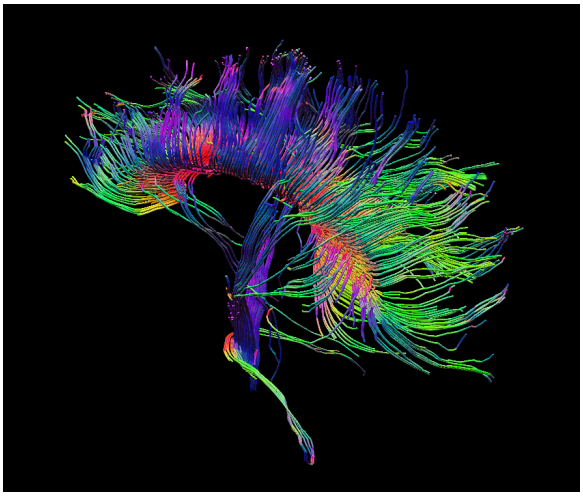
DW-MRI analysis in BrainVoyager 2.0 and up

Version 1.2



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Before You Start

BEFORE YOU START
The DTI module in BrainVoyager $>$ 1.9 requires an additional license, which can be obtained free of charge by sending an e-mail to `sales@brainvoyager.com`.
Please state your HASP dongle ID (in BrainVoyager: `Help-->License Information-->HASP Dongle ID`) your name, and your affiliation.

How to use this document

This document is a step-by-step manual for an analysis of a diffusion weighted MRI data set in BrainVoyager QX. It is assumed that the reader has basic understanding of the principles behind Diffusion-Weighted Imaging. It starts with data import and how to create a DMR: a **D***iffusion weighted* **MR** dataset.

The next stage is co-registration of a DMR project to an anatomical data set (VMR). If you are familiar with BV, than you will immediately appreciate the similarity with FMR/VMR co-registration.

The manual will then show you how to calculate fractional anisotropy and mean diffusivity maps, and how to display them on the VMR.

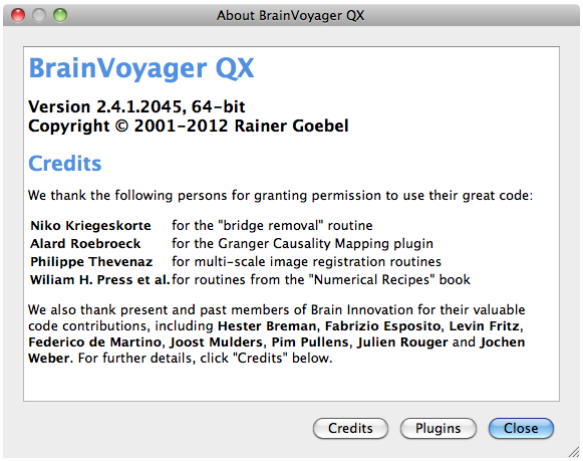
We will then go into 3-D space and show how to display the tensor data. Fiber tracking, both ROI-based and interactively, will be treated next. Finally, some spatial transformations and fiber import/export are treated.

Menu/button commands etcetera are displayed in a `typewriter` font.

Further support

If you have any questions regarding DTI analysis in BrainVoyager after reading this manual, please contact `support@brainvoyager.com`.

BrainVoyagerQX version used for this manual



Chapter 1

Single subject DW-MRI Analysis

1.1 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. A few recommendations for data acquisition can be found at
`http://support.brainvoyager.com/diffusion-weighted-imaging/61`.

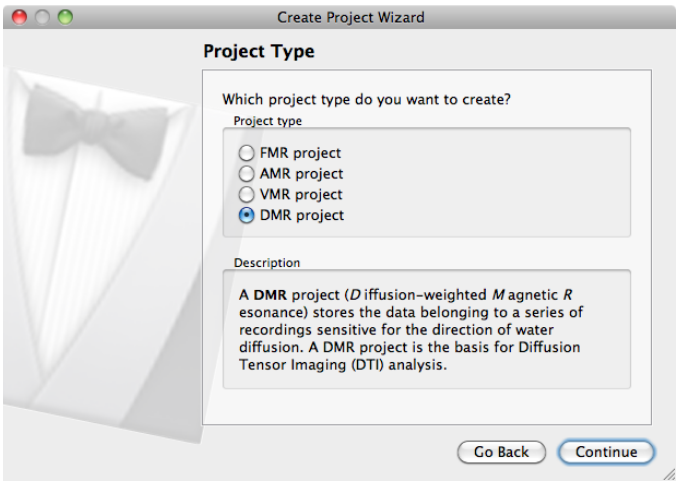
In this manual, we use a DWI scan measured with 31 diffusion directions: 1 b0 and 30 diffusion weighted directions. The gradient file for this measurement can be found in appendix 1.6.1. Furthermore, in the same session an ADNI (modified MPRAGE) anatomy was acquired. Details of the measurement are given below.

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

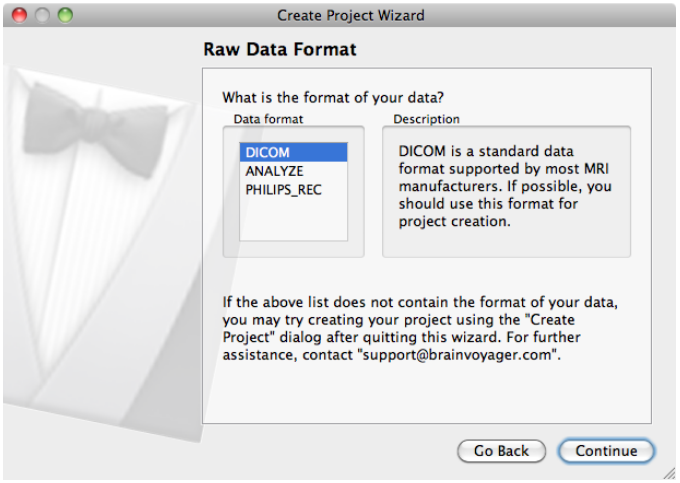
The sample data can be downloaded from the Brain Innovation ftp server on request, by emailing `support@brainvoyager.com`. Please put the data in `\BVQXSampleData\DTI\Human31dir\` or equivalent folder.

1.2 Creation of a Diffusion MR (DMR) Project

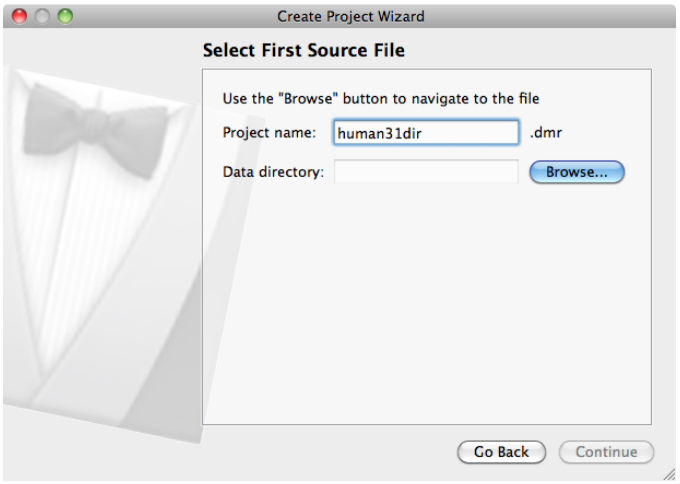
1. The create project wizard can be found in the menu `File --> Create Project Wizard...`. A welcome window will appear, click `Continue`.
2. Now it is time to specify the project type. Choose `DMR Project`.



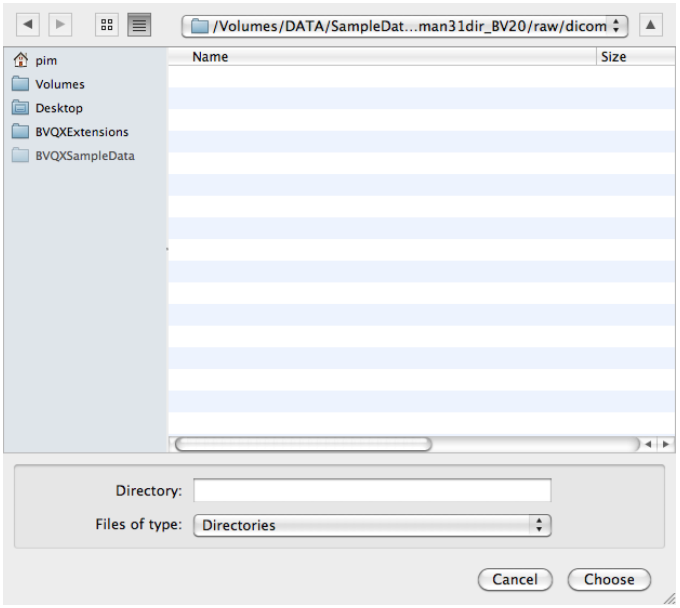
3. Next step is to define the data type. In our case, this is Siemens DICOM, but Philips PAR/REC and ANALYZE are also supported. If you have Nifti data, please consult `http://support.brainvoyager.com/available-tools/49/166`.



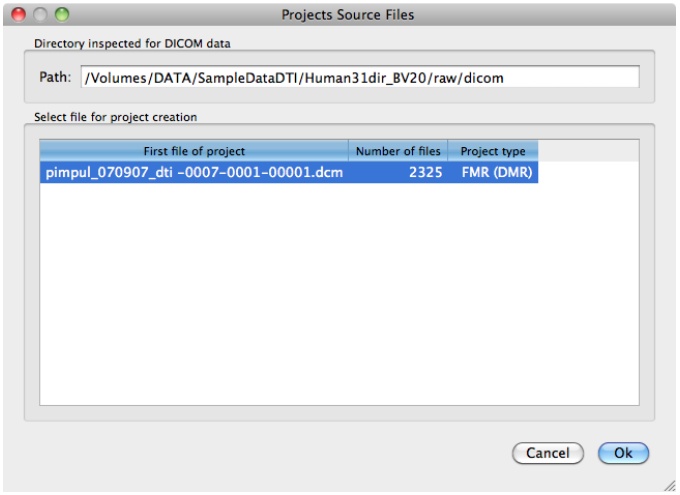
4. Set the name of the DMR project to `human31dir.dmr`.

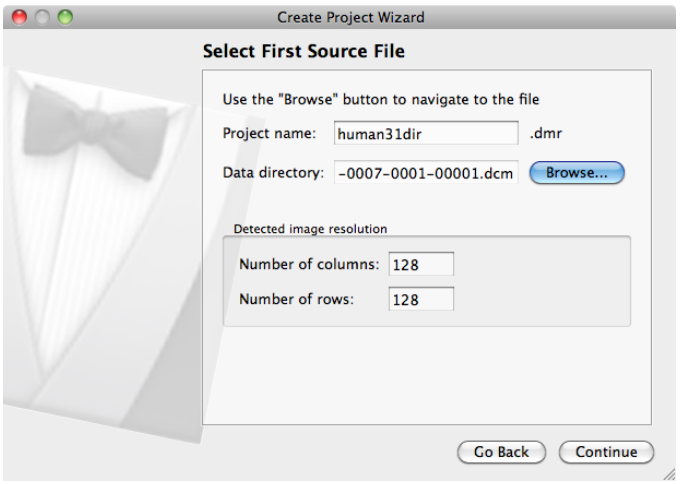


5. Click `Browse` to navigate to the directory containing the DICOM files. Note: in the browse window, the DICOM files will not be shown (the directory appears empty). So, you need to know where your DICOM files are, and select that specific directory.

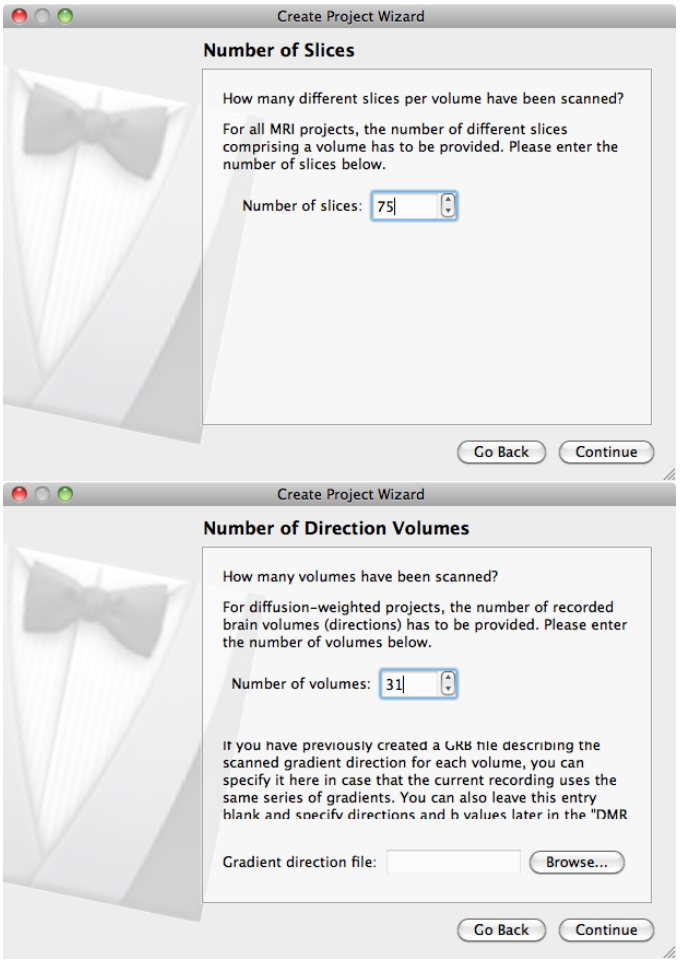


6. In the next step, BrainVoyager will automatically show you the DICOM files belonging to several experiments you might have performed. Select the DICOM file belonging to the DW-MRI experiment `pimpul_070907_dti -0007-0001-00001.dcm`.



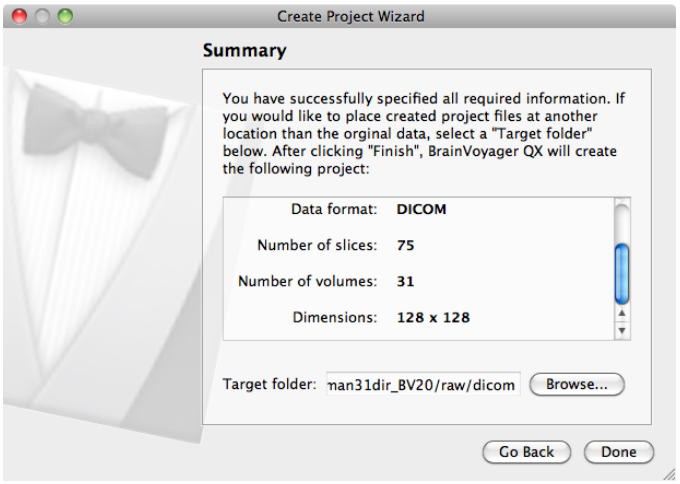


7. Enter the number of slices (75) and the number of volumes (31 = number of diffusion directions) in the next two windows.



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 1.6.1 for details on the file format and contents. Otherwise, leave the field blank and continue by clicking `Next`.

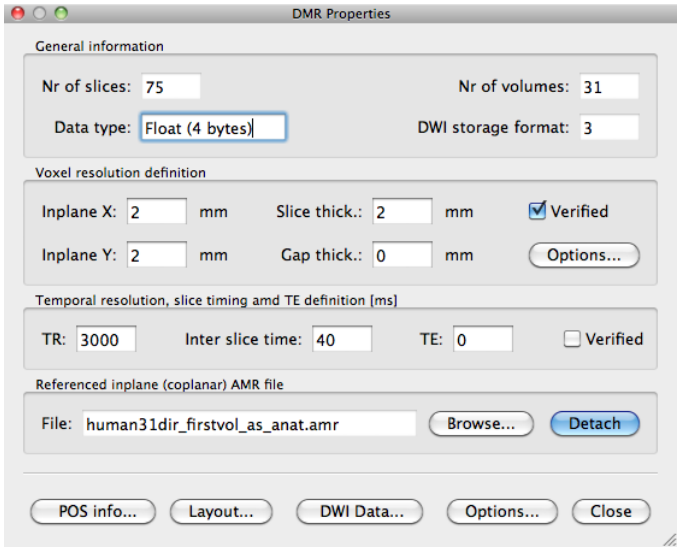
8. BrainVoyager will now give you a summary of the project. Please take a moment to check whether everything is correct. Otherwise, you can use the `Back` button to redo a step.



9. Click `Finish` to start the DMR Project creation.

1.2.1 DMR Properties

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

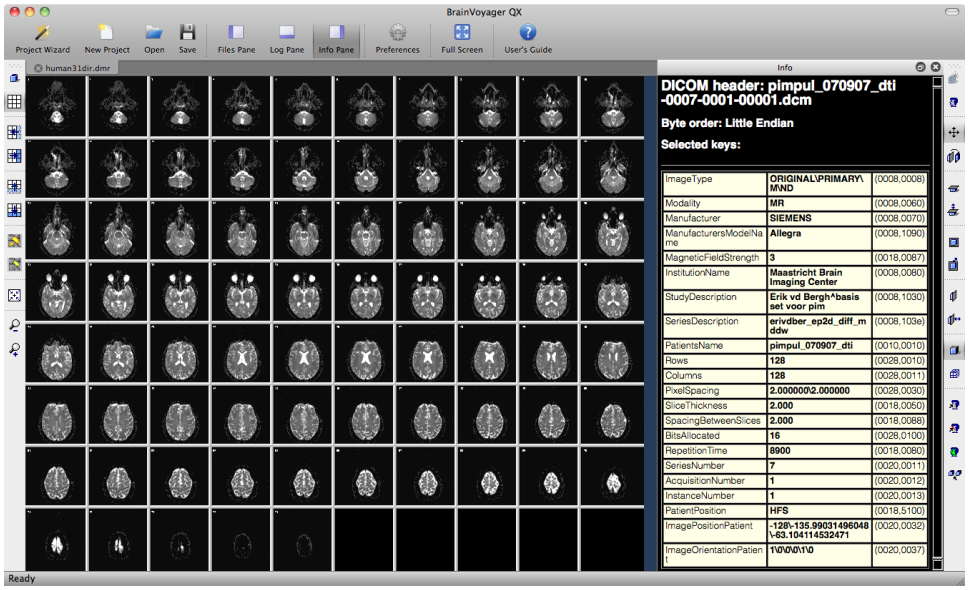


You can inspect here if BrainVoyager has taken the correct parameters of the data.

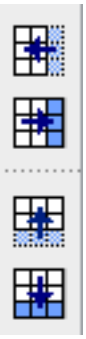
General information	
Nr of slices	
Nr of volumes	should be identical to nr of diffusion directions
DWI storage format	For internal use
Voxel Resolution definition	
X, Y, Z resolution	please check if correct ($2 \times 2 \times 2$mm)
Gap thickness	should be 0
Options	allows you to change in-plane resolution
Temporal Resolution, slice timing	
	Check for accuracy:
TR	8900
TE	78
	Check Verified
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 section1.3.1
Options	opens the options dialog, allows you to change the DWI file prefix and nr of skipped volumes (should be 0 normally)

1.3 Exploring a DMR project

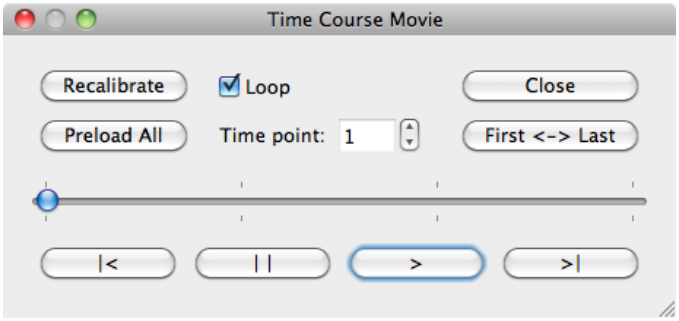
The DMR project just created may look like this, where the first volume is displayed. In this case, it is the b0 volume. This volume contains 75 slices.



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.

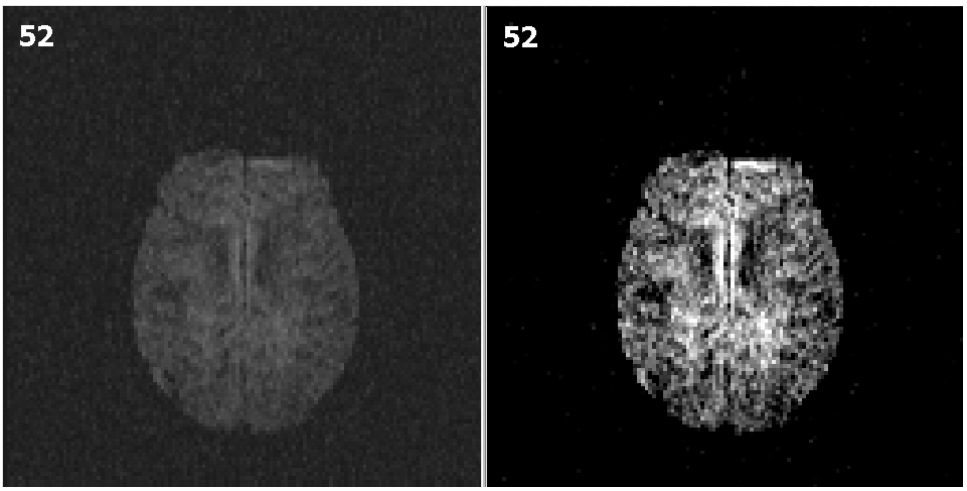


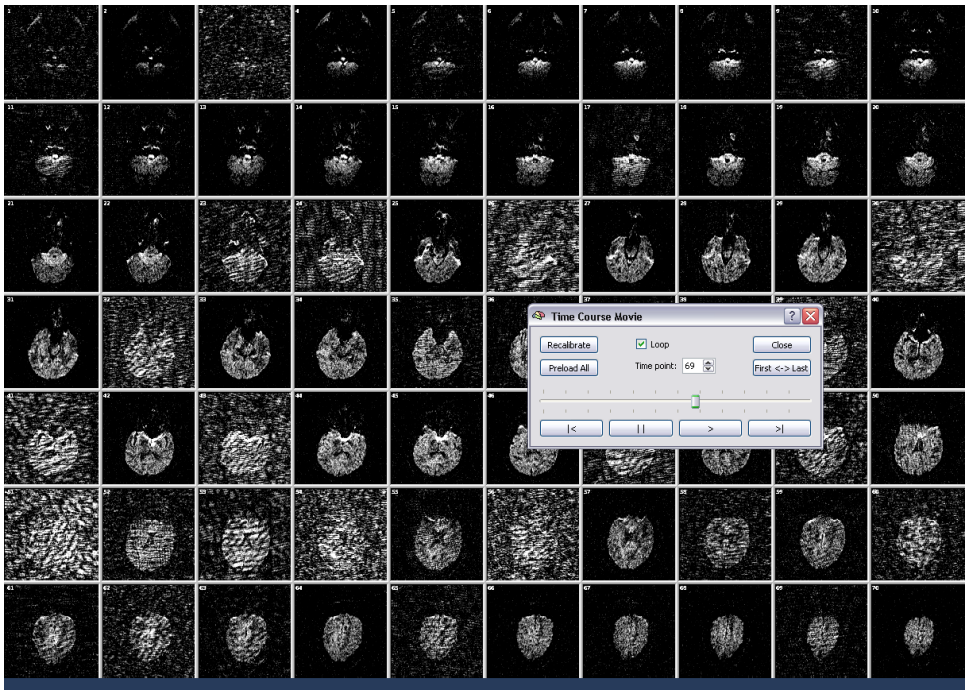
You may explore the data via `Options --> Time Course Movie`. By clicking the play buttons >, BV will move through the volumes or diffusion directions of your measurement. The `Recalibrate` button in the `Time Course Movie` window automatically adapts brightness to the slice you are currently viewing. 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:





1.3.1 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 [BJ02, Kin06c] among others. To recap, Mean Diffusivity is defined as

$$\mathrm{MD} = (D_{xx} + D_{yy} + D_{zz})/3 \equiv \frac{\mathrm{Tr}(D)}{3}, \tag{1.1}$$

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

$$FA = \sqrt{\frac{1}{2}} \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_2 - \lambda_3)^2 + (\lambda_3 - \lambda_1)^2}}{\sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}. \tag{1.2}$$

Fully isotropic voxels have $FA = 0$, while fully anisotropic voxels have $FA = 1$. This is illustrated in figure 1.1.

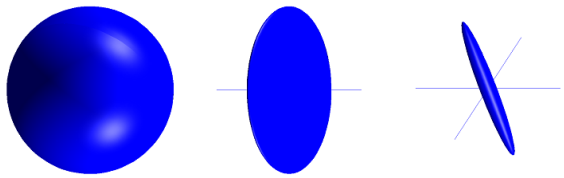
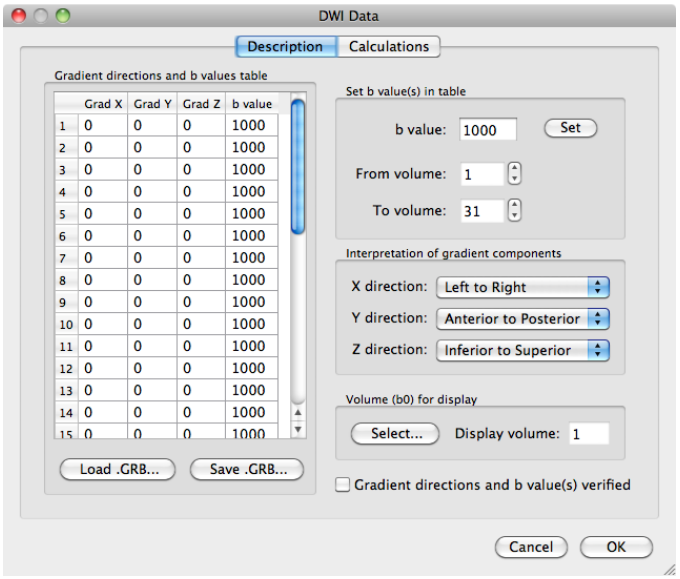


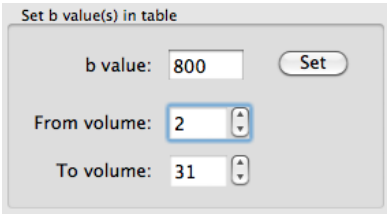
Figure 1.1: From left to right: isotropic tensor, where $\lambda_1 = \lambda_2 = \lambda_3$ and FA close to 0. Oblate tensor where $(\lambda_1 = \lambda_2) >> \lambda_3$ and prolate tensor where $\lambda_1 >> (\lambda_2, \lambda_3)$. FA of the oblate and prolate tensors might be similar.

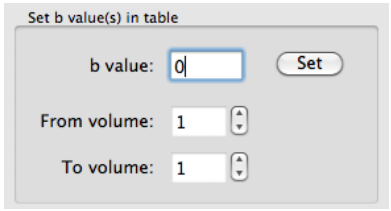
Let's continue with the FA calculation procedure in BrainVoyager:

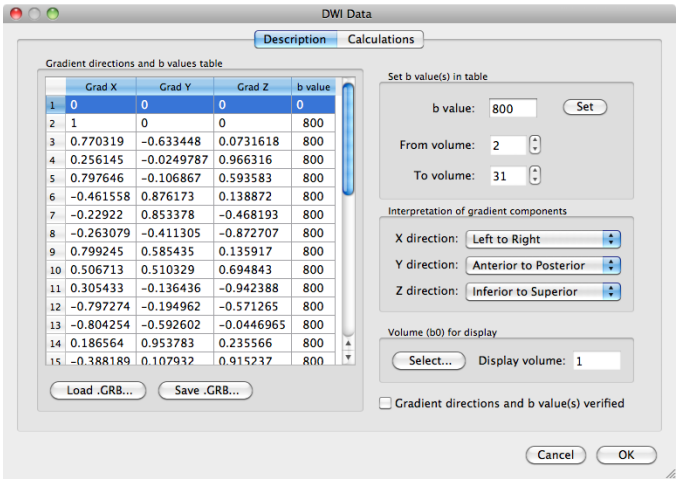
1. Tensor Calculation: Click `File --> DMR Properties --> DWI data`. A dialog pops up, which shows no gradient information, if you did not specify a gradient file during DMR creation:



2. Click `Load GRB` and load the appropriate gradient file `mgh_dti30.grb` (see 1.6.1 for details). Accordingly, the data in the gradient table has changed. To set the right value for b, use the fiels 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.

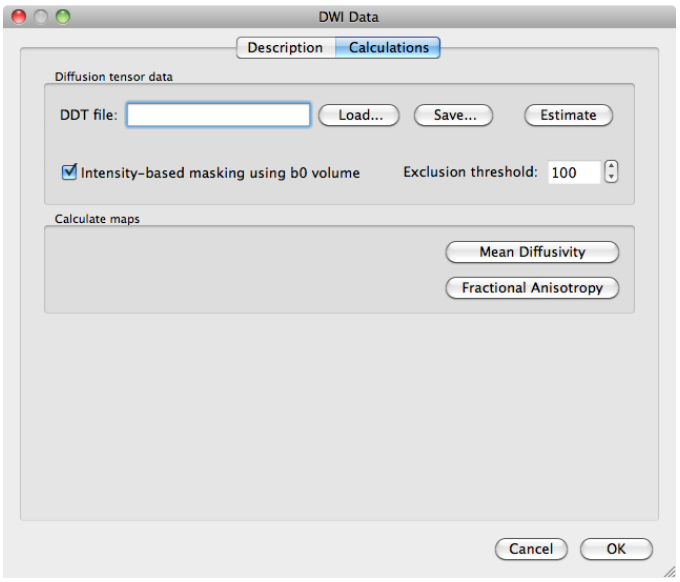






3. Click `OK` and save the DMR (`File > Save`).

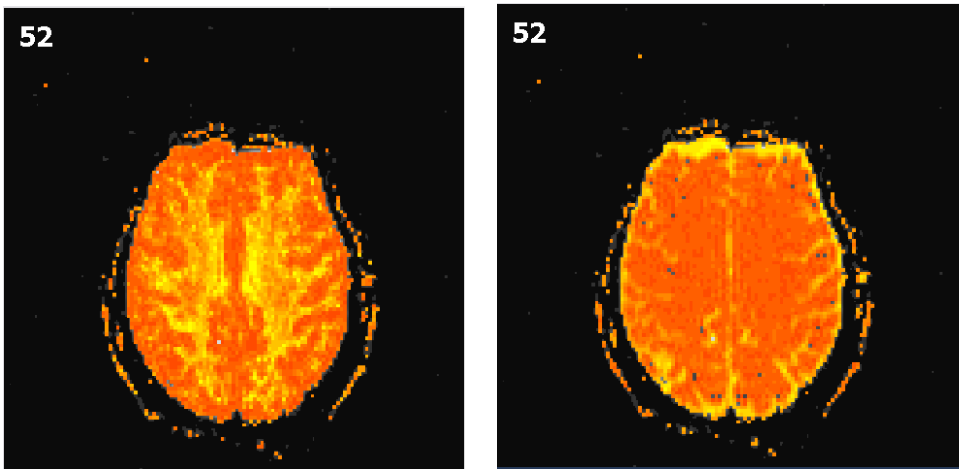
4. Now click on the `Calculations` tab.



   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 1.6.3. 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 overlayed onto the DMR. You may explore the resulting map similar to one of an FMR.

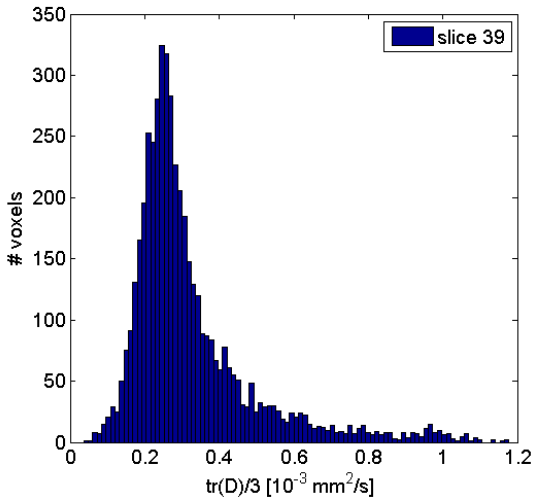
6. Mean Diffusivity: click the `Mean Diffusivity` button.



(a) FA map (b) Mean Diffusivity map

Figure 1.2: Maps calculated on basis of a DMR

In principle, one could start a complete analysis on these maps. For instance, to create a MD histogram of slice 39 (done in Matlab):



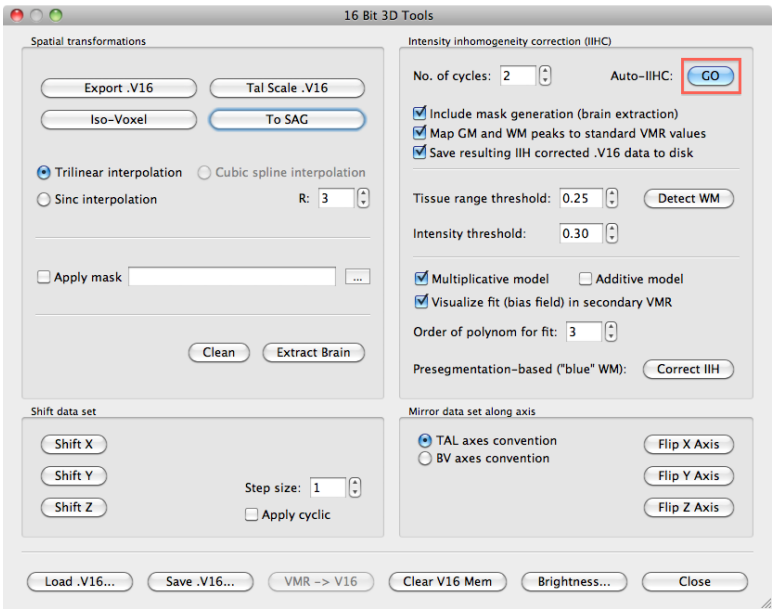
The disadvantage is that we stay in 2-D space. To do an analyis in 3-D, the DMR project has to be co-registered to a VMR, which is explained in the next sections.

1.4 DMR-VMR coregistration

First, the VMR acquired in the same session needs to be created (see the BVQX Getting Started Guide for the procedure). If needed, the VMR can be brought into AC/PC or TAL space. For this demonstration it is not necessary, so we stay in native space. Close all open projects and open the VMR `human.vmr`.

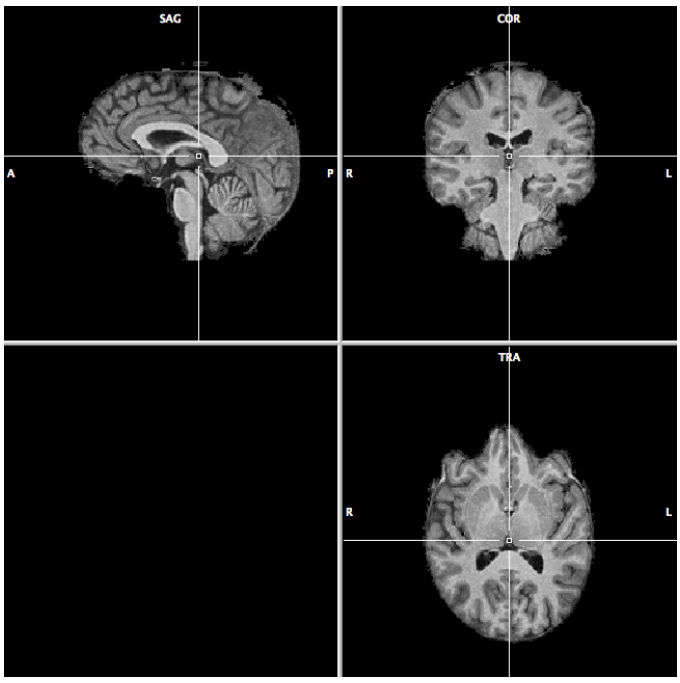
1.4.1 VMR Preparation

For BrainVoyager version 2.4.0 and up BrainVoyager can automatically improve the image quality of the VMR. 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`.

For BrainVoyager $<$ 2.4.0 Co-registration works better if the non-brain tissue is removed in the VMR. Go to `Volumes --> Segregate Brain from Head Tissue`. When BrainVoyager is finished, the result should look like this:

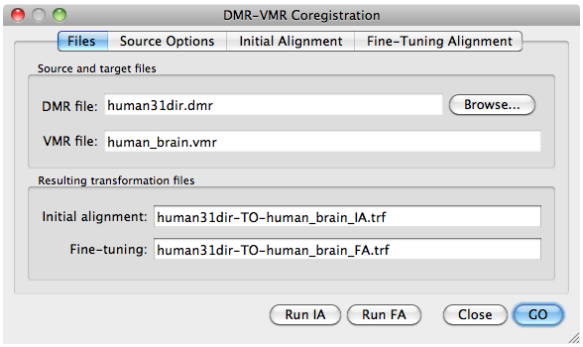


Save the VMR as `human_IIHC.vmr`.

1.4.2 Source Files

Make sure `human_IIHC.vmr` is open. Go to `DTI --> Coregister DMR/DWI to VMR`. A menu appears with 4 tabs, `Files`, `Source Options`, `Initial`

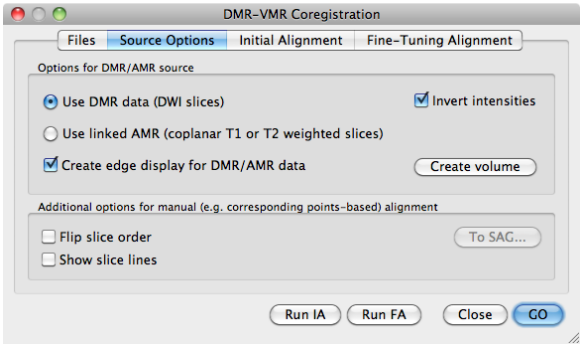
Alignment and Fine-Tuning Alignment. Let's start with the first tab:



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.

1.4.3 Source Options

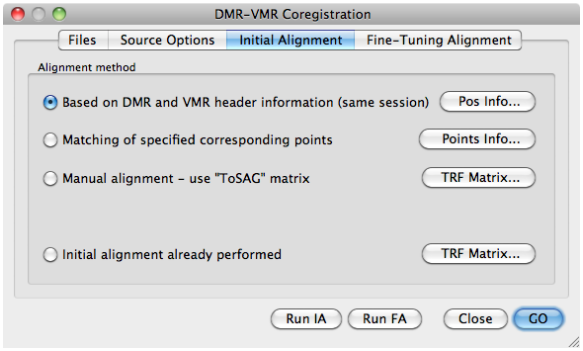


Use DMR data (DWI Slices)	Use the first volume of the DMR data for coregistration. Watch out! First volume should be b0.
Invert intensities	Since intensities in the b0 images are inverted compared to a T1 anatomical image, this option might be used. For instance, the ventricles in a b0 are white, and on the T1 black.
Use linked AMR	Use the AMR created from the first volume of the data for co-registration. Again, watch out! AMR should correspond to a b0 image.
Create edge display for DMR/AMR data	Use this option for calculating edges in the AMR/DMR volume, which may help co-registration.
Create Volume	Applies any of the settings chosen above.
Flip Slice order	**[Advanced]** Use this option together with To SAG if the DMR and VMR data were acquired in different sessions.
To SAG	See above.

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

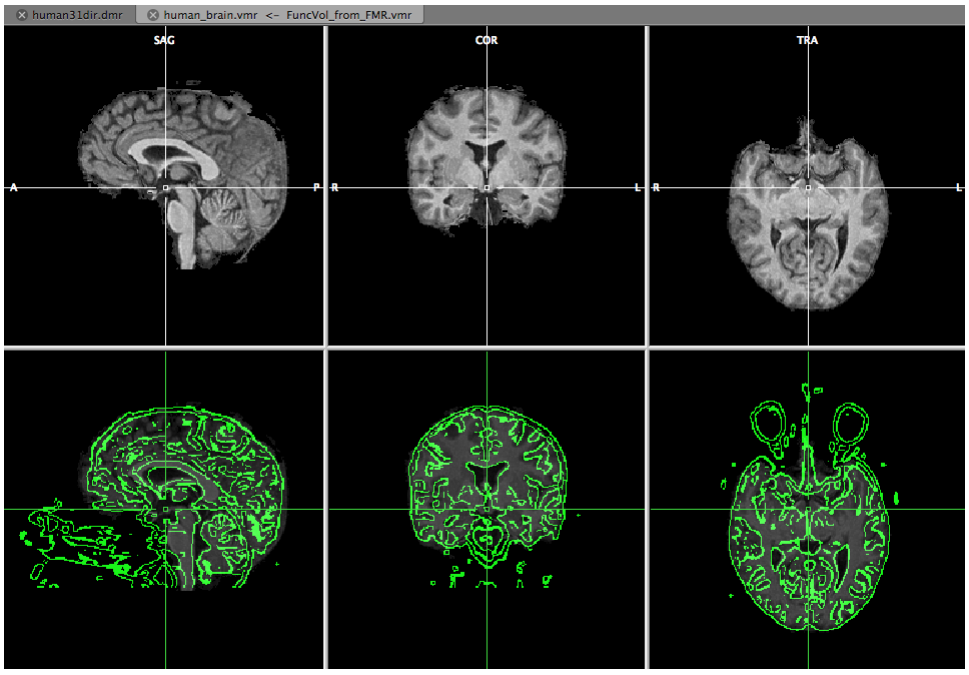
1.4.4 Initial Alignment

Go to the `Initial Aligment` tab.



`Based on DMR and VMR header information (Same session)`	This is the default and easiest option. `POS info` shows you the header information.
`Matching of specified corresponding points`	**[Advanced]** Do the co-registration based on user-specified landmarks. Needed when no header information is available or when the co-registration based on the header information fails. `Points info` shows the defined points.
`Manual alignment -- use "To SAG" matrix`	**[Advanced]** Manual alignment, only used when automatic alignment fails. If in the `Source Options` a `To SAG` matrix was defined, it can be inspected via the `TRF matrix` button.
`Initial Alignment already performed`	Trivial

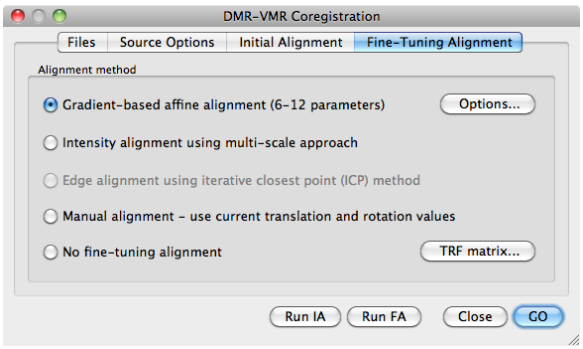
Now it's time to hit the `Run IA` button. A view similar to the one below



appears, and we can inspect the initial aligment 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.

1.4.5 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:



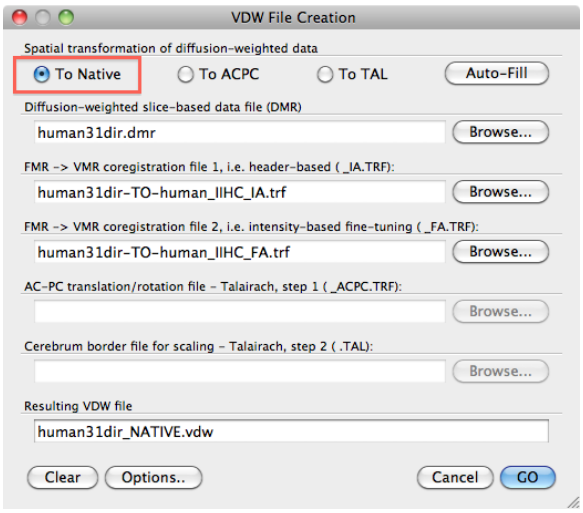
NGF based affine alignment (12 parameters)	Default option
Intensity Alignment using multi-scale approach	Default option in BVQX $<$ 2.0
Edge alignment using iterative closest point (ICP) Method	Not available
Manual alignment - use current translation and rotation values	**[Advanced]**, only recommended when automatic alignment fails.
No fine-tuning alignment	Use if initial alignment is satisfactory.
TRF matrix	shows the current transformation matrix.

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.

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

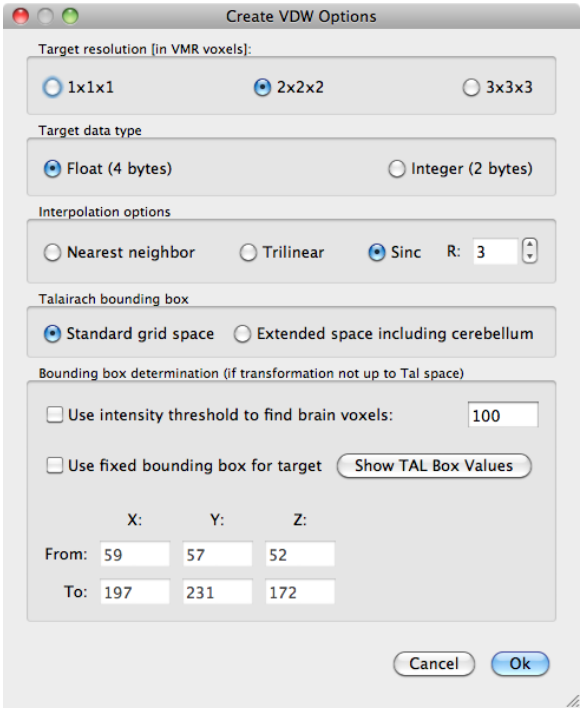
We will now create a VDW data set, using the files created during the co-registration phase. The procedure is quite similar to the VTC creation in fMRI data analysis.

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 `Sinc interpolation` at `Interpolation options` is activated. DWI data is extremely sensitive to interpolation, so the best interpolation setting is required. However, sinc interpolation may easily take hours to compute, so if you don't have that time, take the next best option, which is `Trilinear`. The rest may be left as default. You may choose to turn on or change the `Use intensity threshold to find brain voxels`, but this is not recommended. Use masking, see section 1.6.3 instead.



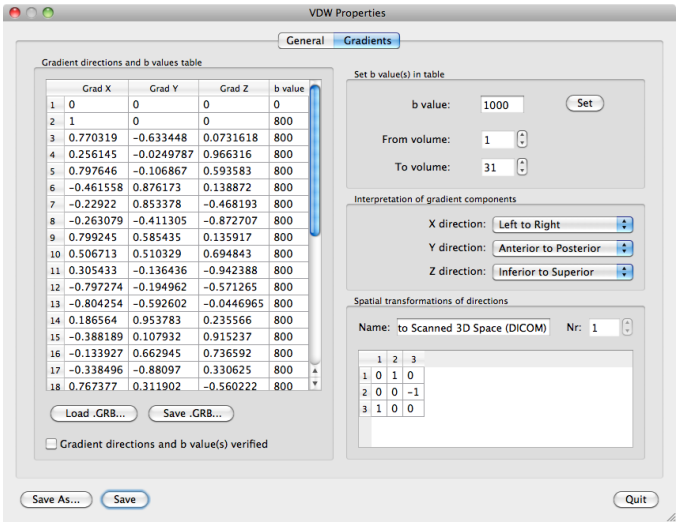
Click `Ok` and `GO` in the `VDW File Creation` window.

1.6 Tensor, Diffusivity and FA calculation

First, close the VMR you may still have open, and reopen it (beware to use the `_ACPC.vmr` or `_TAL.vmr` if you went into standard space). 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 `human31dir.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.

1.6.1 The gradient table



The gradient table can be filled in two ways: manually, by entering the gradient direction and b-value directly into the table, and automatically by loading a so-called GRB *GRadient and B-value* file.

You might have a text file with gradient directions or otherwise you have to ask your MR technician for such a file.

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`. The gradient table can also be found in appendix **??**.

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.

The `interpretation of gradient components` part of the `VDW Properties` window may be used if the data is flipped/reversed. The `Spatial transformations of directions` part may be used if BV makes a wrong interpretation of the scanner versus subject coordinate systems. Both options are explained in Appendix 3.1.1.

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

1.6.2 Tensor, Mean Diffusivity and FA Computation

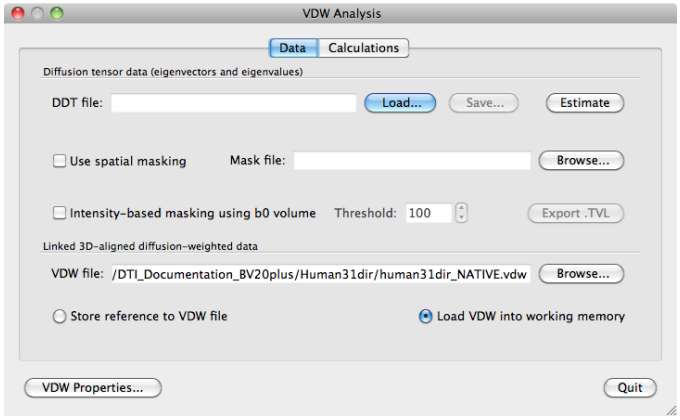
Once the VDW file and gradient information are correct, click `Estimate` in the `VDW Analysis window`. Warning: BV may look irresponsive, but in fact it is busy calculating tensors. A DDT "Diffusion Tensor" file is created, and BV asks you to save this file. Save it as `human31dir_vdw.dmr`. A DDT file may also be saved in TVL format, by clicking the `Export TVL`, for use in the TrackMark software (information via `support@brainvoyager.com`).

1.6.3 Recommended: masking the DDT data

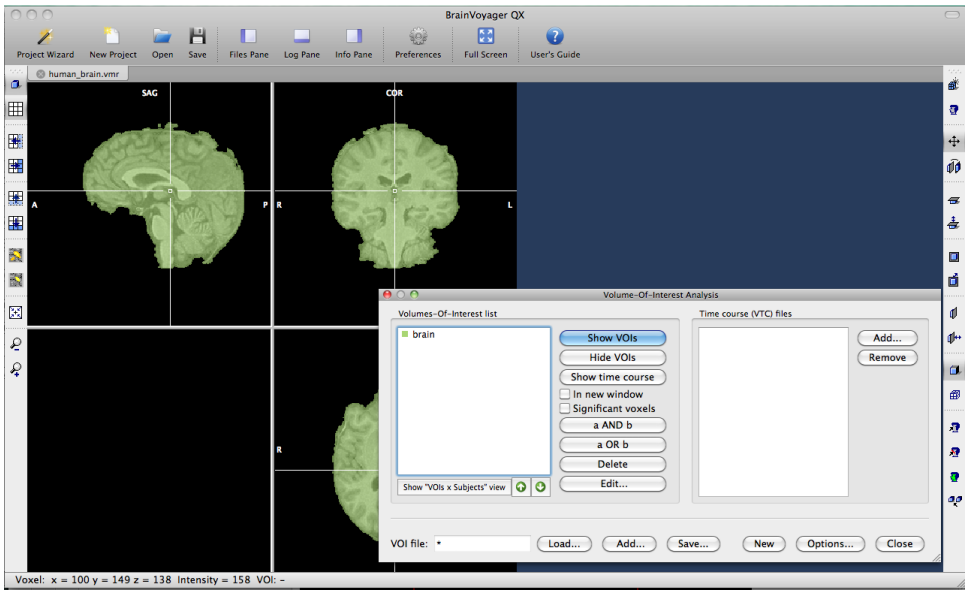
In general you are not interested in data outside of the brain. Due to the nature of the acquisition however, there is noise present outside of the brain, which should be masked out. Besides the visual attractiveness, this also reduces the amount of voxels significantly, which increases processing speed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

For BrainVoyager version 2.4.0 and up 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.

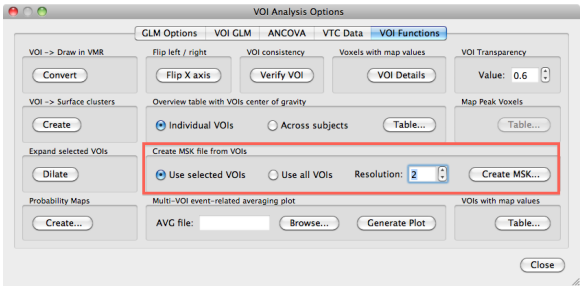
In step 1.4.1 BrainVoyager has automatically created a mask vmr file. Close all open files and open `human_BrainMask.vmr`. BrainVoyager requires the VDW file to determine the right dimensions of the mask. *If the VDW is not linked to the VMR, the mask will be incorrect.* Attach the VDW we've just created via `DTI -> Diffusion Weighted Data Analysis`. Browse for the VDW. The file name will be entered in the dialog:



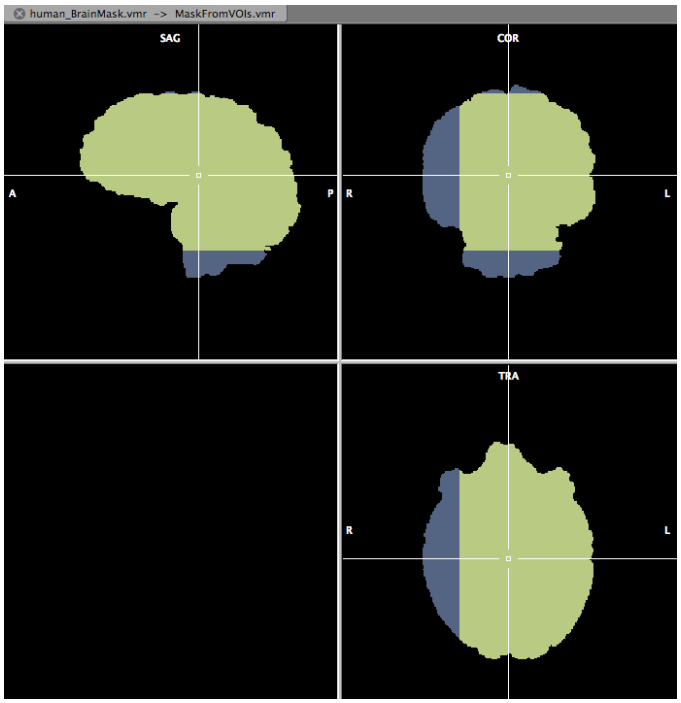
Close the dialog. Now we are ready to create the mask. Now, go to `3D Volume tools -> Segmentation -> Options -> Define VOI`. A dialog pops up and give `brain` as the name of the VOI. Save the VOI using the `Save` button. The BrainVoyager window should look like this:



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.



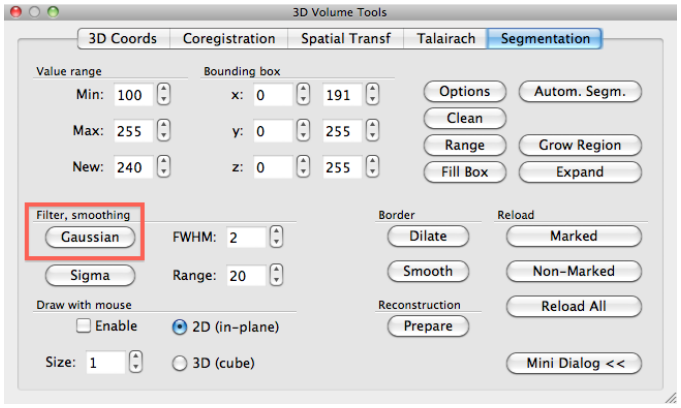
For BrainVoyager version $< 2.4.0$ The pipeline for mask creation is as follows:

VMR $\rightarrow$ Peel brain $\rightarrow$ VOI containing the brain $\rightarrow$ Mask file $\rightarrow$ apply mask file to VDW

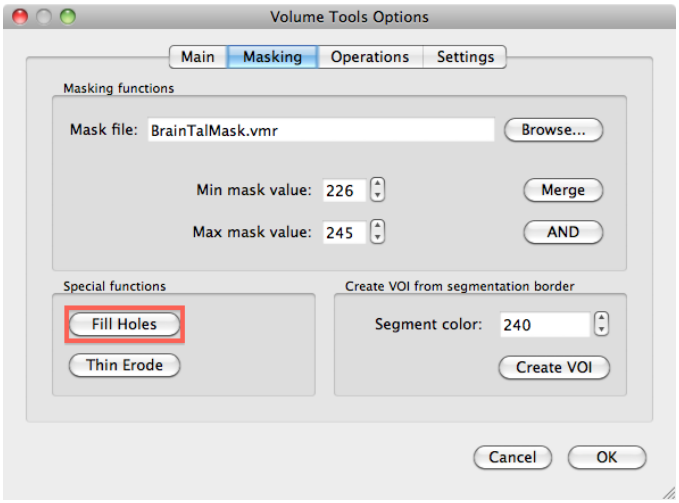
We have already created a VMR containing only brain tissue. Open it and link the VDW file created in section 1.5 to the VMR: `DTI -> Diffusion Weighted Data Analysis`. In the `Linked 3D-aligned diffusion-weighted data` section, locate the VDW that was created earlier using the `Browse` button.

WARNING
Do not forget to link the VDW file to the anatomy before proceeding! The VDW defines the "bounding box" of the mask

Now it's time to define a VOI containing all brain voxels. In order to get a smooth VOI without any holes in it, click the `Gaussian` button in the segmentation tab.

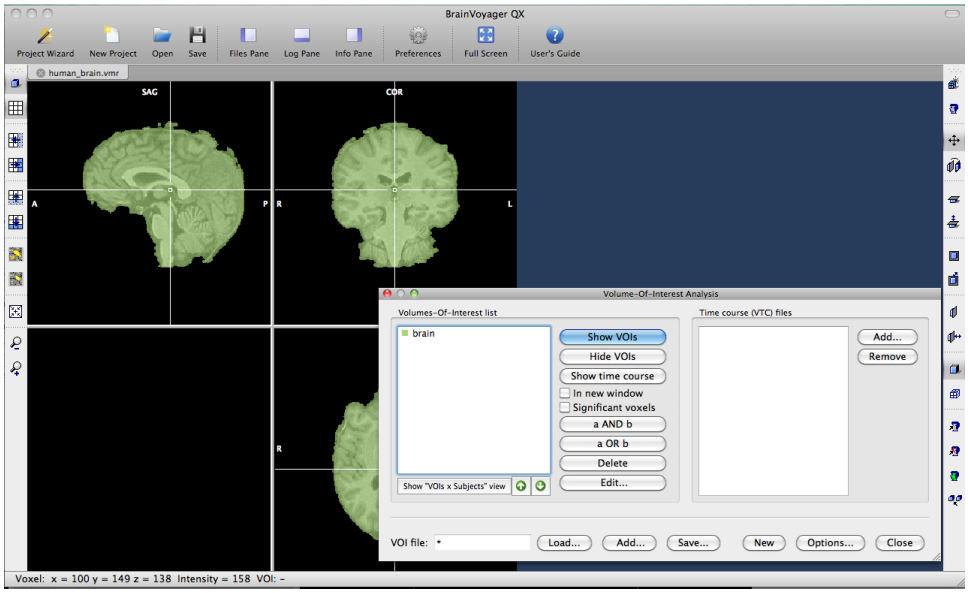


Go to the `3D Volume tools -> Segmentation`. Set `Value range: Min` to 1 and `Value range: Max` to 225, and hit the `Range` button. All brain voxels should be selected now and displayed as blue voxels. Now it's time to fill any holes which might still be present in the mask. Go to `3D Volume tools -> Segmentation -> Options -> Masking`, and click the `Fill Holes` button, and then `OK`.

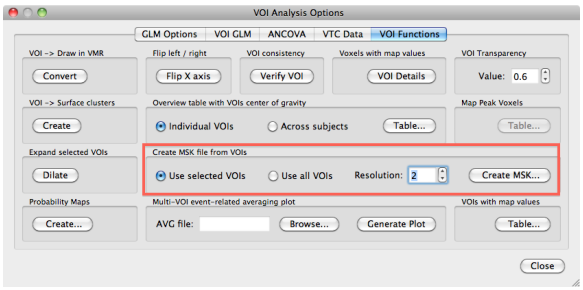


At first, it seems like nothing has happened, but if you click inside a blue region, the screen will be updated and holes will have disappeared.

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:



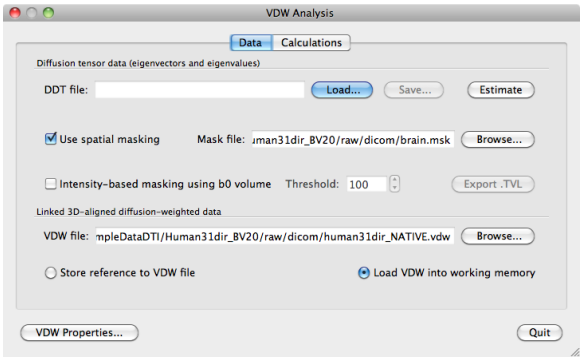
The VOI can now be converted to a mask file. Go to `Analysis->Region Of Interest Analysis`. A dialog will open with the VOI "brain" in it. Save the VOI by clicking the Select this VOI by clicking on it, and hit the `Options` button. In the `VOI functions` tab, set the options as follows:



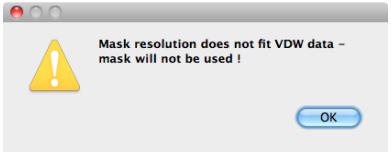
and save the mask file as `brain.msk`.

1.6.4 Tensor calculation

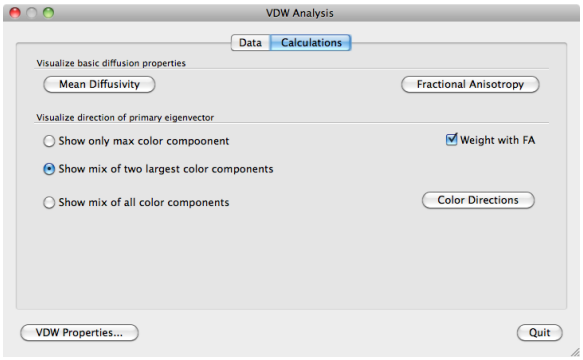
To apply the mask to tensor calculations creation, re-open the file `human_IIHC.vmr`. Go to `DTI -> Diffusion Weighted Data Analysis`. Load the VDW created in section 1.5. Then, tick the `use mask` checkbox, and locate the mask file `brain.msk` with the `Browse` button:



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 1.6.3.*



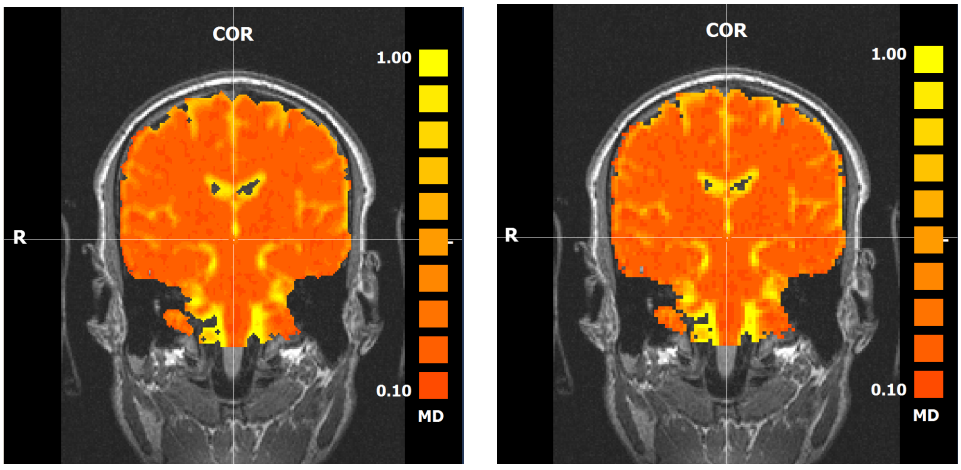
FA and mean diffusivity can be calculated in the `Calculations` tab in the `VDW Analysis` window.



Mean Diffusivity is defined as

$$\mathrm{MD} = (D_{xx} + D_{yy} + D_{zz})/3 \equiv \frac{\mathrm{Tr}(D)}{3}, \tag{1.3}$$

and is in theory limited to the interval $[0, \infty)$. Click the `Mean Diffusivity` button to produce a MD map, overlayed 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 un-checking the `interpolate` checkbox. Also in this window the value range can be set.



(a) MD in VMR resolution (interpolated) (b) MD in DWI resolution

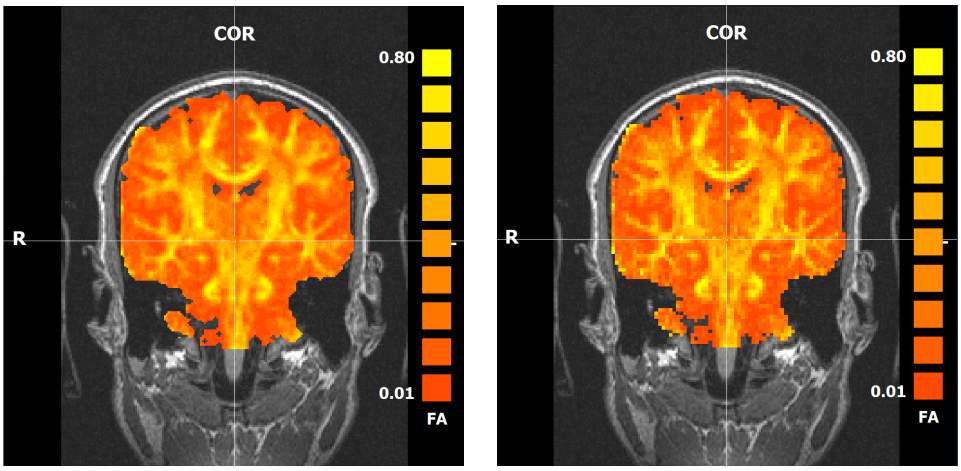
Figure 1.3: Mean Diffusivities

Fractional Anisotropy is defined as

$$FA = \frac{\sqrt{3[(\lambda_1 - \lambda_2)^2 + (\lambda_2 - \lambda_3)^2 + (\lambda_3 - \lambda_1)^2]}}{\sqrt{2(\lambda_1^2 + \lambda_2^2 + \lambda_3^2)}}. \tag{1.4}$$

Fully isotropic voxels have $FA = 0$, while fully anisotropic voxels have $FA = 1$. Click the `Fractional Anisotropy` button to calculate a FA map overlayed on the VMR. Again this map is in VMR resolution.

For users of BrainVoyager 1.10 or lower: Be careful! For visualisation purposes, ***FA is scaled up a factor 10 in BrainVoyagerQX*** < 1.10***!.*** **So,** $FA = 2.0$ **in the map is in reality** $FA = 0.2$.



(a) FA in VMR resolution (interpolated) (b) FA in DWI 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.

1.6.5 Alternative Diffusion Measures

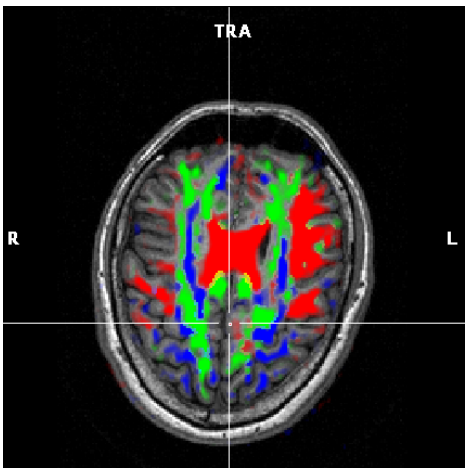
Of course we can extract the values of the eigenvectors and compute alternative diffusion measures such as shape measures, radial/axial diffusivities, trace($\mathbf{D}$) from the tensor file. This is implemented in a Matlab function available on `http://support.brainvoyager.com/diffusion-weighted-imaging/66/349`.

1.6.6 Color coded maps

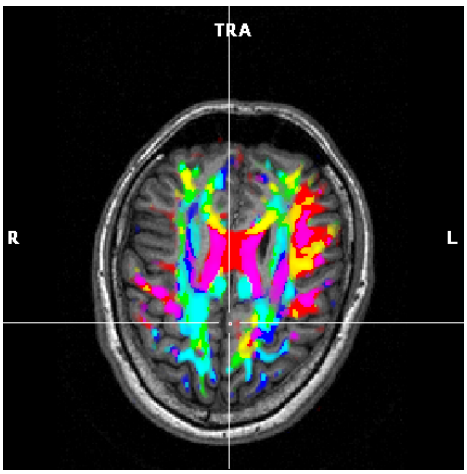
Color coded maps can be displayed by selecting one of the options in the `Visualize direction of primary eigenvector` part of the `VDW analysis` window. It is initially recommended to choose the `Weight by FA` option, see figure 1.4(d). The color options are:

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 $= D_{xx}$:=red, if max $= D_{yy}$:=green, max $= D_{zz}$:=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: $x + y$=red+green=yellow. $x + z$=red+blue=purple. $y + z$=green+blue=cyan.	
`Show mix of all color components`	Colors similar to the mix of 2 components, but where 3 directions mix, the map is colored white.	

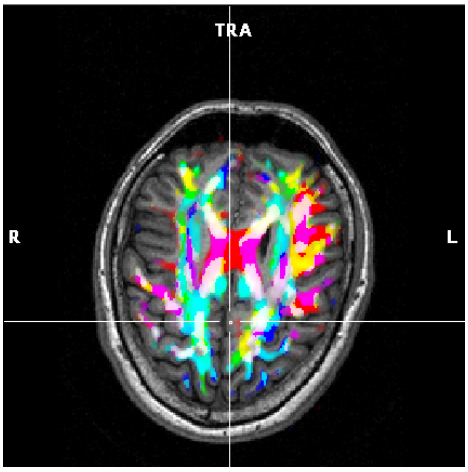
In figure 1.4 the different options are shown. The transparency of the colors may be changed using the `Ctrl+Arrow up/down` key combination.



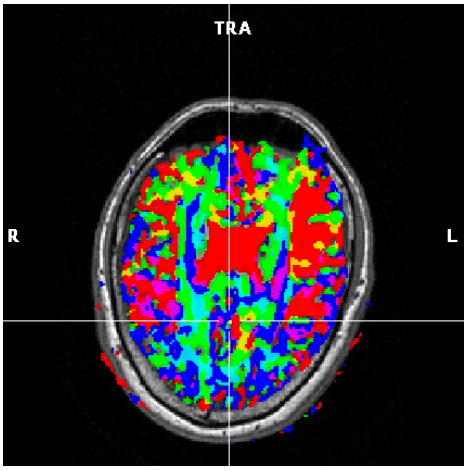
(c) FA map based on 3 max components



(d) FA map based on a mix of 2 max components



(e) FA map based on a mix of 3 components

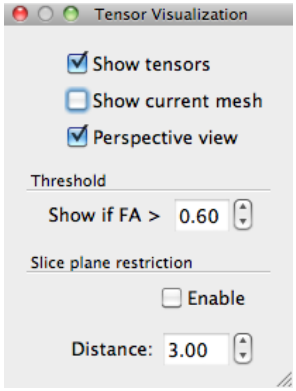


(f) FA map based on 2 components, but not weighted by FA, showing all data.

Figure 1.4: Color options for a FA or MD map, shown for a FA map.

1.7 Tensor visualization

After performing all steps until calculation of the tensors (DDT file creation), the tensors can be visualised in 3D space. Open `human.vmr` and load the DDT file `human31dir_vdw.dmr` 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.



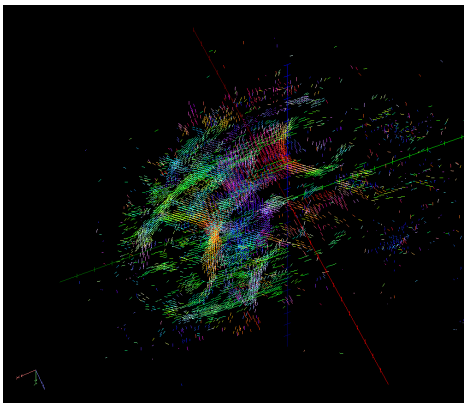
`Show Tensors`	check/uncheck to show/hide tensors
`Show current mesh`	check/uncheck to show/hide a mesh
`Perspective view`	check/unchek to view data in perspective or not in perspective. Also activated by pressing `P` on your keyboard.
`Threshold`	FA threshold for tensor display. High threshold → few 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:

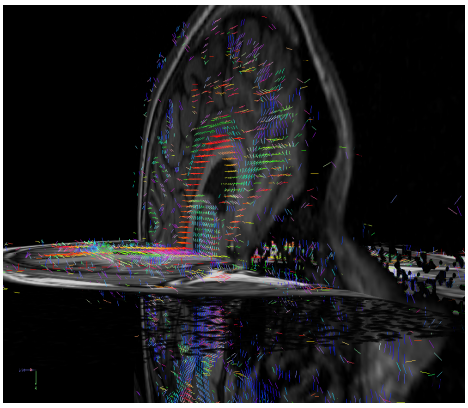
gesture	effect
hold left + move mouse	rotation
hold right + move mouse	translation
hold left + right + move mouse	zoom

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 1.5.b the view is shown.

Transversal slice cut Sagittal slice cut Coronal slice cut



(a) Tensors in the whole volume. $FA > 0.6$.



(b) Tensors limited to a sagittal and transversal plane. $FA > 0.20$

Figure 1.5: Tensor viewing options

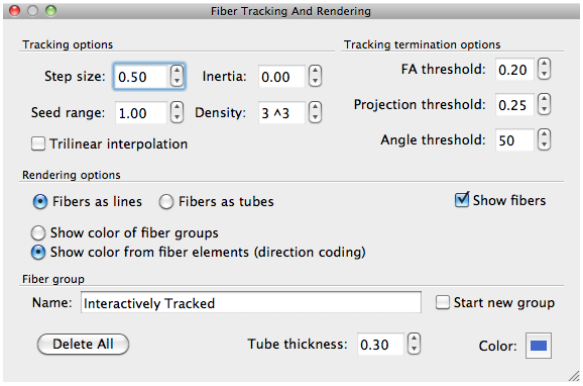
1.8 Fiber Tracking

1.8.1 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:

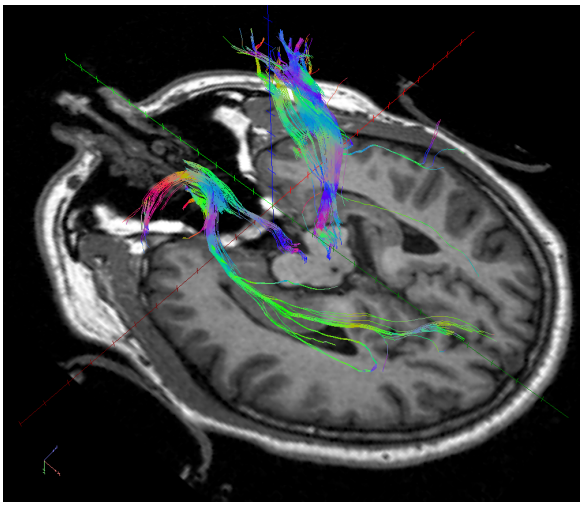
1. Open a VMR
2. Open a DDT file
3. (optional) calculate FA/MD maps
4. Go to `DTI --> Fiber Tracking and Rendering`
5. Display a slice by using the buttons from table **??**
6. use `Ctrl+Left mouse click` to paint fibers on the slice

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.



Parameter	Meaning	Recommended value
	Tracking Options	
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 [WMM+02]. Determines how much the shape of neighbouring tensors are used as a tracking guideline in the current voxel.	depending on the application.
Angle treshold	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:

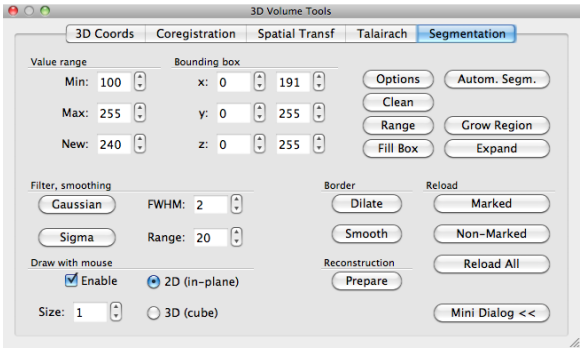


1.8.2 Fiber tracking from seed regions (VOI/ROI)

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.

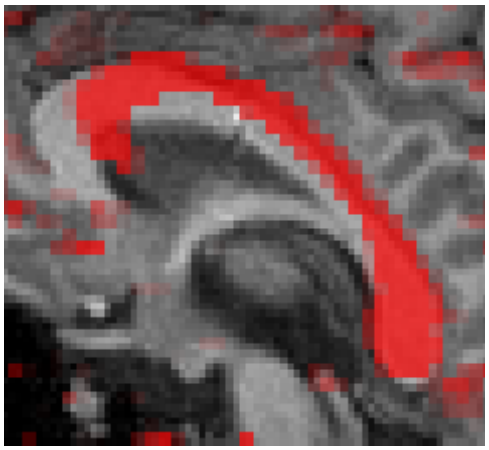
Anatomically defined VOIs Anatomical VOIs are defined by drawing them on a VMR with or without an overlayed FA/MD map.

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 overlayed, 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.



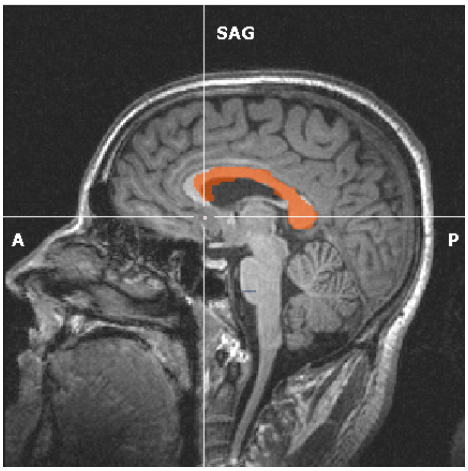
In the `Draw with mouse` section on the lower left of the tab, check the `Enable` box. We have now enabled a drawing pen, and the properties of this pen can be changed 1) by size and 2) 2D or 3D: in 2D, the pen draws a square ie 2×2 voxels, in 3D a cube with dimensions set by `Size`, ie $2 \times 2 \times 2$ 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 overlayed on T1 anatomy.

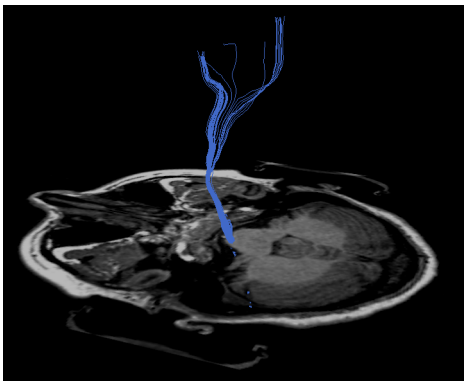


A VOI can be drawn now on the corpus callosum using `Ctrl+left mouse click`. With `Shift+left mouse click`, voxels may be removed from the VOI. When drawing is finished, click the `Options` button on the `Segmentation` tab. A new window pops op, click the `Define VOI` button. Then you'll be asked to 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.



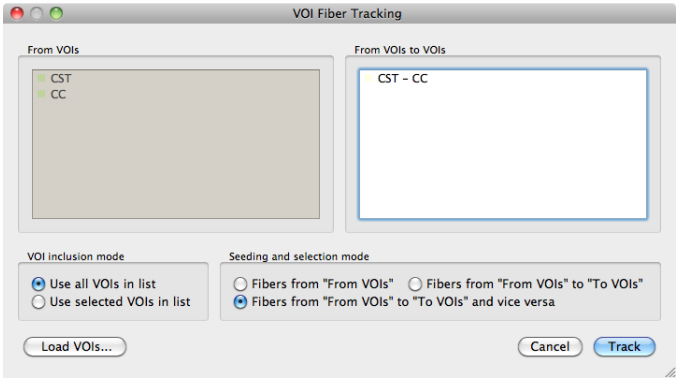
(a) VOI at the corpus callosum in orange.



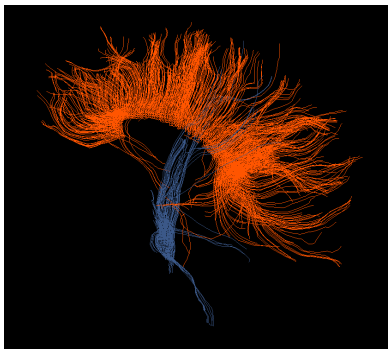
(b) VOI at the brainstem for the corticospinal tract in blue.

Figure 1.6: VOIs

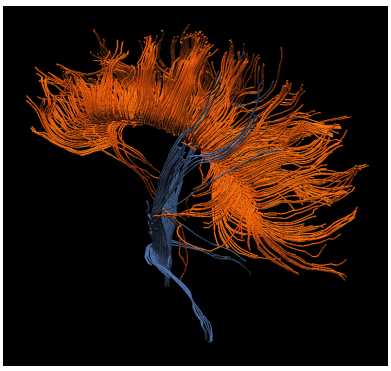
Next, set the parameters for fiber tracking in the `DTI --> Fiber Tracking and Rendering` window. Fibers from these VOIs can be tracked via `DTI --> Track fibers from VOIs`.



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



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

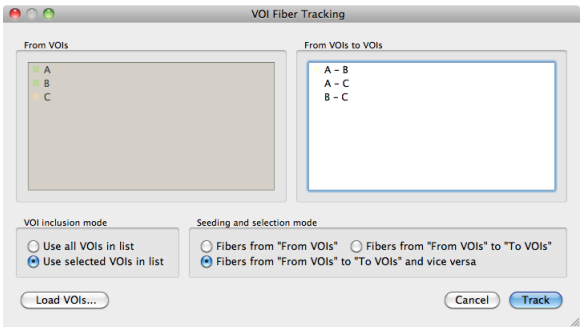


(b) Fibers rendered as tubes

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

Figure 1.7: 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:

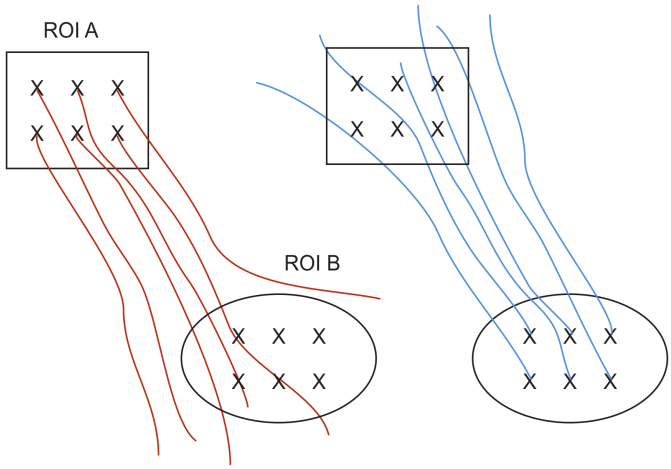


$$A \rightarrow B$$
$$A \rightarrow C$$
$$B \rightarrow C$$

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

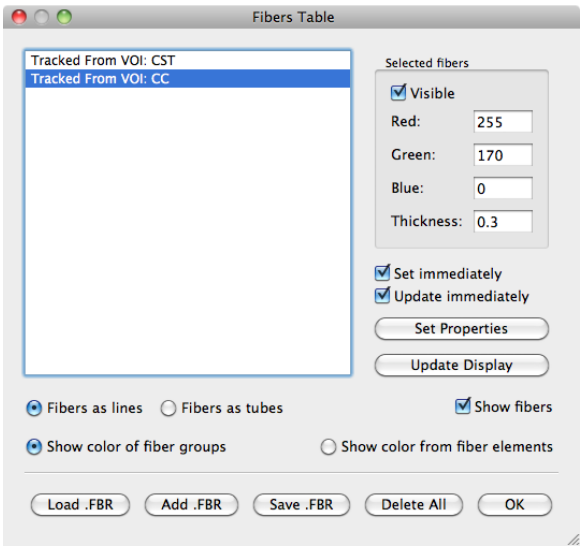
$$A \rightleftharpoons B$$
$$A \rightleftharpoons C$$
$$B \rightleftharpoons C$$

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.



1.8.3 Loading and editing fibers

Once you have tracked fibers, you can save them into an fbr file. 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.

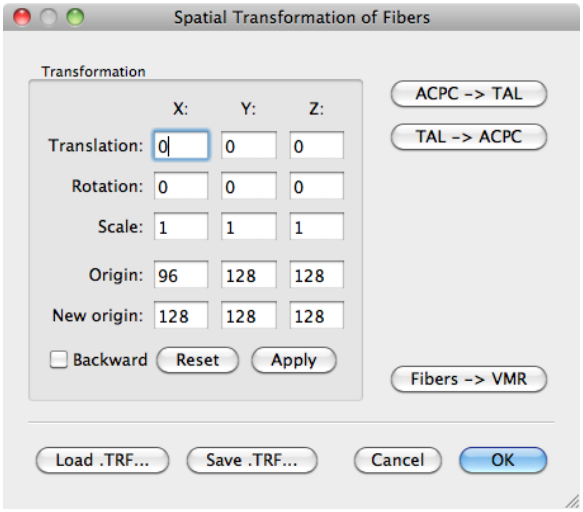


1.8.4 Spatial Transformations of fibers

ACPC/TAL Transformation Fibers may be transferred into ACPC or TAL space from native space. In this case, the only thing that is transformed, are the fiber bundles. There is no transformation of the original diffusion weighted data, as happens when you would transform the original DWI data into TAL or ACPC.

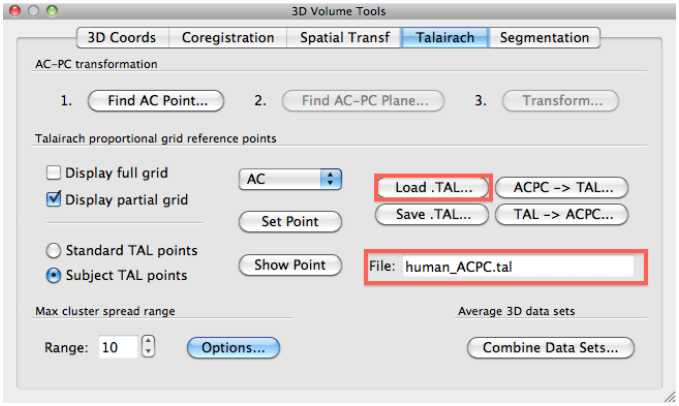
In order to do this, you need to bring the VMR into ACPC or TAL space. The transformation files that are created by BV during these steps are used now to transform the fiber bundles.

ACPC transformation In the `DTI --> Spatial Transformations` dialog, click `Load .TRF`, to load an `<subject>_ACPC.TRF`. Click the `Apply` button to perform the transformation and `OK` to finish.



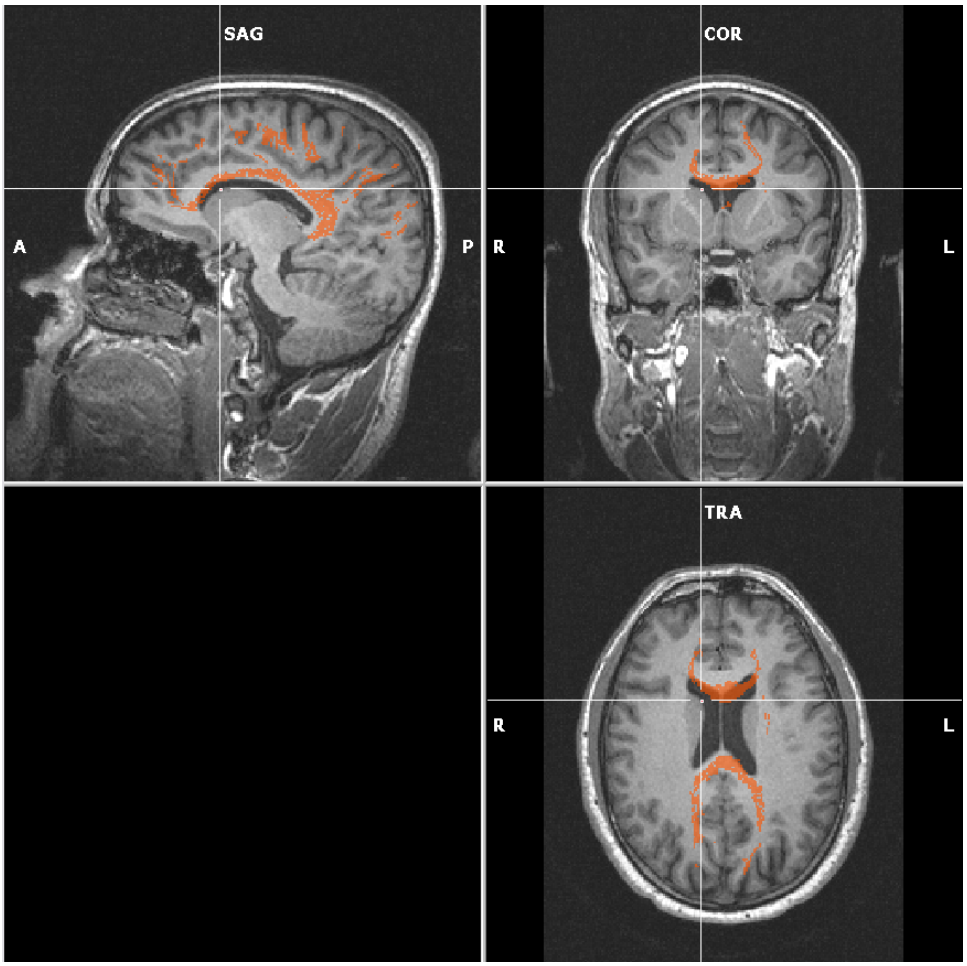
Save the fibers as `<subject>_ACPC.fbr`.

TAL transformation After the ACPC transformation, you can apply a Talairach transformation. To do this, load the `<subject>.TAL` file in the `3D Volume Tools > Talairach > Load .TAL` dialog. The TAL file name will show up.



Then, go to `DTI --> Spatial Transformations` and click the `ACPC -> TAL` button and `OK` to finish.

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, so it can also be used to get statistics from fibers, as explained in the next section.

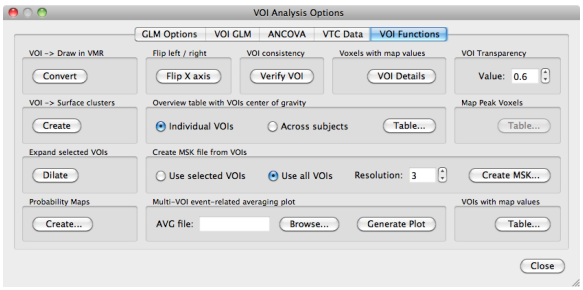


1.9 Statistical Analysis

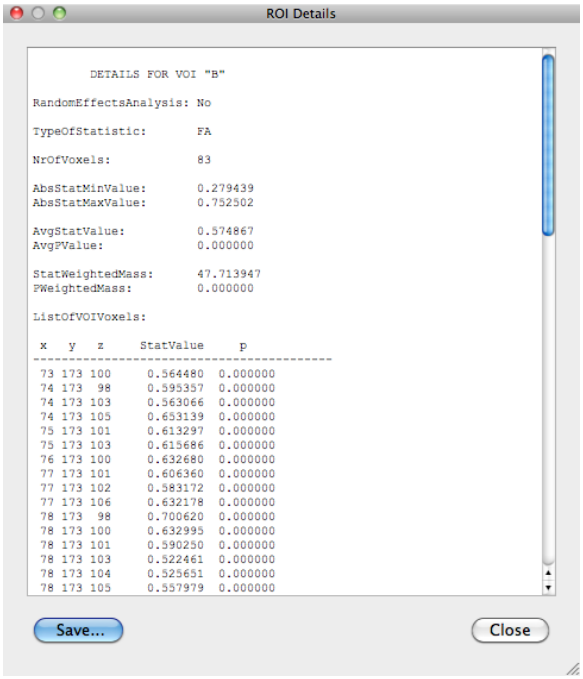
1.9.1 VOI Statistics

An example of using VOI statistics is given in this section. First, make sure you have a VMR and a FA or MD map loaded. Either create a VOI first, or point to `Analysis --> Region of Interest Analysis` to open the VOI dialog and load previously defined VOIs, either drawn or created by backprojection of fibers on a VMR.

Because a FA/MD map is loaded, BV can extract the FA/MD values at the VOIs. Open the VOI dialog if you haven't done this already. To show the data, select the VOI of your choice (here: corpus callosum) and click `Options` in the lower-right corner of the window. In the `VOI Analysis Options` dialog, go to the `VOI functions` tab.



Click the `VOI details` button and a window showing (in this example) the FA values of the VOI at all voxel locations is displayed, in column `StatValue 1`.



The details can be saved as a textfile, and then processed outside of BV, for instance to show the FA profile of the corpus callosum in figure 1.9.

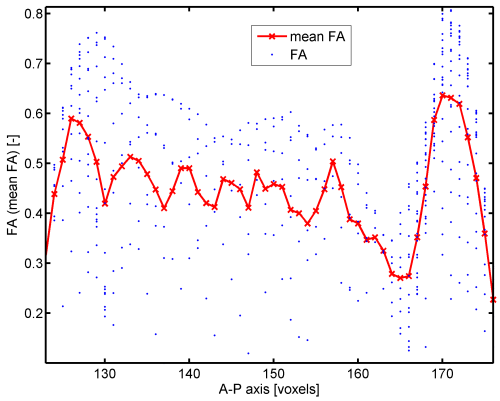


Figure 1.8: FA distribution of the corpus callosum in the anterior-posterior direction.

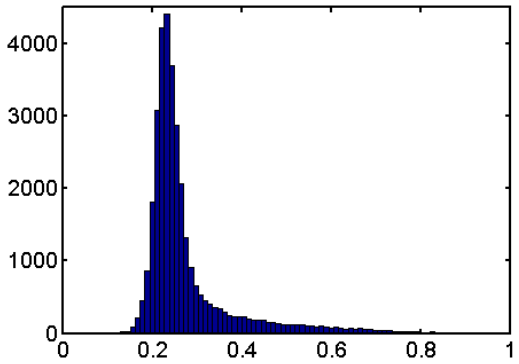


Figure 1.9: ADC distribution of the fibers of the corpus callosum.

Chapter 2

DWI Group Analysis

Before you begin

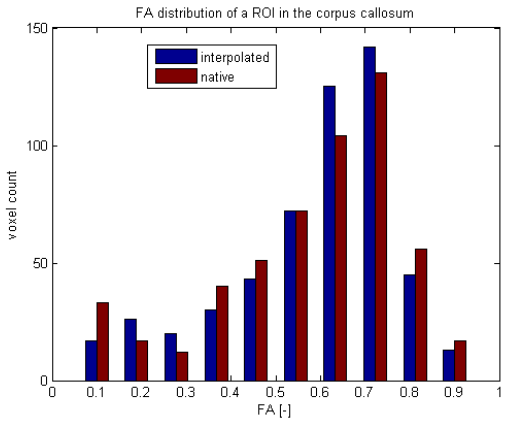
For DWI group analysis, you need BrainVoyagerQX 2.2 or higher.

Introduction

As more and more research is done on white matter morphology, the obvious question to ask is whether differences can be found between individuals or between groups, ie patients vs controls. Before we begin, I'd like to summarize some important acquisition issues.

Data Acquisition

- make sure you acquire data on each subject *exactly* the same. Be careful to use *exactly* the same TR/TE, b-value, voxel size and number of slices.
- *always* measure iso-voxel data. It's easy to understand why: when acquiring non-isovoxel data, and if a fiber structure would be aligned parallel to the long axis of a voxel, more contrast is added there due to the summation of diffusivity. Ergo, more artificial signal decay in that direction!
- try to *avoid* interpolating your data. This has a dramatic effect on derived measures such as *FA*. This is illustrated below, where the *FA* distribution for a native resolution VMP versus interpolated VMP is shown for a ROI in the corpus callosum.



- be very careful with interpretation of differences in *FA* or *ADC*. They might not be of anatomical nature but due to the acquisition, data processing etc.
- include a T1 weighted high-resolution anatomy in the session.

About native and Talairach space

We recommend computing the tensor and derived measures in native space (that is the space as the data was scanned in), and to do the group analysis in common space by converting the scalar FA/ADC maps to TAL space. This prevents introducing artefacts in the tensor data by interpolation. Interpolation of a tensor is not trivial and may introduce tensor deformation in the processing. For more information, see reference [AFPA06].

2.1 Group analysis of FA/ADC maps

2.1.1 Anatomical data Preparation

We will now start by preparing the anatomical data. The anatomy is used to transfer the data into a common space (Talairach space, abbreviated as TAL). The transformation files are later on used to transfer the DW-MRI data into TAL space as well.

It is assumed that you know how to put an anatomical data set into TAL space. If not, please go through the BVQX *Getting Started Guide*.

For each subject, create the `<subject>_TAL.vmr` file. Make sure you do not delete `<subject>_ACPC.trf` and `<subject>.TAL`.

2.1.2 Diffusion Data Preparation

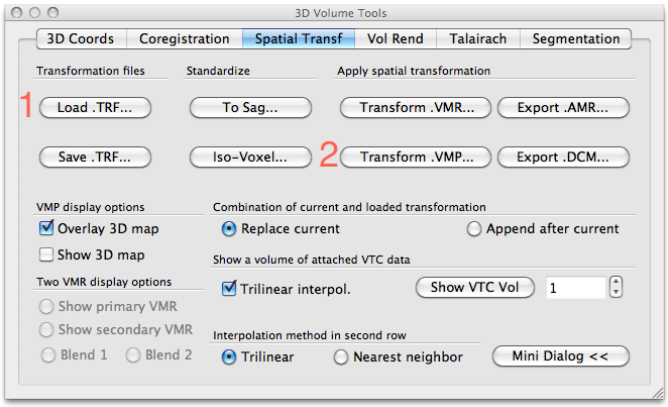
For each subject in your study, do the DW-MRI data analysis in native space, up to the point of creation of *FA* and *ADC* maps. Save each map as `<subject>_FA.vmp` or `<subject>_ADC.vmp` respectively.

2.1.3 Creation of talairach *FA* or *ADC* maps – starting in native space

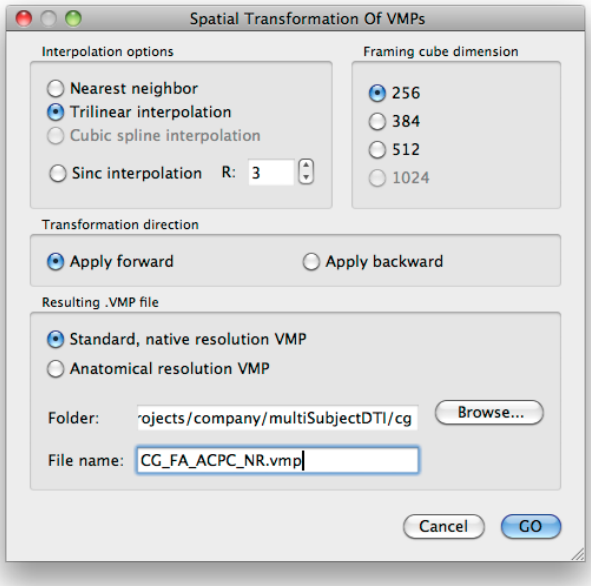
The processing of *FA* maps is demonstrated here, but it is the same for *ADC* maps. It consists of two steps: 1) bringing the map to ACPC space and 2) going from ACPC to TAL space.

Map to ACPC space Open the native space VMR, `<subject1>.vmr`. Go to `Analysis -> Overlay Volume Maps`. Click `Load VMP` and load the file `<subject1>_FA.vmp` you have created earlier. Close the dialog. You should see a *FA* map overlayed on anatomy.

Now, go to `3D Volume Tools -> Spatial Tranf`. Load the `<subject>_ACPC.trf` file created earlier and click `Transform .VMP`.

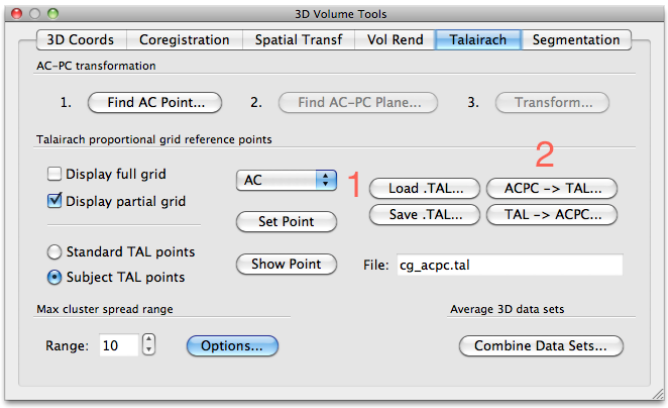


Save the result as `<subject>_FA_ACPC.vmp`:

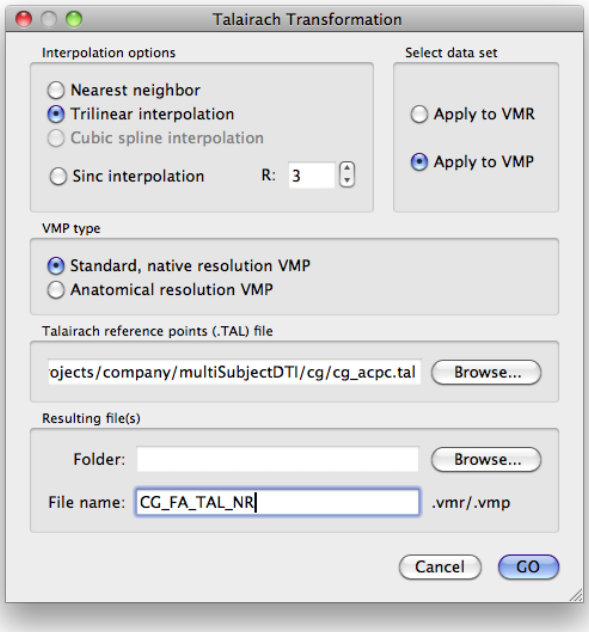


The ACPC transformation is done. Close the VMR.

Map to TAL space from ACPC Now, open the file `<subject>_ACPC.vmr`. Load the *FA* map: `<subject>_FA_ACPC.vmp`. Go to `3D Volume Tools -> Talairach`. Load the TAL file `<subject>_ACPC.TAL` by clicking the `Load TAL` button. Next, click `ACPC -> TAL`.



Save the results as `<subject>_FA_TAL.vmp` (make sure the `Apply to VMP` checkbox is checked!):

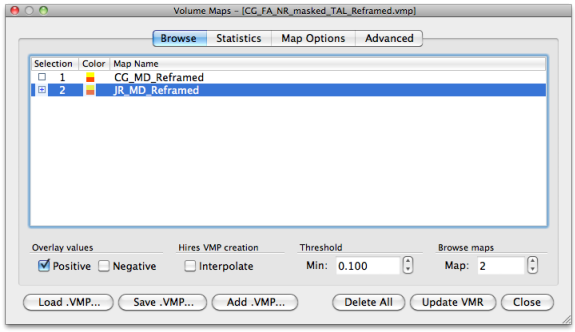


Repeat the talairach process for each subject.

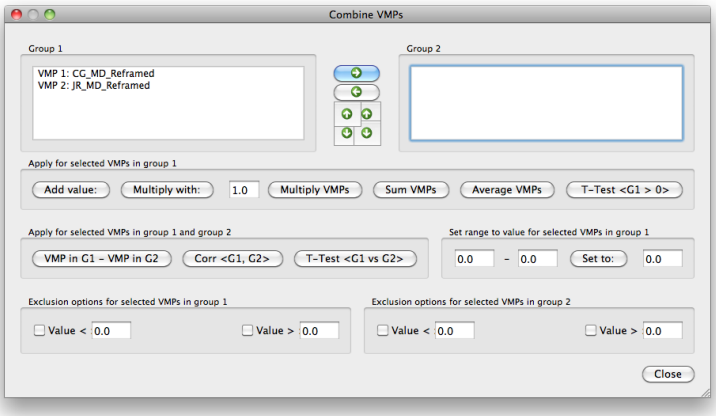
2.1.4 Combining the maps

Now that we have created FA maps in TAL space, and have reframed them for each subject, it's time to do simple statistics. For analysis, first a TAL VMR needs to be opened. You may use the best VMR in your data set, but you can also create an average VMR from all data sets (`Volumes > Combine 3D data sets`).

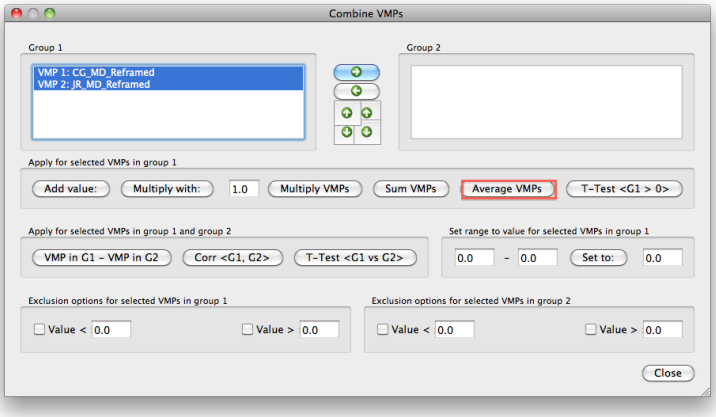
Open the `Analysis > Overlay Volume Maps` dialog. This dialog can also be opened using the `Ctrl+M` shortcut. Now, load the FA map of each subject:



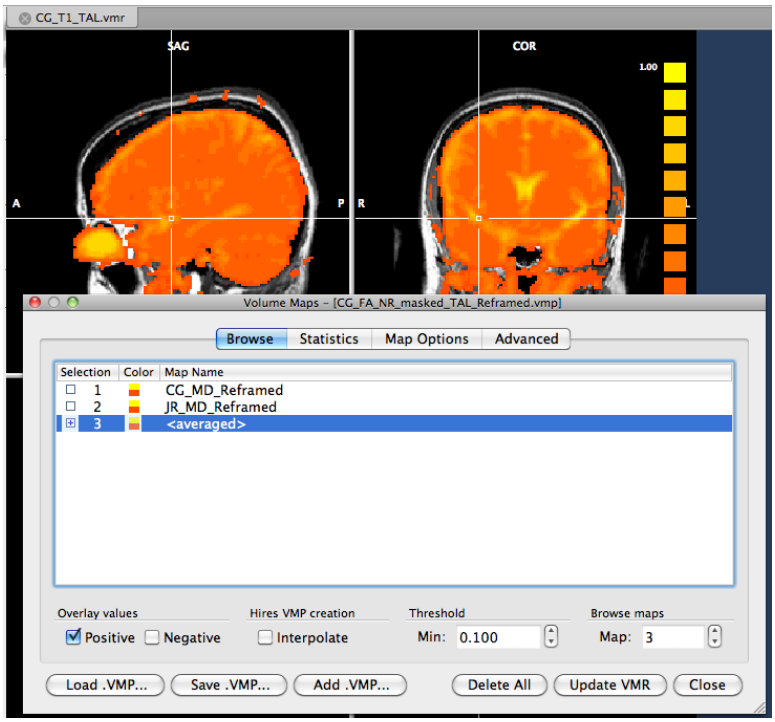
Browse all maps to see whether they correctly align with the VMR and inspect for other irregularities. Now we can use the `Combine VMPs` option in the `Advanced` tab. The dialog is divided into 4 parts. The top part shows the subjects maps, and gives you the opportunity to discriminate between 2 groups G1 and G2. A second part that can be used to analyze the maps without splitting them into groups. A third part that enables specific statistics on the basis of the maps separated into groups. Finally, an "exclusion" option that will help to shape specific maps according to their values and a value range selected by the user.



First, we try the statistics that are available for the single group (in the first field). We mark all subjects maps and use the `Average VMPs` option.

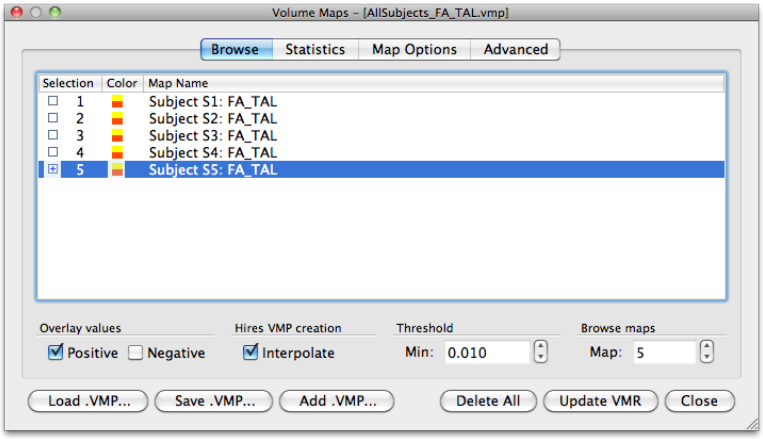


As the result, a new map will be created in the main dialog (at the end of the map list). We check the map to visualize the result of the average procedure.



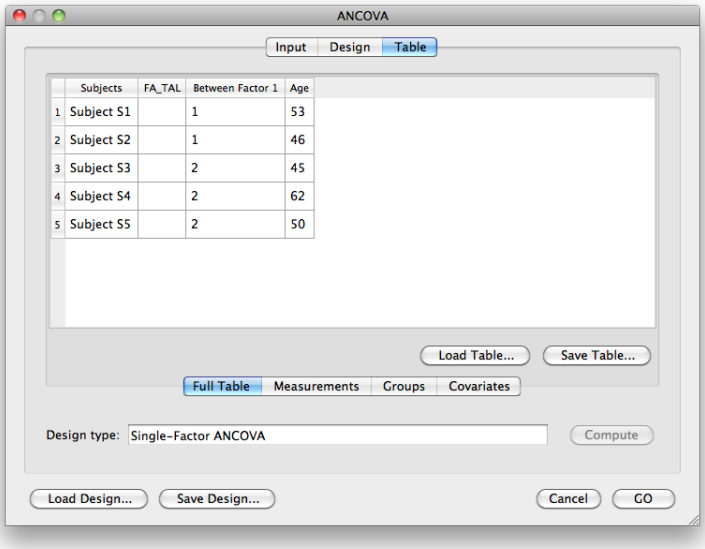
2.1.5 ANCOVA Analysis of FA/ADC maps

For this step, first create a map containing all maps (VMPs) of all subjects, and use the naming convention `Subject <initials>: FA` or the like:



Then, go to the `Advanced` tab of the `Volume Maps` dialog. From there on, you can use the ANCOVA tool just as you would for an fMRI ANCOVA analysis. I'd like to refer you to the description in the User's Guide in the Basic Analysis, Random Effects Group Analysis section. You can also have a look at the description in `http://web.mac.com/rainergoebel/RainersBVBlog/Rainers_BV_Blog/Entries/2007/9/25_The_'C'_in_ANCOVA.html`.

As an example, I've divided 5 subjects into two groups (Dummy example, i.e. excellent readers in group 1 and poor readers in group 2), and I've added age as a covariate. The design table of the experiment looks like this:

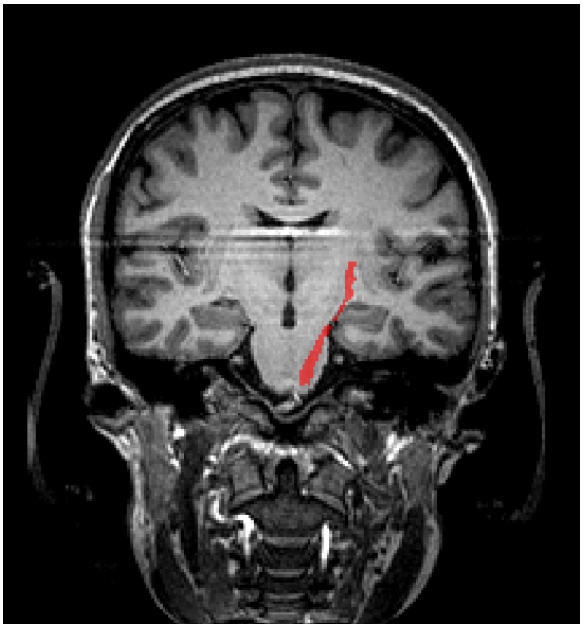


Click `GO` to start the analysis.

2.2 Group analysis of fiber tracts

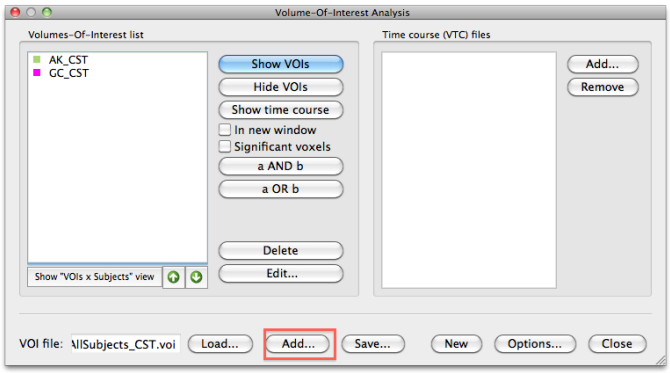
Again, we will start with preparing the data in native space. Do the DTI preprocessing up to the tensor estimation, so you can start tracking fibers. The next step is to select the tract you are interested in, in the `DTI > Fibers Table` menu. Then, transform the fibers to ACPC or TAL space, as explained in 1.8.4.

Next, go to `DTI > Spatial transformations` and click the button `Fibers -> VMR`. This will project the 3-D fiber reconstruction onto the 2-D VMR slices. The result is a volume of interest (VOI) on the VMR. As explained earlier, if you add a VMP in Talairach space, you can extract the MD/ADC values from that VOI.

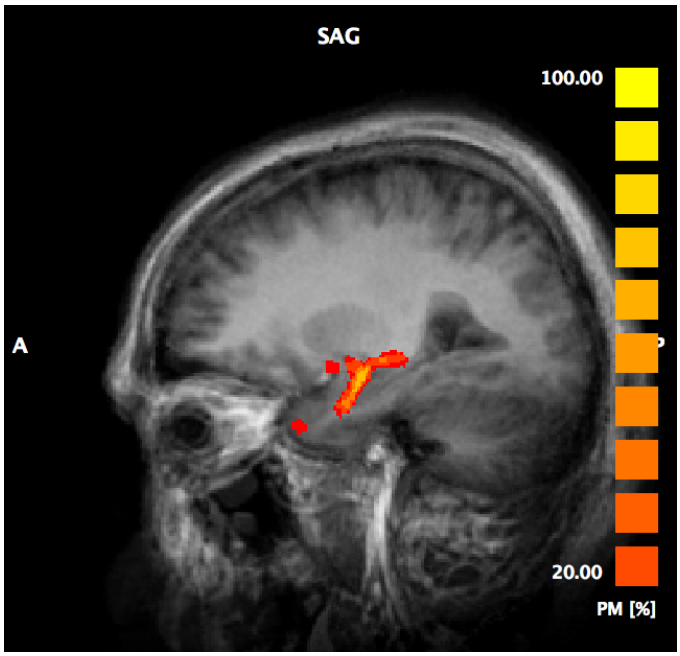


2.2.1 Tract probability maps

Ofcourse we could overlay the tracts from all subjects on a TAL vmr, but a nicer option is to create probability maps of the tracts across subjects. To do this, convert the tracts from all subjects into TAL space, and use the naming convention `<subject>_tractname` for each voi, eg `CG_CST`. Add the vois of all subjects into one voi file, by using the `Add` function in the VOI analysis dialog.



Then, click `Options > VOI functions > Probability Maps, Create`. Make sure you see only the tract name and not all subject names. You can use the `Naming Convention` radio buttons to change. Set the map resolution to `1x1x1` and click `GO`. The result is a VMP showing overlapping tracts. The colors indicate in what degree the tracts are overlapping. The percentage value is calculated according to $100 * (\text{number of times a tract overlaps})/(\text{number of subjects})$.



Chapter 3

Frequently Asked Questions

WARNING
If your acquisition matrix is larger than 128x128, the automatic DMR-VMR co-registration feature in BrainVoyager QX will possibly fail. This means, you might need to do manual co-registration.
We strongly recommend the acquisition matrix to be at maximum 128x128, since a larger matrix will be zero-filled in k-space (=interpolated in image space), resulting in data redundancy. Please ask your MR technician to turn off interpolation for DW-MRI acquisition.

3.1 General

3.1.1 Incorrect color coding FA maps

FA color coding is incorrect. Why? Because co-ordinate system of scanner and BrainVoyager is different. This is not a BV problem, since co-ordinate systems are not standardized.

Normal color coding:

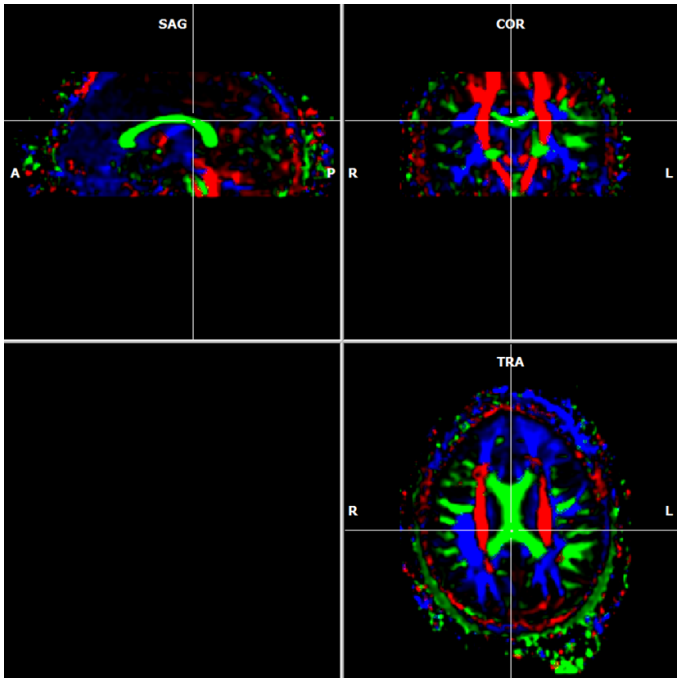
Red Left-Right vv (= X direction)

Green Anterior-Posterior vv (= Y direction)

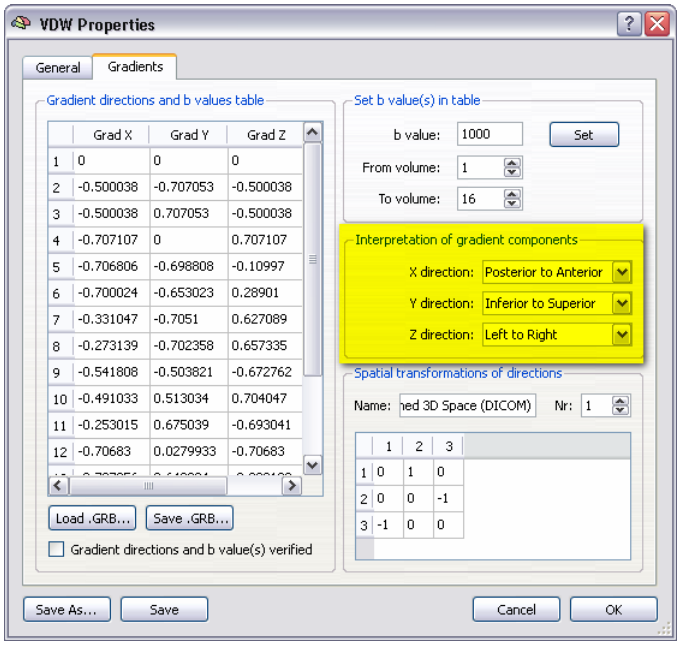
Blue Inferior-Superior vv (= Z direction)

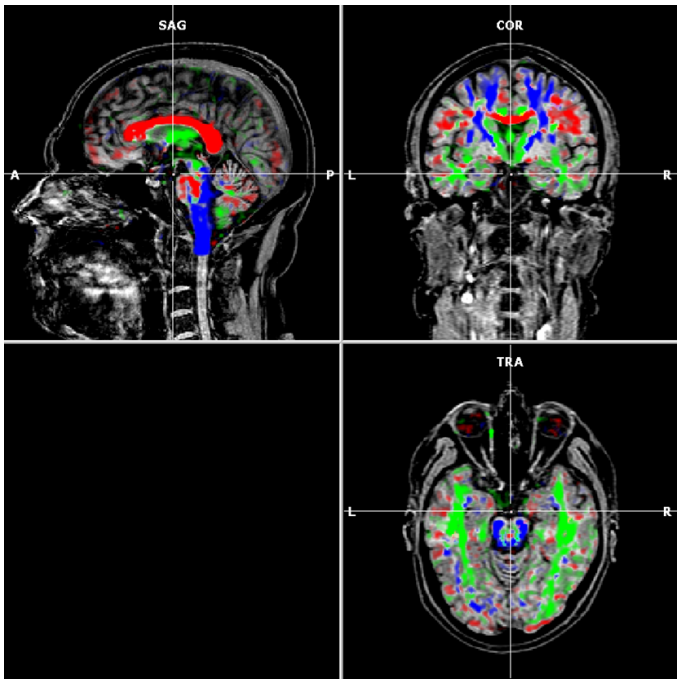
An example of abnormal color coding:

Example: Original color	**Proposed change**
Ant-Post = blue	X: direction = Inf-Sup
Inf-Sup = red	Y: direction = Left-Right
Left-Right = green	Z: direction = Ant-Post



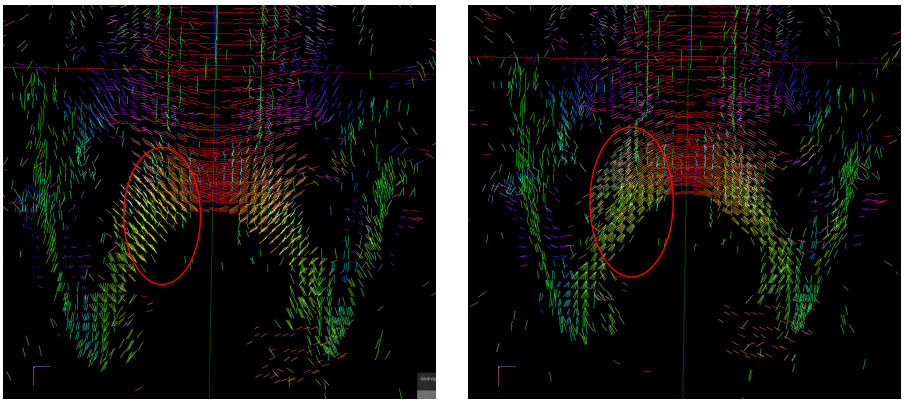
Procedure to correct:
go to `DTI -> Diffusion Weighted Data Analysis -> VDW Properties -> Gradients`. Change x, y and z to what you think is correct. *This is a mathematical operation and has nothing to do with orientation in the brain.* Next, click the `OK` button.





Re-calculate the tensors by clicking the `Estimate` button. In the `Calculations` tab, create the color coded FA maps and check them for the right colors.

Then, Go to `DTI -> Tensor visualisation` and check for tensor directions. I always use the splenium of the corpus callosum to check for correct orientation.



(a) incorrect tensors (b) correct tensors

Figure 3.1: Splenium of the corpus callosum, view from the top

3.2 Project Creation related

3.2.1 I can't get my data into BrainVoyager, or the values are all wrong

Before calling BV support, please try to convert your data to Nifti, and try to import it using the Nifti plugin, which can be found in `Plugins > Nifti Converter`.

An excellent DICOM to Nifti convert is MRIcron by Chris Rorden, to download for free from `http://www.sph.sc.edu/comd/rorden/mricron/`.

3.2.2 The create project wizard does not work or crashes BrainVoyager

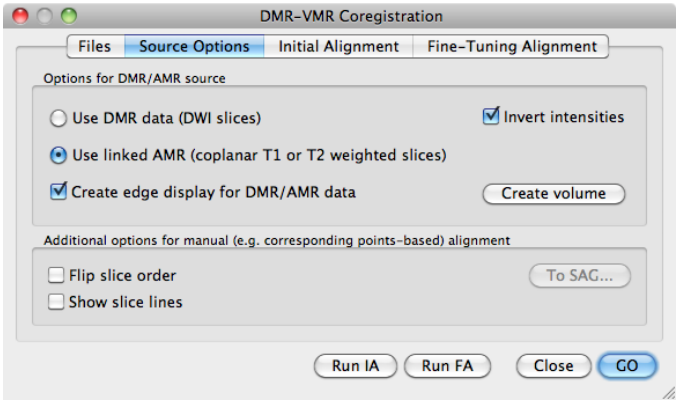
- BrainVoyager crashes while executing the create Project wizard
- My acquisition matrix is larger than 128×128. BrainVoyager incorrectly reads my data?
- I need byte swapping (can occur with PHILIPS PAR/RECdata), that is: from little Endian to big Endian or vice versa.
- the number of bytes per pixel of my raw data $\neq 2$?
- the Siemens MOSAIC matrix is incorrectly read by BrainVoyager?

Please check out `http://support.brainvoyager.com/diffusion-weighted-imaging.html` or contact the support team at `support@brainvoyager.com`.

VDW related

3.2.3 Fine-Tuning alignment does not work properly

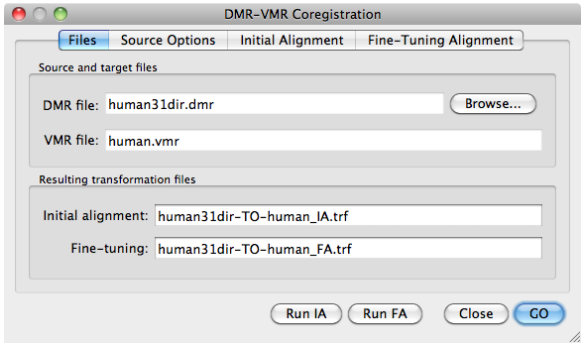
By default, Fine-Tuning alignment uses the first volume in the data set. It might be, that this is a diffusion weigthed image instead of a b0. The fine alignment fails at this point. The solution is to set the display volume to a b0 volume (see `DMR Properties > DWI Data > Volume (b0) for display`), and *save the DMR*. Then, in the alignment procedure, use the AMR as input.



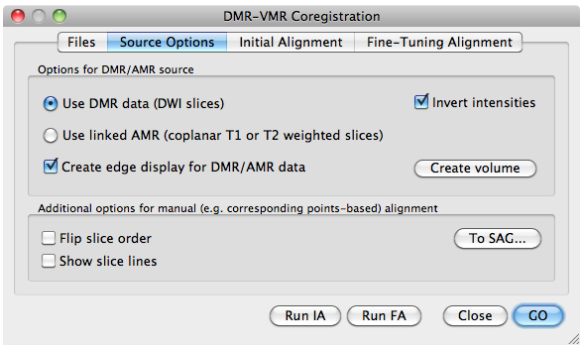
3.2.4 Optional: Manual Co-registration of DMR with VMR

In some cases the position information may be lost or incorrectly read by BrainVoyager. The automatic co-registration will not work, and you are forced to use manual co-registration. In this section, the procedure is discussed step-by-step.

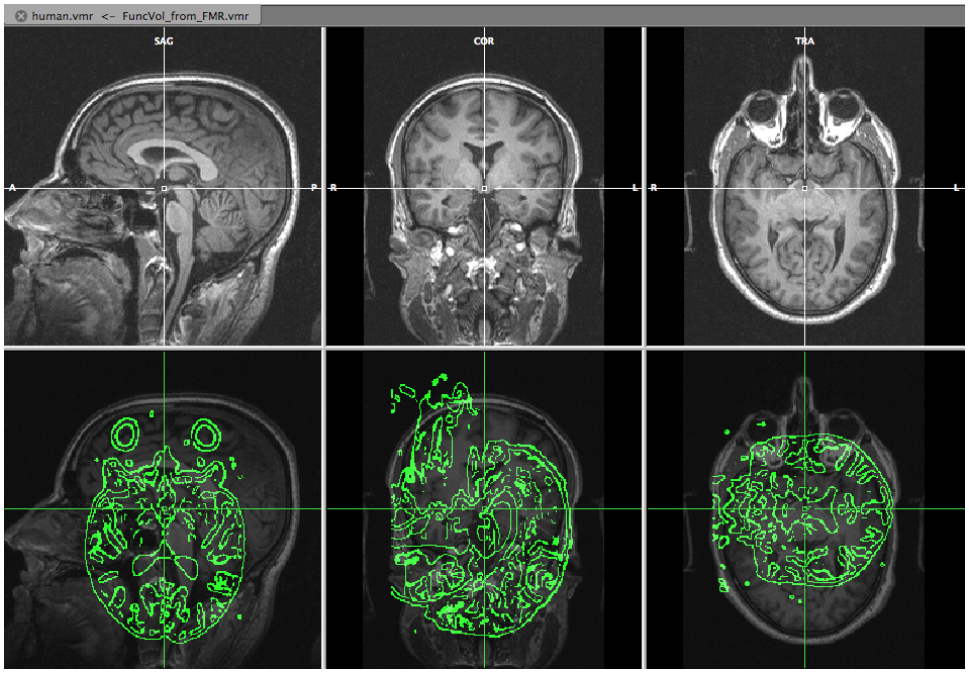
1. Open the VMR corresponding to the DTI data set, `human.vmr`.
2. Go to `DTI-->Coregister DMR-DWI to VMR`. Via the `Browse` button, locate the DMR `human31dir.dmr`.



3. Go to the `Source Options` tab. In most cases, BrainVoyager has created an AMR file from the first volume, but if this did not happen, choose the `use DMR data (DWI Slices)`, and check the `invert intensities` box. This has to be checked, since a DWI images has T_2 contrast, while T_1 contrast is needed for co-registration. Check the `create edge display for DMR/AMR data` box. Next, hit the `Create Volume` button. This will create a VMR from the first DMR volume.

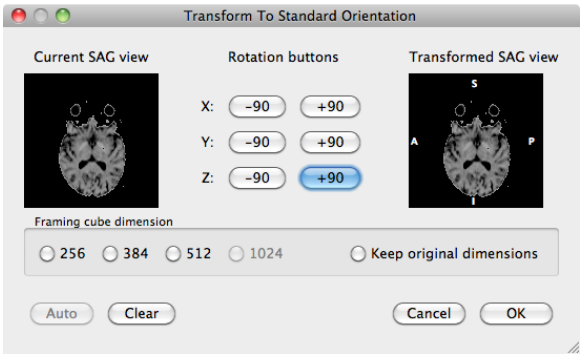


4. The window will look like this:

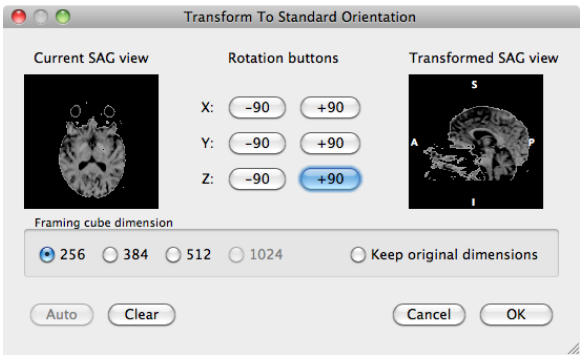


On the top row, we see the VMR, overlayed with the slice orientation of the DMR data set (light yellow lines) The bottom rows shows the VMR overlayed with the DMR data. The green lines represent the edges of the DMR data. As is immediately clear, the DMR is scanned in a transversal way, while the VMR is sagittally oriented. We will solve it in the next step, by converting the DMR to sagittal orientation.

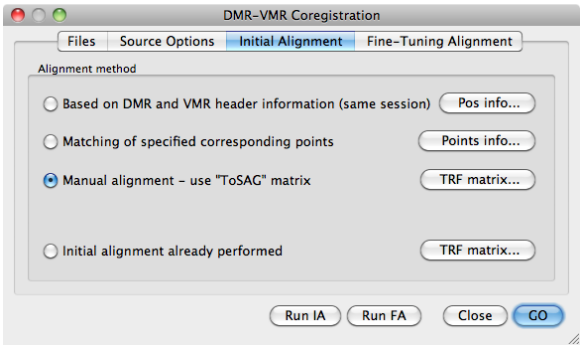
5. Click the `To SAG` button in the co-registration dialog. A dialog pops up:



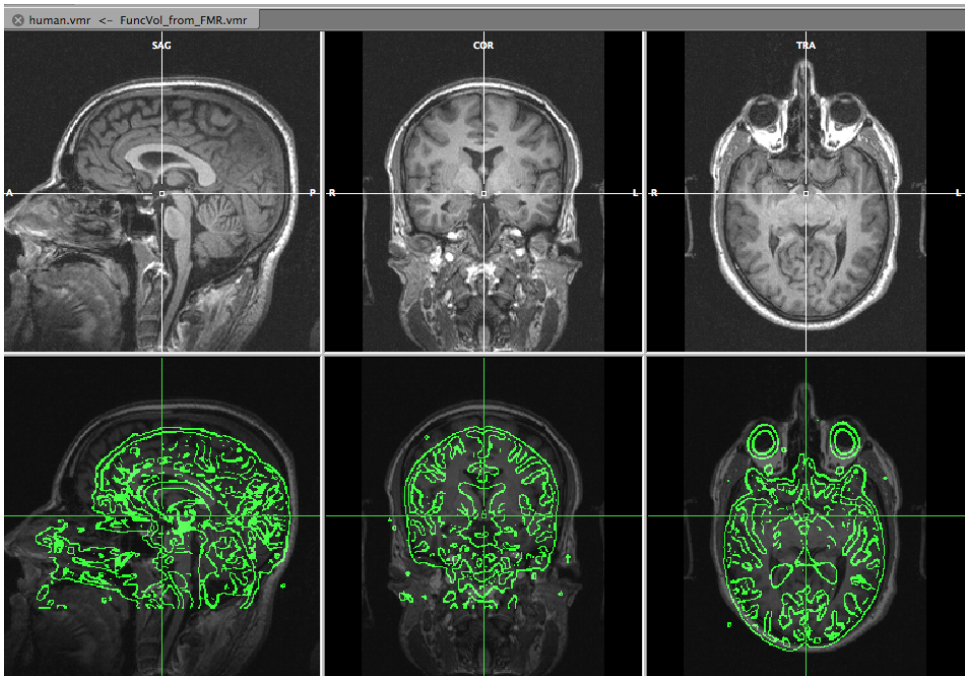
By manipulating the data via the middle buttons, change the right view to a sagittal view. In this case, it means hitting the `X: +90` button once, and `Y: -90` button one, but in your data it may be different. Check the `Framing cube dimension: 256` radio button, and click `OK`.



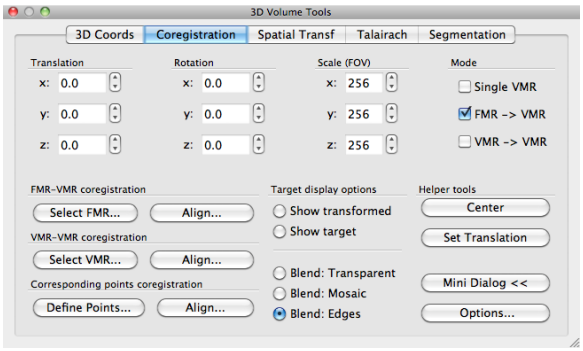
6. Go to the `Initial Alignment` tab of the coregistration dialog and check the `Manual Alignment -- use "To SAG"` option. Click `Run IA`.



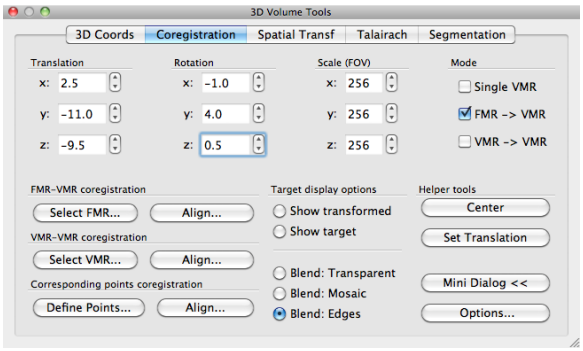
The result is the DMR in sagittal orientation overlayed on the VMR:



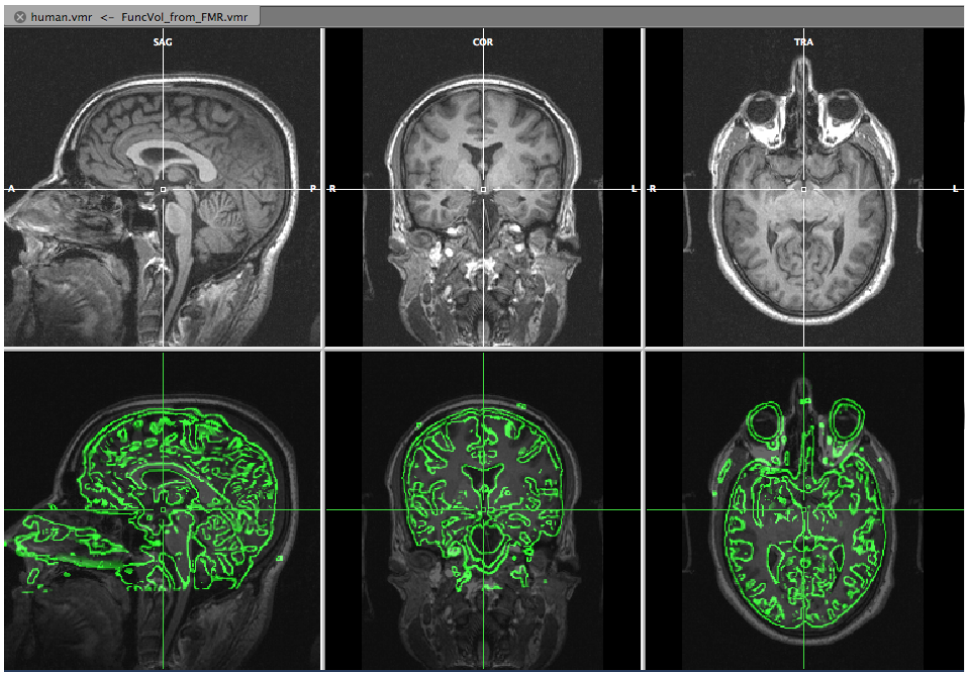
7. The result is a very crude alignment, so it needs to be adjusted. This is done by transformations and rotations. Go to the coregistration tab of the `3D Volume Tools`:



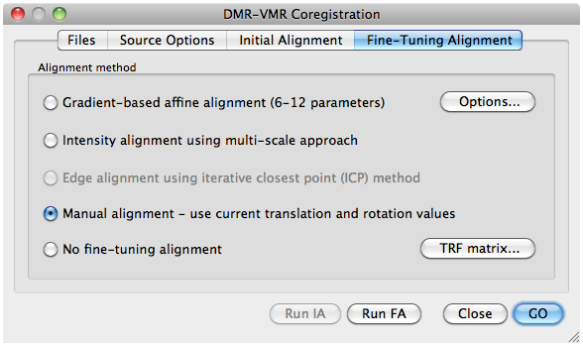
Using x, y, z translations and x, y, z rotations, try to align the DMR as good as possible to the VMR data set. In the bottom row of the data display, you can freely browse the data, and this is of course highly recommended. When aligning, concentrate on aligning gyri and sulci rather than the ventricles, since the tissue around ventricles suffers from (large) distortions in EPI data such as DMR. Try to be as precise as possible! For the current data set, the following parameters were found:



and the window looks like this:

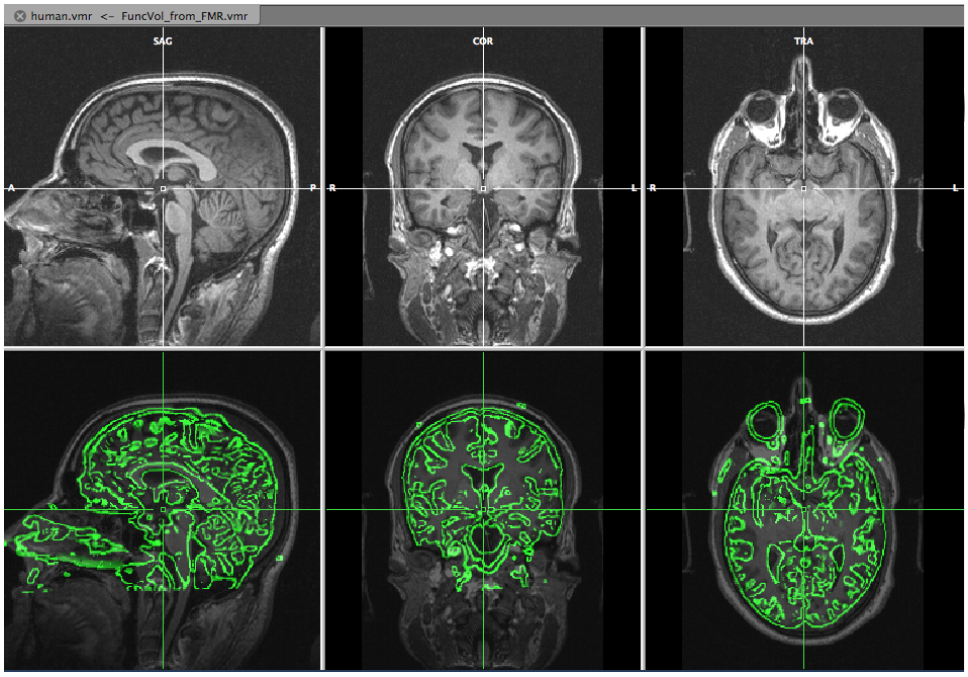


8. Now, return to the DMR-VMR coregistration dialog, via `DTI-->Coregister DMR/DWI to VMR`. Go to the `Fine Tuning Alignment` tab, and check the `Manual alignment -- use current translation and rotation values` option:



Hit the `Run FA` button.

9. Result of the manual alignment procedure:



BrainVoyager has saved the transformation values in the files `human31dir-TO-human_IA.trf` and `human31dir-TO-human_FA.trf`

Further Reading

[AFPA06] Vincent Arsigny, Pierre Fillard, Xavier Pennec, and Nicholas Ayache. Log-Euclidean Metrics for Fast and Simple Calculus on Diffusion Tensors. *Magnetic Resonance in Medicine*, 421(April):411–421, 2006.

[BJ02] PJ Basser and DK Jones. Diffusion-tensor MRI: theory, experimental design and data analysis - a technical review. *NMR Biomed*, 15:456–467, 2002.

[CHPJ02] M Catani, RJ Howard, S Pajevic, and DK Jones. Virtual in vivo interactive dissection of white matter fasciculi in the human brain. *NeuroImage*, 17:77–94, 2002.

[Jon04] DK Jones. The effect of gradient sampling schemes on measures derived from diffusion tensor MRI: A monte carlo study. *Magnet Reson Med*, 51:807–815, 2004.

[Kin06a] PB Kingsley. Introduction to diffusion tensor imaging mathematics: Part i. tensors, rotations, and eigenvectors. *Concept Magn Reson A*, 28A(2):101–122, 2006.

[Kin06b] PB Kingsley. Introduction to diffusion tensor imaging mathematics: Part ii. anisotropy, diffusion- weighting factors, and gradient encoding schemes. *Concept Magn Reson A*, 28A(2):123–154, 2006.

[Kin06c] 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.

[LBPAL06] D Le Bihan, C Poupon, A Amadon, and F Lethimonnier. Artifacts and pitfalls in diffusion mri. *J Magn Reson Imaging*, 24:478–488, 2006.

[MB99] S Mori and PB Barker. Diffusion magnetic resonance imaging: Its principle and applications. *Anat Rec*, 257:102–109, 1999.

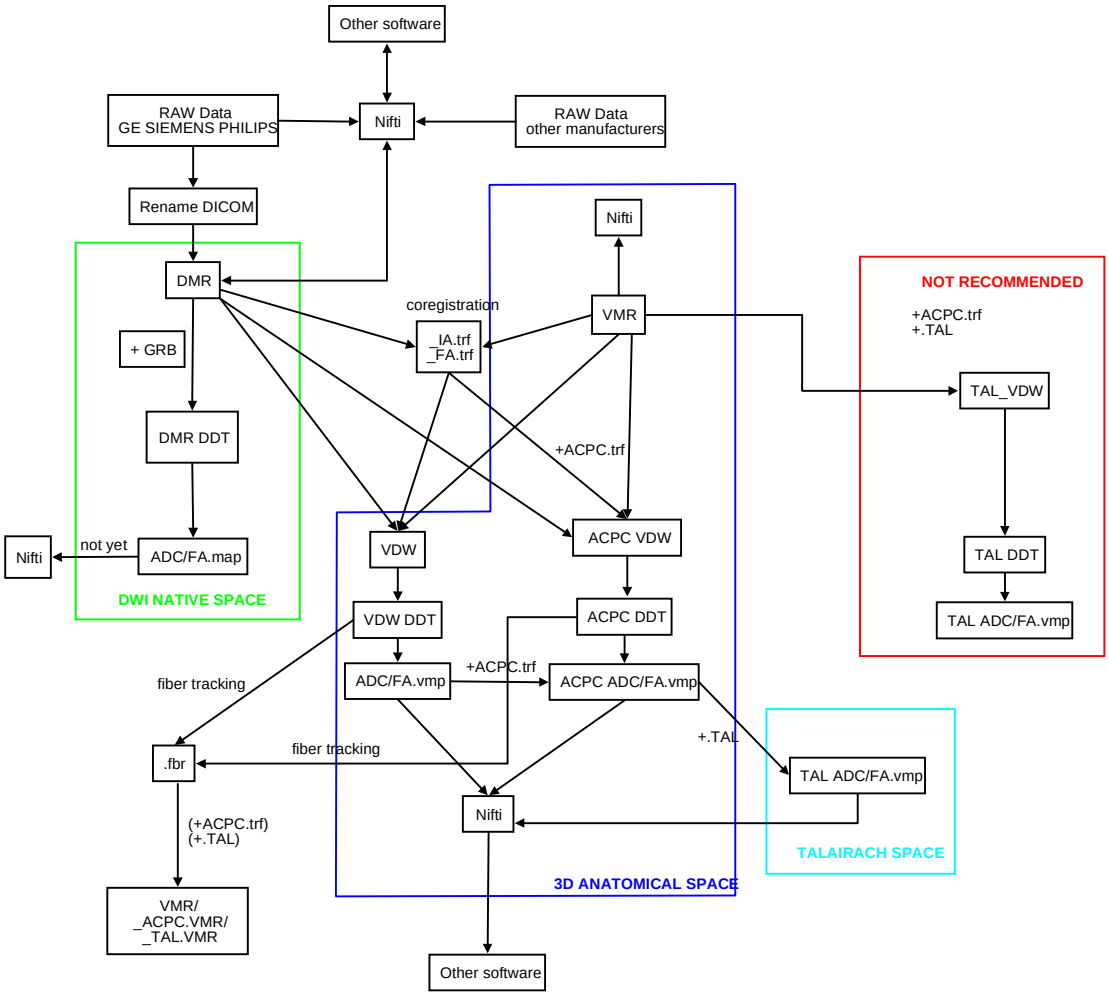
[Mor07] S Mori. *Introduction to Diffusion Tensor Imaging*. Elsevier, 2007.

[MWNPVZ05] S Mori, S Wakana, LM Nagae-Poetscher, and PCM Van Zijl. *MRI atlas of human white matter*. Elsevier, 2005.

[WMM+02] 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.

Appendix A

Overview of DTI Procedures



Appendix B

File types

DMR	Diffusion MR project	text file, describing the project which data is in a DWI file (compare FMR ↔ STC)
DWI	Diffusion Weighted Images	binary file containing raw diffusion weighted data
TRF	TRansformation File	text file, containing transformation parameters
VDW	Volume Diffusion Weighted file	binary file, 3-D diffusion weighted data set (compare to VTC)
GRB	Gradient directions and b-values	text file, containing gradient directions and b-values
DDT	Diagonalized Diffusion tensors file	
TVL	Tensor Volume file	binary tensor file for use in TrackMark
VMP	Volumetric Map	Binary file containing FA or mean diffusivity values for each voxel.
FBR	fiber file	text file containing the fiber points
VOI	Volume of Interest	text file, containing voxel positions for each voxel in the VOI/ROI

B.1 BrainVoyager Fiber Coordinate system

This is the coordinate system in the OpenGL/Surface window.

Origin: $[x, y, z]$ = 0.5*VMR slice X-resolution, 0.5*VMR slice Y-resolution, 0.5*number of slices

x-axis: anterior to posterior 0 to X-resolution y-axis: superior to inferior 0 to Y-resolution z-axis: right to left 0 to Z-resolution

B.2 Contents of the DDT file

DDT file format, for each voxel, with v_{ij} the eigenvector entries and eigenvalues $\lambda_1 > \lambda_2 > \lambda_3$, there are 12 values:

$$\begin{bmatrix} v_{1x} & v_{1y} & v_{1z} & v_{2x} & v_{2y} & v_{2z} & v_{3x} & v_{3y} & v_{3z} & \lambda_1 & \lambda_2 & \lambda_3 \end{bmatrix}$$

If you want to reconstruct the tensor $\mathbf{D}$, use the following:

$$\mathbf{DE} = \mathbf{E\Lambda}$$

$$\begin{pmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{pmatrix} \begin{pmatrix} v_{1x} & v_{2x} & v_{3x} \\ v_{1y} & v_{2y} & v_{3y} \\ v_{1z} & v_{2z} & v_{3z} \end{pmatrix} = \begin{pmatrix} v_{1x} & v_{2x} & v_{3x} \\ v_{1y} & v_{2y} & v_{3y} \\ v_{1z} & v_{2z} & v_{3z} \end{pmatrix} \begin{pmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{pmatrix}$$

and

$$\mathbf{DEE}^T = \mathbf{D} = \mathbf{E\Lambda E}^T$$

$$\mathbf{E}^T\mathbf{E\Lambda} = \mathbf{\Lambda} = \mathbf{E}^T\mathbf{DE}.$$

Appendix C

GRB file for the sample data set

C.1 Format of grb files

GRB files are plain text files. The format of a GRB file is as follows, demonstrated as an example here for a 6-direction + b0 scheme, each line having 3 entries `X Y Z`:

```
FileVersion:    1

IncludeBValues: no

NrOfEntries:    7
X   Y   Z
0   0   0
0.577   0.577   0.577
-0.577  -0.577  0.577
0.577   -0.577  -0.577
-0.577  0.577   -0.577
0.707   0.707   0
0.707   0   0.707
```

If the b-values (1000 in this case) are included, the file looks like this: Note that IncludeBValues is changed to "yes", and that each line now has 4 entries, `X Y Z b`.

```
FileVersion:    1

IncludeBValues: yes

NrOfEntries:    7
X   Y   Z b
0   0   0 0
0.577   0.577   0.577 1000
-0.577  -0.577  0.577 1000
0.577   -0.577  -0.577 1000
-0.577  0.577   -0.577 1000
0.707   0.707   0 1000
0.707   0   0.707 1000
\label{appendix:grb}

FileVersion:          1
```

```
IncludeBValues:      no

NrOfEntries:          31
X   Y   Z
  0.0           0.0           0.0
  1.0000000000  0.0000000000  0.0000000000
  0.7703189794 -0.6334477240  0.0731618129
  0.2561448687 -0.0249786863  0.9663156169
  0.7976459349 -0.1068670680  0.5935826751
 -0.4615578229  0.8761728334  0.1388723949
 -0.2292204126  0.8533775040 -0.4681931632
 -0.2630794898 -0.4113047154 -0.8727070603
  0.7992449025  0.5854349684  0.1359171940
  0.5067126566  0.5103287334  0.6948430524
  0.3054330813 -0.1364364527 -0.9423883102
 -0.7972741706 -0.1949622700 -0.5712649212
 -0.8042542270 -0.5926021950 -0.0446964971
  0.1865635668  0.9537832611  0.2355663949
 -0.3881893823  0.1079319091  0.9152375137
 -0.1339272628  0.6629447625  0.7365919699
 -0.3384961835 -0.8809697404  0.3306246365
  0.7673774759  0.3119018842 -0.5602222989
  0.4065245350 -0.6656047592  0.6258658858
  0.2871876223 -0.7612264361 -0.5814271946
 -0.7661480348  0.4319864923  0.4758201964
 -0.1793153505 -0.5264136055  0.8311045187
 -0.7673768974 -0.3119020115  0.5602230203
  0.2179780246 -0.9751760272  0.0389524925
  0.4189866219  0.8397110024 -0.3454499142
  0.1777380470  0.4786928124 -0.8598036857
 -0.3397814897 -0.8554854208 -0.3907598163
 -0.7844890989  0.5119797541 -0.3499336868
 -0.4197498720  0.2604620840 -0.8694650929
  0.7734515702 -0.3550403437 -0.5250895379
 -0.9984481940  0.0477096943  0.0287226207
```

Appendix D

Recommended DW-MRI scan protocols

Date: May 21, 2010

Disclaimer: this document contains recommendations for optimal DW-MRI acquisition. We (Brain Innovation BV) are not responsible for any damages caused in any way resulting from following these recommendations.

Sequence double-refocused single shot EPI reduces eddy current distortions.

Field of View minimal 240 mm (square)

k-space coverage symmetrical

Number of Slices minimum needed to cover entire brain including cerebellum (usually > 55)

Slice orientation axial

Voxel size Isotropic, 2.5 x 2.5 x 2.5 minimum recommended

Matrix size square 96x96, 128x128, etc

Slice gap 0 mm

Angulation none, could cause mis-calculation of tensors

TR shortest to accommodate all slices

TE minimum needed for full acquisition

Zero-filling No zero-filling or interpolation

Parallel imaging SENSE (factor 2) or GRAPPA

Diffusion directions > 6 directions for MD, > 20 directions for FA and fiber tracking, > 80 directions for HARDI applications

b0 1 b0 for every 6-10 diffusion weighted images

b-value 600-1200 s/mm^2 for DTI, > 2000 for HARDI/q-ball etc

Averages As many as possible given the scan time. Do not average real-time on the scanner, but save each repetition as a seperate data set.

Supported Raw data formats in BVQX DICOM, DICOM MOSAIC, PAR/REC, Nifti via Nifticonverter plugin

Sources:

- BIRN Imaging protocols `http://nbirn.net/research/morphometry/imaging_protocols.shtm` May 21, 2010;
- S. Mori Introduction to Diffusion Tensor Imaging Elsevier 2007;
- ISMRM Diffusion and Perfusion study group mailing list