making functional MRI easy

NordicNeuroLab

nordicBrainEx

Tutorial – DTI Module

Please note that this tutorial is for the latest released nordicBrainEx.
If you are using an older version, please upgrade.

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Contents

1 Introduction to DTI analysis

The nordicBrainEx DTI computation can analyze DTI data acquired with all major MR vendors. DTI datasets acquired with two b–values, i.e. one or multiple b=0 images and 6 or more diffusion weighted images where $b \neq 0$ (typically b=1000 s/mm ^{2}) can be analyzed in nordicBrainEx. For datasets with 6 diffusion weighted images the analysis is done by taking the analytical solution of the Stejskal and Tanners diffusion equation system, while for datasets acquired with more than 6 diffusion directions a least–square fit approach using Singular Value Decomposition (SVD) is used.

The DTI analysis in nordicBrainEx generates parametric maps of the various attributes of the diffusion tensor, including Eigenvector color map (cDTI), Fractional anisotropy index (FA), Mean diffusicity (ADC), Tensor eigenvalues (λ_1 , λ_2 and λ_3), Trace weighted (TraceW) and Axial and Radial diffusivity. Additionally, fiber tracking of the entire volume is performed, using a variant of the algorithm commonly referred to as Fiber Assignment by Continuous Tracking (FACT) (Mori et al. Ann. Neurol. 1999;45:265–269).

2 DTI settings

When you first load a DTI dataset into the database, nordicBrainEx tries to automatically extract the DTI gradient configuration from the header file of the series. If this is not possible, you have to define the DTI gradient configuration yourself.

DTI settings can be accessed from two different locations in nordicBrainEx, which both will open the DTI settings window (see Figure 1).

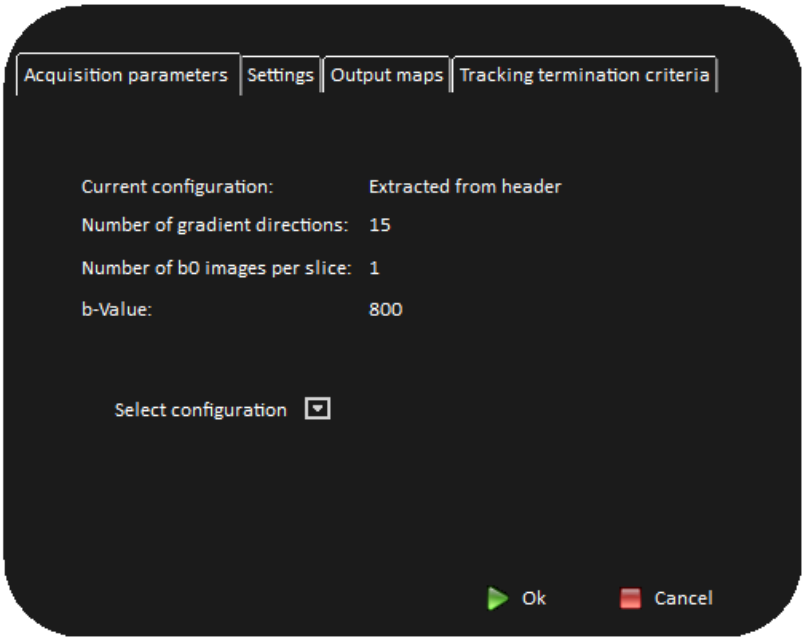

Figure 1: The DTI settings interface.

- In the *Select patient data* window, right click on the selected DTI series in the *Series* tab and choose *Edit DTI settings*.
- In the *Visualization* interface, right click on the DTI series' thumbnail in the *Data panel* and choose *Edit DTI settings*.

Read more about how to configure the DTI settings in 'Details on configuring DTI settings' on page 11.

3 Interacting with DTI results

When the DTI analysis is completed, the *Visualization* interface will open. The generated output maps (FA maps, ADC maps, etc.) as selected in the settings step (see section 'Output maps' on page 15) are displayed as thumbnails under the *Derived data* to the left (see Figure 2). The *DTI* tab in the right panel contains the tools for interacting with the data. The available features are described in the following sections.

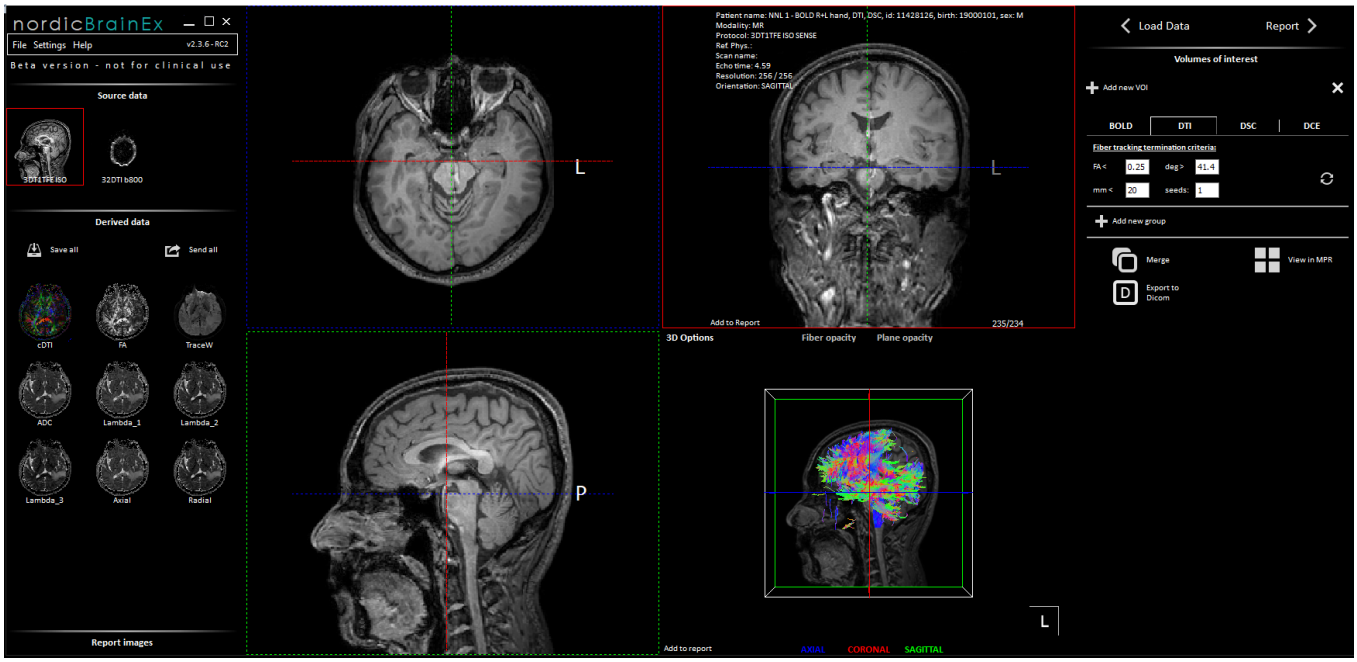

Figure 2: Visualization and interacting with DTI results in nordicBrainEx.

3.1 Fiber tracking

When loading a DTI dataset, the fiber tracts from the entire brain is automatically generated using an exhaustive search, and visualized in the 3D view of the MPR. To visualize fibers from smaller areas of the brain, the *Volume-of-Interest* tool is used.

In order to visualize fibers using VOIs, do as follows:

1. Add a VOI by clicking on *Add new VOI*, and choose its geometrical shape. See section 'Volume-of-Interest (VOI)' in 'Tutorial – Visualization and Interaction for more details.

2. Place the VOI in the image volume.
3. Assign the VOI with AND, OR or NOT logical operators. E.g. adding a VOI assigned as
    - AND will only visualize the fibers passing through that VOI (if several VOIs are marked with AND, only fibers passing through *all* these VOIs will be visualized).
    - OR will visualize the fibers passing through this and any other VOIs defined.
    - NOT will disregard all fibers passing through that VOI.
4. Add additional VOIs similarly.

The visualization of the fiber tracts in the 3D MPR will be updated automatically, as the attributes (SEED, AND, OR, NOT) changes. See section 'Intereacting with the 3D viewer' in 'Tutorial – Visualization and Interaction' for a description of the various options and features available in the 3D viewer.

Alternatively, the VOI can be assign as a *Seed* attribute, see section 'Using VOIs with DTI fiber tracking' in 'Tutorial – Visualization and Interaction'. This will re-do the fiber tracking analysis using only voxels inside the VOI as seed point. To reset the fiber tract to show all the brain's fibers after the *Seed* attribute has been used, choose no attributes (-), and answer *yes* to the prompted question.

The fiber tracking termination criteria and number of seeds per voxle (default 1) is shown in the DTI tab and can be edited. Hit  to recalculate with new settings. The default fiber tracking termination criteria are: FA < 0.25, turning tract angle (deg) > 41.4 and minimum fiber length 20 mm. Changing the fiber tracking termination criteria here will be the same as chaning them within the DTI settings (see section 4.4 Tracking termination criteria).

3.1.1 Segmented VOI

If you have DTI and BOLD datasets in the same session, *segmented* VOIs based on the BOLD activations can be created. Assigning this with AND will visualize all fibers running through this activation. This is done by first VOI that surrounds the activation, and then pressing *Create segmented VOI*, located under each VOI listed in the *Volume-of-Interest* tool.

3.2 Creating fiber groups

The visualized fibers can be used to create one or multiple fiber groups that can be used to represent different structures/connectivity of interest (see Figure 3). The groups can be used to visualize different fiber connections with different colors, extract various information about the fibers (such as number of fibers, mean FA, ADC etc.), and to export fiber data to DICOM datasets.

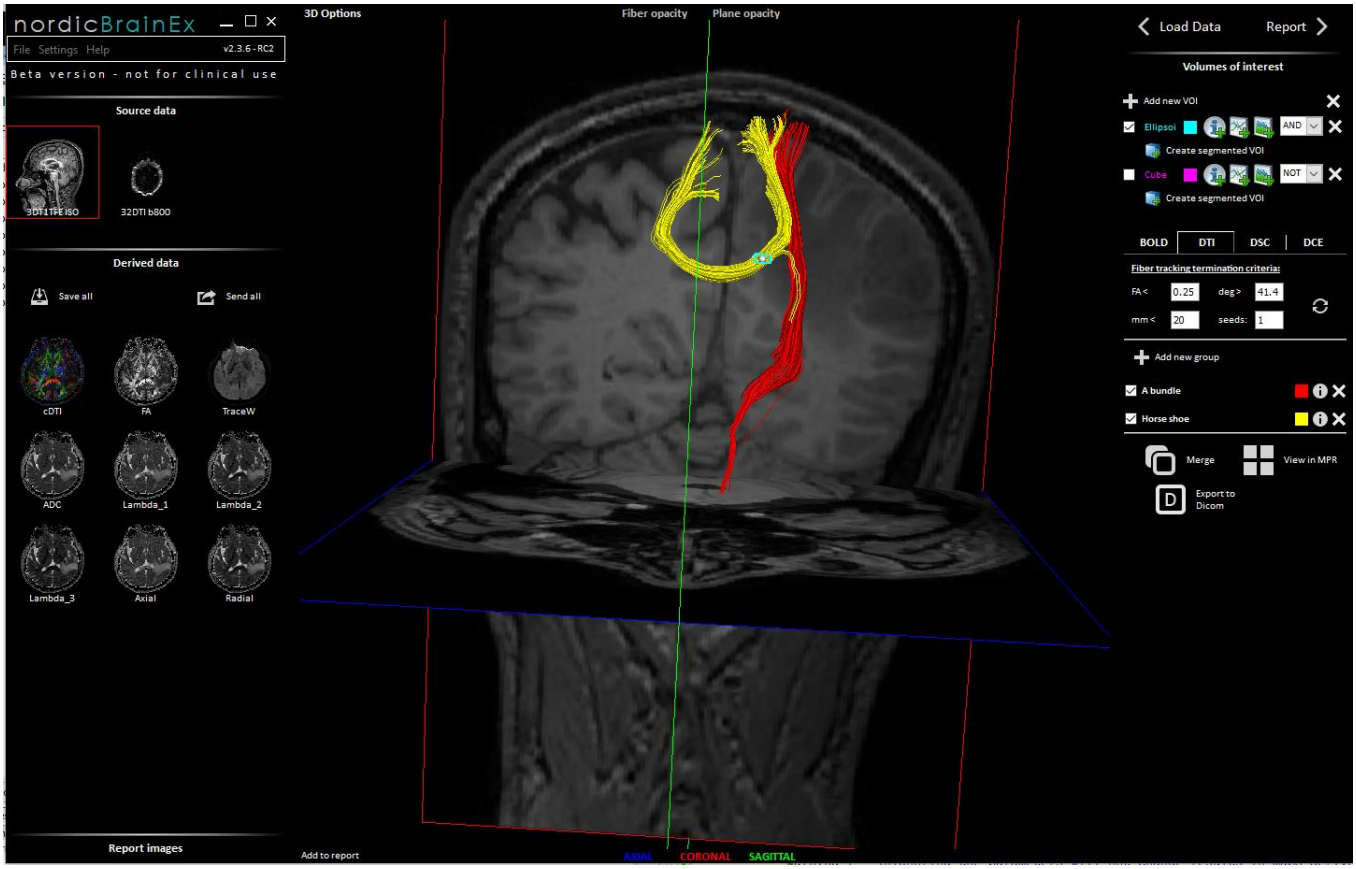

Figure 3: Two fiber groups have been added in the 3D viewer. To maximize the 3D viewer as in this illustration, double click in the 3D viewer.

In order to create a fiber group do as follows:

1. Perform fiber tracking as described in previous section.
2. Apply VOIs with assigned logical operators to select a given fiber structure.
3. Click the *Add new group* button (see Figure 4) to make a group of the current visualized fibers. You will then be prompted to provide a name to the group.

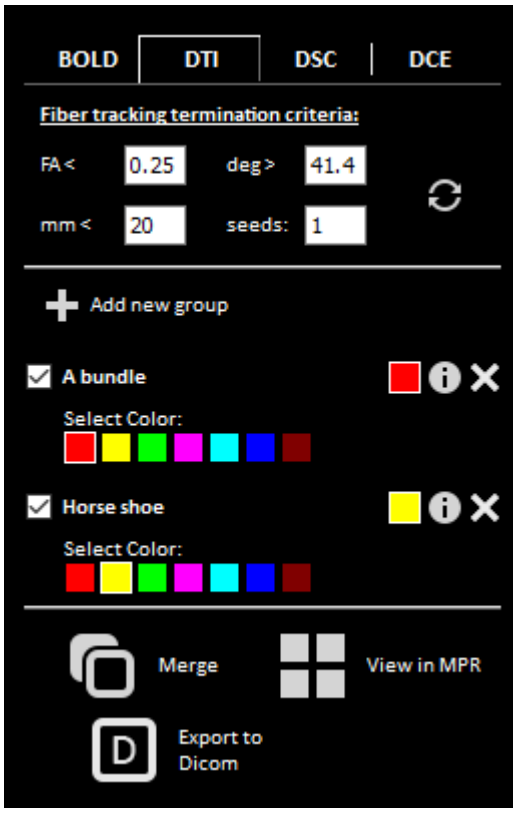

Figure 2: The list of fiber groups is available under the DTI tab in the Visualization interface.

Steps 2 and 3 can be repeated to create multiple groups. Each group will be listed under the *DTI* tab in the interaction panel as illustrated in Figure 4, where the following interactions are available:

- *Add new group* as described above.
- *Click on the color indicator box to change the fiber group color.*
- *Click on the 'i' to list additional information about the fiber group.*
- *Merge* will create an export of the fibers on a format chosen in *Export results as...* under the *Settings* menu in the upper left corner of the *Visualization* interface. The different export formats are suitable for different neuronavigation devices.
  - *Color export*
    The output is a new DICOM image series where the fibers are represented with non-zero pixel values where the fibres cross the image planes. The image geometry is the geometry of the current underlay image series. This DICOM image series can be viewed together with a structural volume on various neuronavigation workstations.
  - *White pixels on greyscale*

The output is a new DICOM image series that is a copy of the underlay series with pixel values at the points of fibre crossing set to the hightest available value, i.e the underlay is merged with the fibers.

– *Vector format*
The output is a file containing the coordinates of the fiber tracts and a header describing the geometry. This allows for the fibers to be visualized in external viewers able to read and interprete this file format. The validity of the visualization of the fibers in an external viewer must be verified by the user of the viewer. For further details about this format, please contact NordicNeuroLab.

The new image series (using *Color export* or *White pixels on greyscale*) can be saved to the local database and sent to remote entities such as PACS or a neuronavigation system. Please note that neither saving to the database, nor sending is done automatically, but must be done by right-clicking on the thumbnail or by selecting *Save all* or *Send all* in the left panel of the interface.

You can choose to apply smoothing to the merged fiber group. Turn on smoothing by selecting this in the Settings menu. If smoothing is turned on, this applies to both the fiber group displayed in MPR, and the merged series.

- Export to Dicom will create a DICOM Tractography Results object, an information entity containing all the fibres with coordinates

- Show in MPR will display the selected grouped fiber as a overlay in the 2D MPR planes. In the *Overlay options* that will show on in the *Interaction* panel on the right, you can change the color palette and opacity of the overlay. You can also choose to visualize the overlay as a checker board with a choice of predefined number of squares.

- Toggle on/off the checkbox located to the left of the group name to show/hide the group's visibility in the 3D viewer.

After adding a fiber group, the fibers in the group will remain visible when you use the Volume-of-Interest tool to select a new fiber structure.

More details on how to work with the 2D and 3D MPR views in nordicBrainEx is described in section 'Visualisation panels and thumbnails' in 'Tutorial – Visualization and Interaction'.

3.3 DTI spike detection

Spike detection is a DTI quality check by visual inspection of the DTI series, which can be performed by the user. The user can exclude those slices or volumes from the analysis which contain spikes. The spike detection is normally done if there are "outliers", i.e. images/slices where the signal-to–noise ratio is low or when the results of the DTI analysis have not induced the expected results. In that case you can have a closer look at the DTI series and exclude spike slices or volumes.

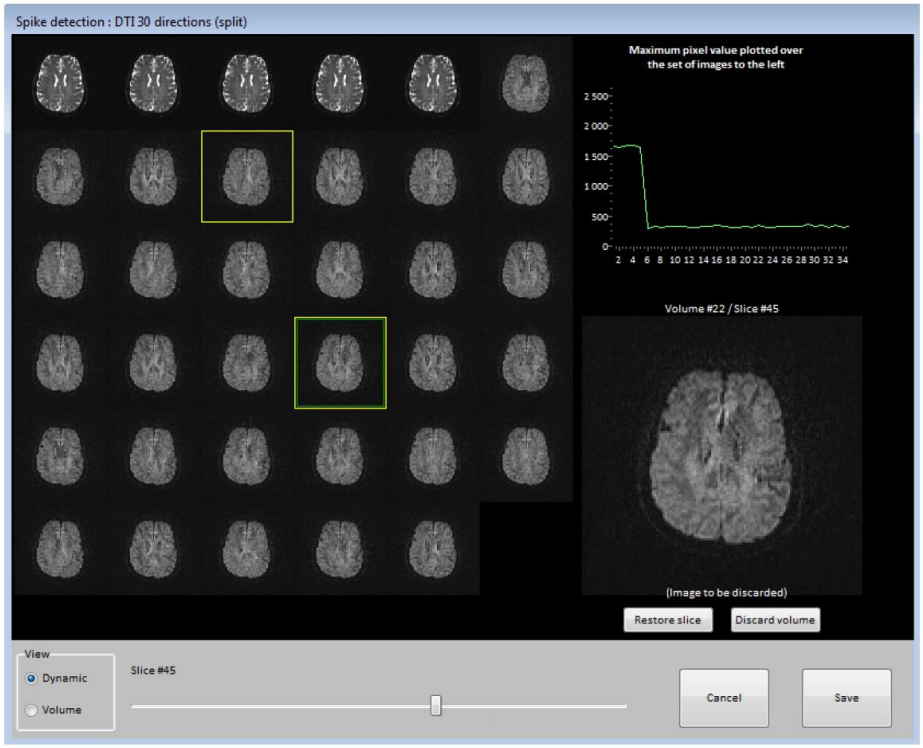

Figure 3: The spike detection interface for DTI in nordicBrainEx. In this example, for each slice there are five B0-images followed by 30 gradient directions with b ≠ 0.

Figure 5 illustrates the spike detection interface. The images/slices in the DTI dataset are displayed by thumbnails, and the *View* controls at the bottom of the page controls how the data are visualized. Select between *Dynamic* or *Volume*, where the former will display all volumes (first the b0-images, then the different gradient directions with b $\neq$ 0) for a given slice and the latter will display all slices in a given volume (first the b0-images, then the different gradient directions with b $\neq$ 0). Use the slider to scroll through the images in the dataset.

The curve in the upper right corner shows the maximum pixel value of all the images to the left. If you have a slice/volume with high pixel values, this can be shown on the curve.

If you have detected a spike slice, click on the slice in order to mark it, and then choose *Discard slice*, or *Discard volume* if you want to discard the entire volume at the specific time point. The following border colors are used in the *Spike detection* interface:

- A *green* border indicates the current slice/volume.

- A *yellow* border indicates that a slice/volume is marked to be discarded.
- A *red* border indicates that this slice/volume has been saved as discarded in a previous session.

Slices/volumes can be restored by choosing *Restore slice* or *Restore volume*. When you have marked all slices/volumes you would like to discard, click on *Save,* see Figure 5. All discarded slices will be excluded from the DTI analysis. Note that you can not discard b0-slices.

3.4 Motion correction results

Right click on the DTI series' thumbnail in the *Data panel* of the *Visualization* interface. Motion and eddy current graphs will be displayed for the chosen series. This option will only be available if motion correction and/or eddy current correction were done as part of the DTI preprocessing steps. You can read more about motion correction and eddy current correction in sections 'Motion correction (BOLD/DTI/DSC)' and 'Eddy current correction (DTI)' in 'Tutorial – Visualization and Interaction'.

3.5 Saving DTI results

There are several different ways of saving the DTI results.

- *Saving the session* can be done by choosing *File -> Save Session*. This will save all output maps, fiber tracts, fiber groups and applied VOIs so that it can be restored in a subsequent session without having to redo the analysis and interaction steps. The session name that you entered will appear in the session table on the *Select patient data* window. Read more about saving sessions in section 'Saving, loading and sending a Session' in 'Tutorial – Handling Image Data'.
- *Send*, accessed by right clicking on a series' thumbnail in the *Data panel* will send the series to a remote entity (for example PACS). Read more about saving sessions in section 'Saving data to database and PACS' in 'Tutorial – Handling Image Data'.
- If choosing *Merge* in the *Interaction panel*, the selected DTI fiber groups overlaid on the structural datasets can be merged into a new DICOM series.
- In the *Slice editor* window, accessed by right clicking on any of the three planes in the MPR, and then choosing *Slice selection* (and clicking on *Slice*) or *Slice all*, slices can be
  - Saved to the database
  - Saved and sent to a remote entity (for example PACS)
  - Added to report
  - Saved as AVI-file
- Similarly, *View slices* can be selected for the derived data (FA-map, ADC, etc.), by right clicking on the series' thumbnail in the *Data panel*, and the *Slice viewer* window as described above will open.

- By right clicking on any of the three planes of the current volume in the MPR, choosing
    - *Create snapshot* will open the *Slice viewer window* of the current slice.
    - *Create snapshot of MPR* will open the *Slice viewer window* of the three current planes of the MPR, as well as the visualized fibers in the 3D viewer.
    - *Copy* will copy the current slice to the clipboard, so it can be pasted into other programs (like word, etc.).
- In the 3D viewer, animations can be made by right clicking in the 3D viewer and choosing *Create snapshots/animations*. This will create a new thumbnail that can be saved, for example as an AVI-file. How to make and save animations are described in more details in 'Tutorial – Visualization and Interaction' in the section 'Interacting with the 3D viewer'.
- *Add to report* (bottom left of any plane in the MPR) can be chosen to add the current slice to Report (see section 'Report' in 'Tutorial – Visualization and Interaction').

4 Details on configuring DTI settings

4.1 Acquisition parameters

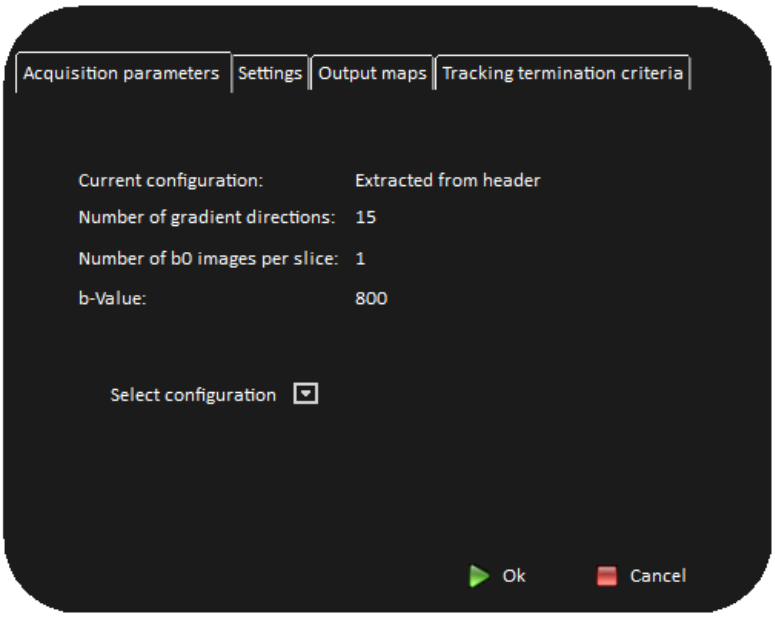

Figure 4: Manual configuration of DTI acquisition parameters.

The acquisition parameters define the imaging protocol settings needed for the DTI analysis (see Figure 7):

- Current configuration

This field indicates which settings are currently being used. When this field reads "Extracted from header" it means that the acquisition parameters are read out from the DICOM header of the input DTI images. Alternatively this may specify a previously user–defined configuration. If the field says 'Not specified' you need to define the parameters manually by clicking on the *Select configuration* button, see below.

- Number of gradient directions
  The number of diffusion gradient directions that were used to acquire the dataset. If the dataset has multiple repetitions, i.e. the same gradient table was applied multiple times during the acquisition, this will also be listed here. In this case you can choose to average across the repetitions prior to the analysis, see 4.2 Settings.

- Number of b0 images per slice
  The number of b=0 images that was used when acquiring the dataset. If there are more than one b=0 image, they will be averaged prior to the analysis.

- Select configuration
  - Choose among previously imported/created gradient configurations in the dropdown.
    - Select. This option will be greyed out for gradient configurations that do not match the current dataset.
    - Edit configuration. Details below.
    - Delete stored gradient configurations.
    - Export. Choose a location and name for the file. This will export the DTI gradients to a text file, as they are shown in the gradient table.
  - Import new gradient configurations from file.

- Assign to similar
  This can be used to automatically assign the current gradient configuration to other similar DTI datasets. New datasets with identical series description, slice count and volume count will be assigned this configuration.

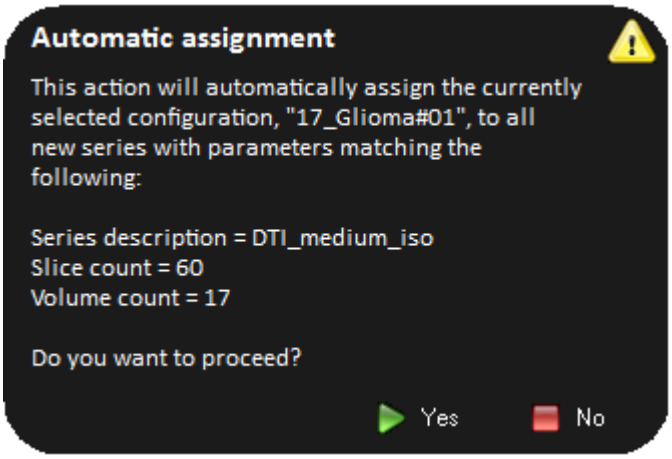

Figure 5: Setting up automatic assignment for matching series.

- Edit configuration

  Click Select configuration, choose a configuration, and press edit to open the Diffusion Gradient Configuration dialog (see Figure 8).

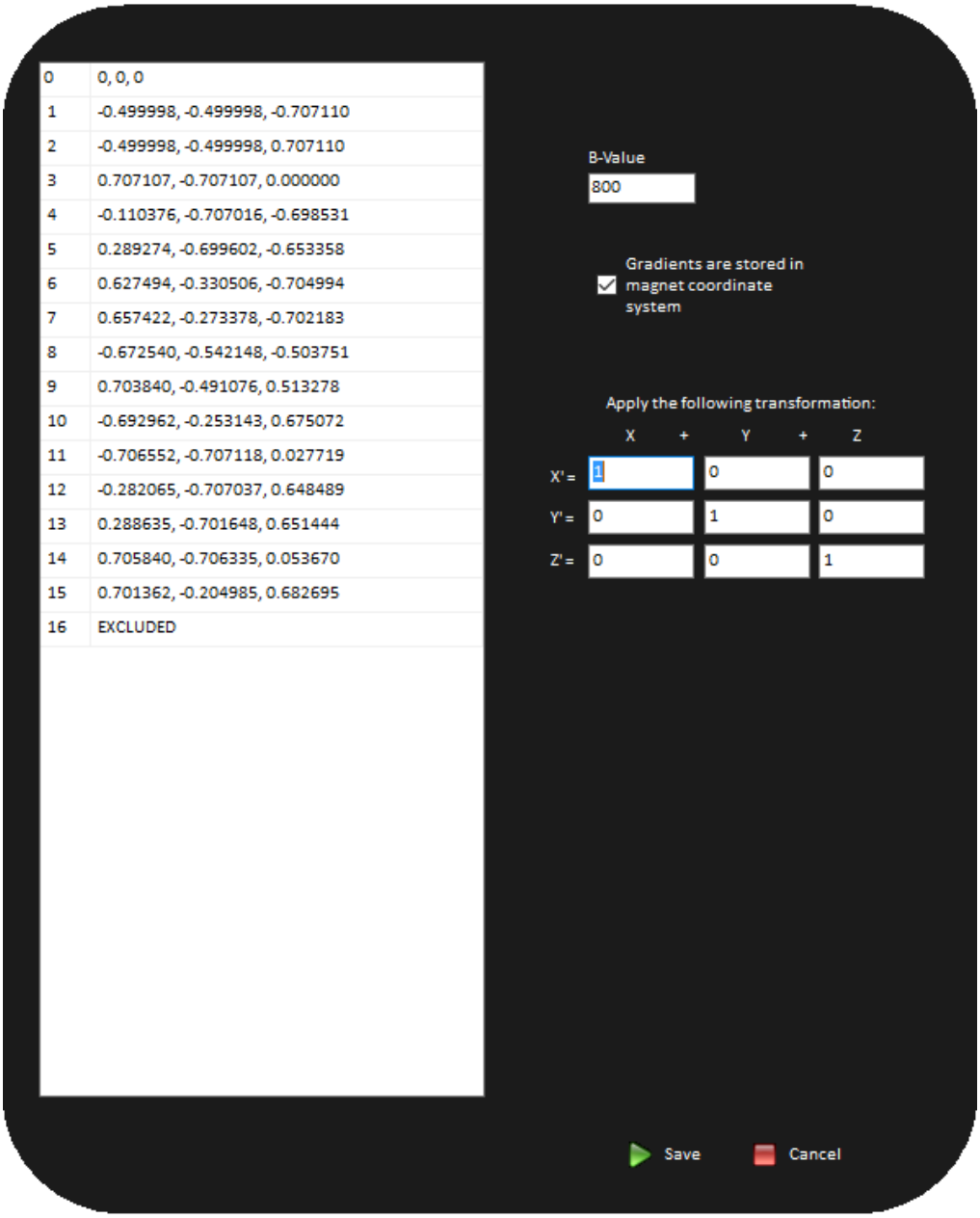

Figure 6: In The Diffusion Gradient Configuration window, diffusion gradient directions can be edited manually. The gradient directions are shown in the white box on the left side.

The *Diffusion Gradient Configuration* window shown in Figure 8 can be used to manually modify the diffusion gradient directions for a given DTI gradient configuration.

The gradient direction table is shown in the white box on the left side. To edit the list, click on the line you want to edit. A small, dotted box will be visualized at the end of the line. Click on this to insert, duplicate, edit or delete entry, or clear the entire table.

Parameters that are available are:

- *B–Value*
  Shown in the upper right corner and can be edited.

- *Gradients are stored in magnet coordinate system*
  Enable this if the diffusion gradients are defined in the magnet system and thus needs to be rotated to the image slice orientation. If the gradients are already defined in a reference system aligned with the in– and through–plane axes, leave this unchecked.

- *Apply the following transformation*
  The transformation that will be applied to the gradient directions prior to the analysis. This can be used to specify the reference frame of which the gradient directions are defined, as this may vary depending of MR vendor and the protocols used. For fiber tracking it is important that the directions are transferred to the image (voxel) coordinate system prior to the analysis. Note that only integer values are valid in these fields, as it is intended to reverse or change axes and not to perform custom rotations/transformations.

4.2 Settings

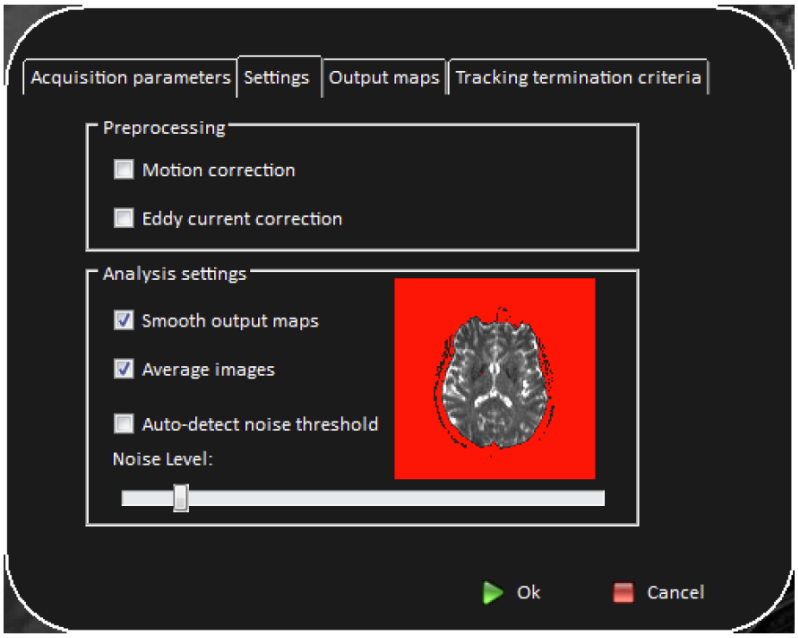

Figure 7: Available settings for the DTI analysis that can be performed in nordicBrainEx.

- The settings (see Figure 8) define what preprocessing steps will be performed before and the settings used when analyzing the DTI data: *Motion correction*

Apply motion correction to the DTI data, see section 'Motion correction (BOLD/DTI/DSC)' in 'Tutorial – Visualization and Interaction'.

- *Eddy current correction*
  Apply eddy current correction to DTI data, see 'Eddy current correction (DTI)' in 'Tutorial – Visualization and Interaction'.

- *Smooth images*
  Apply nearest neighbor smoothing to the output image maps.

- *Average images*
  This option will be applied if the input DTI dataset contains one or more repeated gradient configurations, i.e. the same gradient table were applied multiple times during the acquisition. If checked, the repeated images will be averaged prior to the analysis to improve the signal–to–noise ratio. If not checked, the repeated images will be interpreted as separate additional diffusion weighted images, e.g. if the dataset contains 4 repetitions of an DTI protocol with 30 directions the analysis will be done assuming the dataset has $4 \times 30=120$ directions.

- *Auto–detect noise threshold*
  Toggle on/off whether automatic detection of noise threshold should be done to the data. If checked, the current noise threshold will be estimated automatically. If unchecked, a static threshold will be applied, that can be defined manually by using the Noise Level slider bar.

4.3 Output maps

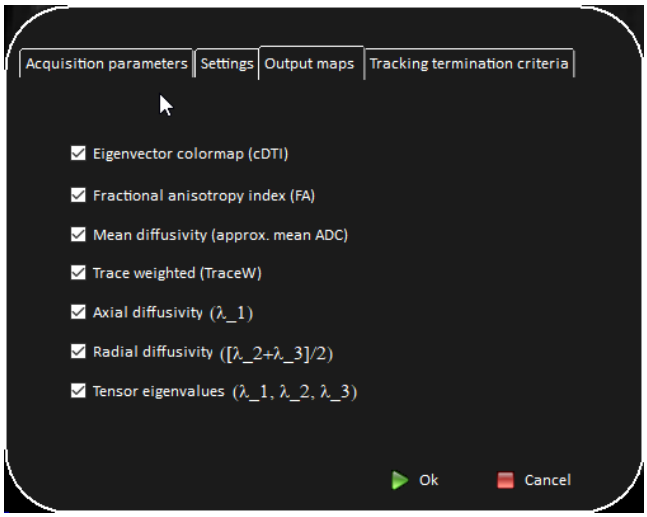

Figure 8: Define which output maps to generate.

The DTI output maps are the available parametric maps representing various attributes of the diffusion tensor (see Figure 8). They can be toggled on/off depending on what maps you want to generate during the analysis.

- *Eigenvector color map (cDTI)*

Generates a diffusion tensor color map (color DTI) where the pixel color reflects the direction of the diffusion tensor in that voxel. The intensity of the colors are scaled with the Fractional Anisotropy (FA) index.

- *Fractional Anisotropy Index (FA)*
  Generates a map reflecting the fractional anisotropy of each voxel. The index range is 0–1. The values are calculated according to

$$\mathrm{FA} = \sqrt{\frac{3}{2}}\sqrt{\frac{(\lambda_1 - \langle\lambda\rangle)^2 + (\lambda_2 - \langle\lambda\rangle)^2 + (\lambda_3 - \langle\lambda\rangle)^2}{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}} \quad (1)$$

  where $\langle\lambda\rangle = (\lambda_1 + \lambda_2 + \lambda_3)/3$

- *Mean diffusivity (ADC)*
  Generates a map reflecting the trace of the diffusion tensor (Tr(D)/3). The mean diffusivity map is scaled so that the pixels are in units of 10^{-5} mm^2/s.

- *Tensor eigenvalues ($\lambda_1, \lambda_2, \lambda_3$)*
  Generates three maps reflecting the individual eigenvalues, $\lambda_1, \lambda_2, \lambda_3$, of the diffusion tensor. The eigenvalues are sorted in descending order, i.e. $\lambda_1 > \lambda_2 > \lambda_3$.

- *Trace Weighted (TraceW)*
  Generates a map reflecting the geometric average of the individual diffusion weighted images. These maps are comparable to orthogonal DWI, and have a contrast reversal as compared to the ADC image.

- *Axial Diffusivity* is the diffusivity along the principal direction of diffusion, i.e. λ_1.

- *Radial Diffusivity* is defined as $\lambda_\perp = \frac{\lambda_2 + \lambda_3}{2}$, a measure of the diffisivity in the plane orthogonal to the prinicipal direction of diffusivity.

4.4 Tracking termination criteria

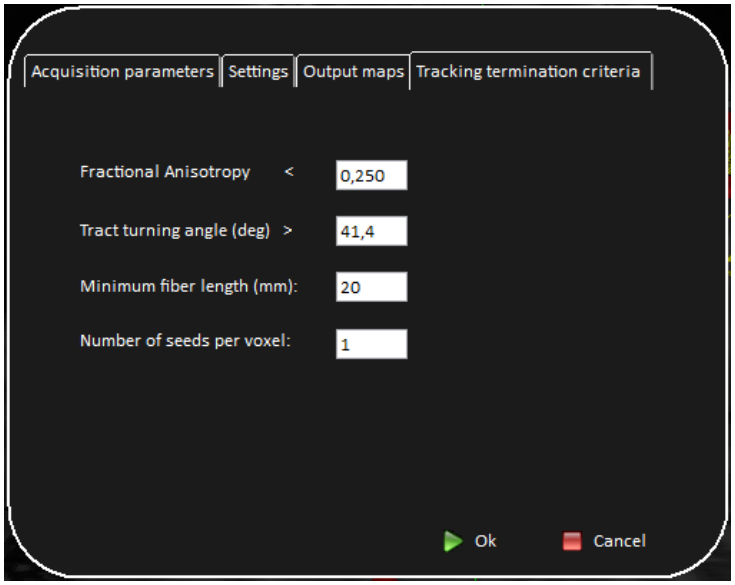

Figure 9: The tracking termination will terminate when it reaches values defined here.

The propagation of fiber tracts must be terminated at some point. The most intuitive termination criterion is the extent of anisotropy. In a low anisotropy region, such as gray matter, there may not be a coherent tract orientation within a pixel and the orientation of the largest principal axis is more sensitive to noise errors. Another vital criterion is the angle change between pixels. For the linear line propagation model being used, large errors occur if the angle transition is large. It is therefore preferable to set a threshold that prohibits a sharp turn during the propagation. Thus the fiber tracking is terminated when it reaches a voxel with where the following conditions apply (see Figure 11):

- *Fractional anisotropy*
  If the FA index of the voxel being propagated to is less than this threshold, tracking of the current tract is terminated.
- *Tract turning angle (deg)*
  If the angle (in degrees) between two successive principal eigenvectors is larger than this threshold, tracking of the current tract is terminated.
- *Minimum fiber length*
  Threshold on the minimum length (in mm) of a reconstructed fiber tract to be kept. This option can be used to suppress very small spurious tracts.
- *Number of seeds per voxel.*
  How many seeds (starting points) are selected per voxel. The default value is 1. For exhaustrive search, the maximum number of seeds is 8, but if tracking from seed, a higher number can be used. If a higher value than 8 is selected for exhaustive search, a warning will be given and the number will be reduced to 2. The reason for this is that doing an exhaustive search of the entire brain with a very high number seeds per voxel will be too comptationaly heavy for the computer.