6 MR FiberTrak

This postprocessing function provides an additional step in the Diffusion package, and is meant to visualize diffusion tensor data in the form of white matter tracts in Diffusion studies.

NOTICE

Visualization of fibers can be used to visualize the white matter structure in the brain. Together with other forms of MRI data it can give a more complete diagnosis.

Valid imaging series

A valid series for the FiberTrak step of Diffusion package is a Diffusion Tensor series containing at least 6 diffusion directions and a minimum of 2 b-values.

Indications for Use

The MR FiberTrak application supports the user with the viewing, processing and analysis of Diffusion Tensor Imaging (DTI) data from MR diffusion imaging and with the creation and visualisation of white matter tracks (or diffusional structure) in the brain and spinal tracts.

User Interface

Screen layout

The MR FiberTrak step of the MR Diffusion package has a default layout of a main viewport with three reference viewports to the right, and a toolbar, and task guidance panels to the left.

Main viewport

The large viewport contains a view of the selected dataset as a combination of three orthogonal slices. Rotating, panning and zooming this view allows viewing of white matter tracts from all angles.

Reference viewports

The small viewports each contain an orthogonal view and serve as reference views (from top to bottom: transverse, coronal, sagittal view). Each of the views is overlaid by colored lines indicating the position of the shown slices. The slices in the main viewport are linked to the slices in the orthogonal views.

300006338791_A/881 * 2021-06-30

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Task Guidance

Similar to all packages on the IntelliSpace portal, also the MR FiberTrak step provides a task guidance panel in the left part of the screen. The task guidance panel provides the following steps:

- Select Underlay & Overlay
- Track Fiber Bundle
- Save Fiber Bundles

The Workflow section later in these Instructions for Use is based on this Task Guidance. For details, see section “Workflow” on page 85.

NOTICE

Follow the steps of the Task Guidance to make optimal use of the FiberTrak function.

Guidance

While you are locating fiber bundles, a guidance panel is optionally available on the right side of the main display area. The guidance panel provides information about locating common fiber bundles. Details of how to use this panel are provided in the following workflow description.

Toolbar

Orientation

Click the arrow next to the **Orientation** tool to display the slices in the main viewport in one of the following predefined orientations:

-  **Axial Feet**
-  **Anterior** (frontal)
-  **Sagittal Left**

View Slices

Click a slice indicator to show or hide any of the following slices in the main viewport:

-  **Transversal Slice**
-  **Coronal Slice**
-  **Sagittal Slice**

3000063387791_A/881 * 2021-06-30

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Layout

Click the arrow next to the **Layout** tool to select one of the following layouts for the main display area:

-  **Layout 1x1**
-  **References at Right**

Each of the reference views displays one orthogonal slice. The other 2 orthogonal slices are represented by lines. The color of the lines indicates the plane of the slice.

In the reference views, you can adjust the position of slices by using the **Plane Position** interactor on the displayed slice, or by dragging the lines of the other slices. The position of the slice is shown in the upper-right corner of each reference view.

The plane of the slice is also shown in the upper-right corner of each reference view, and indicates the direction of fibers perpendicular to the slice.

Fiber Bundle Settings

1. The **Fiber Bundle Settings** dialog box is displayed. You can modify the following settings:
   - Minimum FA
   - Maximum Angle Change
   - Minimum Fiber Length

Optimum settings for the FiberTrak algorithm

It is difficult to define the best settings for tracking fibers. They depend on the quality of the data, the curvature of the expected tracts, and many other qualities of the underlying data. Lowering the FA and enlarging the Angle options will yield more fibers. This should only be done as long as the resulting tracts are shown as a coherent fiber bundle. Erroneous fibers will be shown when these values are too low.

WARNING

When fibertract settings are changed to low values (meaning no signal threshold, very low FA, and very high curvature acceptance) the white matter tracts may include erroneous results.

This may consequently lead to misdiagnoses. It is advised to use default settings whenever possible.

NOTICE

Low SNR in the DTI dataset can influence the results, leading to limited or no tracts.

3000063879l_A/881 * 2021-06-30

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Follow Mouse

You can use the single point fiber tracking, also known as fiber probing.

To probe fibers, move/hover the mouse in the main viewer.

A fiber strand is displayed for the voxel at the current pointer position in the main viewer. Statistical values of the fiber strand are displayed beneath the main viewer (coordinates, fractional anisotropy (FA), and apparent diffusion coefficient (ADC)).

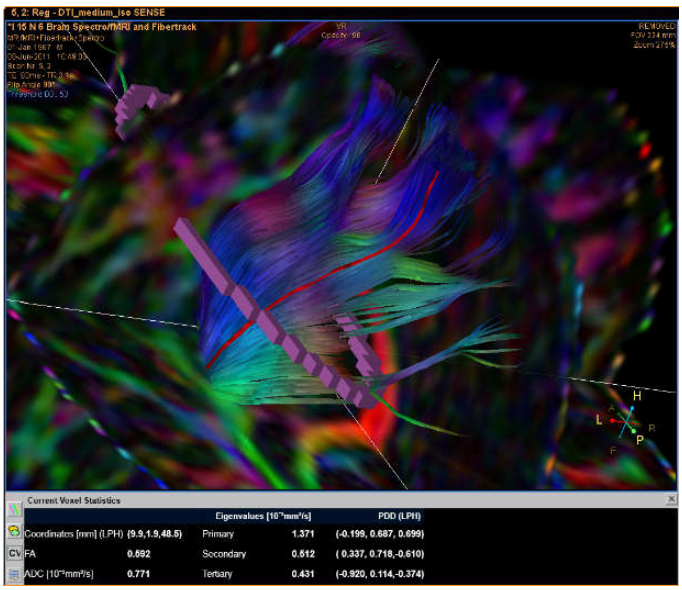

Fig. 37: Fiber probing with the Follow Mouse function

Single ROI in high density

An alternative fiber tracking algorithm uses neighbor voxels (high density) when tracking fibers with a single ROI. The default fiber tracking algorithm does not use neighbor voxels.

Tracking fibers with high density turned on is beneficial if you plan to exclude sections of the fiber bundle using an "exclude" ROI. In this case, turning on the option **Single ROI in high density**provides more consistent results.

NOTICE

This option is for use when tracking fibers with a single ROI only. If you track fibers with multiple ROIs, the default fiber tracking algorithm is recommended.

Delete From Guidance

You can use the **More** menu to delete a fiber bundle from the guidance panel.

1. Click the arrow besides **More**.
2. Click **Delete From Guidance** in the **More** menu.

⇨ The **Delete Fiber Bundles From Guidance** dialog box is displayed.

300006338791_A/881 * 2021-06-30

3. Select the fiber bundles that you want to delete and click **Delete**.

More Functions within the FiberTrak step

In IntelliSpace Portal MR packages, the most important functions can be performed via the Task Guidance and the toolbar. However there are more functions which you can access via the right mouse menus.

For more information, see section “Right mouse menus” on page 12.

Workflow

Launch the MR FiberTrak step from the MR Diffusion package

▷ In the 'Directory' tab of the activity bar:

1. Select a suitable diffusion series.

2. Click 'MR Diffusion'.

   The MR Diffusion package opens.

3. Click the right arrow in the MR Diffusion title panel.

⇨ The MR FiberTrak step opens.

Select Underlay & Overlay

In this step of the FiberTrack process you can select an underlay and an overlay, if desired.

1. To select an underlay, select the check box next to the underlay selector in the task guidance panel.

⇨ A list of available underlays is displayed.

2. Select an underlay from the list, or click **Select Anatomical Series** at the top of the list.

⇨ If you clicked **Select Anatomical Series**, a dialog box is displayed with available anatomical underlays. Select an anatomical underlay and click **OK**. The anatomical series is automatically co-registered with the diffusion input series.

⇨ When used, an underlay adds additional anatomical information to the slices in the main display area.

3. To select an overlay, select the check box next to the overlay selector in the task guidance panel.
4. Select an overlay from the list, or click **fMRI Statistical Parametric Maps** at the top of the list.

⇨ **FA Directional overlay**: The colors used in a directional map indicate the direction of diffusion:

- Blue: head and feet
- Green: anterior and posterior

3000063879l_A/881 * 2021-06-30

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- Red: right and left

⇨ If you clicked **fMRI Statistical Parametric Maps**, a dialog box is displayed with available fMRI maps. Select a map and click **OK**. The map is automatically co-registered with the diffusion input series.

Track Fiber Bundle

In this step of the FiberTrack process you draw ROIs in the main display area to track fiber bundles. A guidance panel is optionally available to help you locate and identify common fiber bundles.

Using the Guidance Panel

1. To display the guidance panel, select **Use guidance** in the task guidance panel.

⇨ The guidance panel is displayed on the right side of the main display area. It provides information about specific fiber bundles.

2. To show guidance for a different fiber bundle, click the fiber bundle name at the top of the guidance panel and select a fiber bundle from the list.
3. The guidance panel can be collapsed or expanded, to accommodate your workflow requirements.

⇨ In expanded mode, all text and image guidance panel for the selected fiber bundle is displayed in one scrollable panel.

- Click  to collapse the guidance panel.

⇨ In collapsed mode, the guidance panel displays only images to indicate the location of the ROIs to track that fiber bundle.

- Click  to view the text guidance associated with the currently displayed image.

⇨ Images are displayed in sequence, according to the actions needed to locate and identify a fiber bundle. Pause the pointer at the bottom edge of the guidance panel to display thumbnails of the images in the sequence, and then click an image thumbnail to display the image.

- Click  to expand the guidance panel.

Tracking a fiber bundle

1. Manipulate the slices in the main display area to display the location of the start of the fiber bundle.

   To manipulate the slices, you can use the following tools in the right mouse menu:

   - **Plane Position**
   - **Pan**
   - **Zoom**
   - **Roll/Rotate**

- **Gray Level**
- **Threshold**
- **Plane Opacity**

2. To change the position of a slice, you can also use the reference views: use the **Plane Position** interactor on the displayed slice, or by drag the lines of the other slices.
3. To display a predefined orientation, select an orientation using the **Orientation** tool in the toolbar.

   You can also select a predefined orientations using the **Switch To View** command in the right mouse menu.
4. To hide or show a slice, click one of the **View Slices** buttons in the toolbar.

   You can also hide or show slices using the **View Slices** command in the right mouse menu.
5. When the location of the fiber bundle is displayed, click one of the ROI tools in the task guidance panel.
   - **Multi ROI Manual Tracking**: This tool allows you to identify multiple ROIs and then manually start tracking them.
   - **Single ROI Auto Tracking**: This tool allows you to identify a single ROI and track it automatically.

6. If the selected ROI tool does not display the type of ROI that you want to use, click the down arrow next to the tool and select one of the following ROI tools:
   -  **Smoothed Polygon**
   -  **Ellipse**
   -  **Freehand Contour**
   -  **Seed 2D**
   -  **Seed 3D**
7. Create an ROI at the location of the fiber bundle.

   To create an ROI using the polygon, ellipse, or contour tool, select the tool and do the following:

   To create an ROI using one of the seed tools, select the tool and then click at the location of the fiber bundle.
   - Click at the edge of the fiber bundle location.
   - Move the pointer and click around the edge of the fiber bundle location.
   - Double-click to complete the ROI.

⇨ If you used **Single ROI Auto Tracking**, the ROI is automatically tracked. If you are manually tracking multiple ROIs, continue with this procedure.

8. If desired, you can remove the last drawn ROI. Do one of the following:
   - Press Ctrl+Z.
   - Right-click the ROI and then click **Delete Last Drawn ROI** in the shortcut menu.
9. If desired, modify the shape of the ROI by pausing the pointer over the edge of the ROI and then dragging.
10. To create another ROI, do the following:
    - Manipulate the slices to display the next location that the fiber bundle passes through.
    - Click the ROI tool in the task guidance panel again.
    - Draw the next ROI.
11. When you have finished drawing ROIs, click **Track** in the Track Fibers task guidance panel to track the fiber bundle.

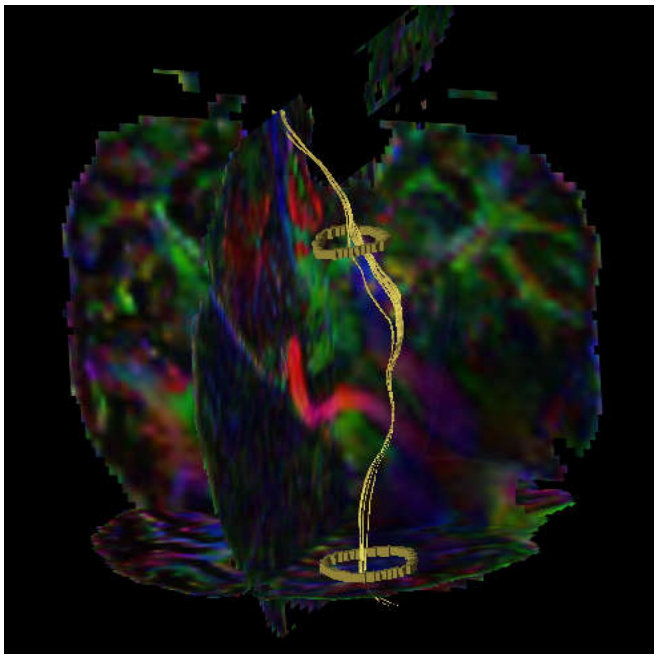

Fig. 38: Tracked fiber bundle

⇨ The tracked fiber bundle is displayed.

Modifying the current fiber bundle

After creating a fiber bundle, you can edit it, or modify its appearance.

1. Right-click the current fiber bundle and then select an option from the shortcut menu.
   - **Edit**

     Use this option to modify or add ROIs.
   - **Hide**

     Use this option to hide the ROI in the display. You can show the ROI again at a later stage using the **Manage Fibers and ROIs** panel in the task guidance panel.
   - **Show ROIs**

300006338791_A/881 * 2021-06-30

- **Use Directional Color**
- **Color**

  Select a color from the submenu. This option is not available if **Use Directional Color** is selected.
- **Delete**
- **Edit settings**

  This option displays the **Fiber Bundle Settings** dialog box, which you can use to set configuration options for the fiber bundle.
- **Rename**

Managing fiber bundles

You can manage fiber bundles that you have created using the **Manage Fibers and ROIs** panel in the task guidance panel.

1. Click the down arrows in the task guidance panel.

   ⇨ The **Manage Fibers and ROIs** panel is displayed. This panel contains color-coded entries for each fiber bundle and associated ROIs that you have tracked.
2. To view the ROIs associated with a fiber bundle, click the plus sign (+) next to the fiber bundle.
3. To display a fiber bundle or ROI in the main display area, click the item in the **Manage Fibers and ROIs** panel.
4. To turn the visibility of a fiber bundle or an ROI on or off, select or clear the check box next to the item.
5. To rename a fiber bundle or an ROI, right-click the item, click **Rename**, and then enter a new name.
6. To delete a fiber bundle (and associated ROIs), right-click the fiber bundle and then click **Delete**.
7. To delete an ROI without deleting the fiber bundle, right-click the ROI and then click **Delete**.
8. To exclude an ROI from the calculation of the fiber bundle track, right-click the ROI and then click **Exclude**.

   The ROI is not deleted, but it is marked as 'excluded', and the fibers contained in the ROI are not included in the tracked fiber bundle.
9. To include an ROI that you have previously excluded, right-click the ROI and then click **Include**.
10. To change the color of a fiber bundle, right-click the fiber bundle and select one of the following options:
    - **Use Directional Color**
    - Select a custom color from the **Color** submenu.
11. To add another ROI to a tracked fiber bundle, do the following:

- Select the fiber bundle and click **Edit** in the task guidance panel, or right-click the fiber bundle and click **Edit**.
- Manipulate the slices to locate the desired position of the ROI.
- Draw the ROI.
- In the task guidance panel, click **Track**.

Excluding fibers

You can explicitly exclude some fibers from a tracked fiber bundle.

1. Select the fiber bundle and click **Edit** in the task guidance panel, or right-click the fiber bundle and click **Edit**.
2. Manipulate the slices in the main display area to display the location of the fibers that you want to exclude.
3. Select an ROI tool in the task guidance panel.
4. Draw an ROI around the location of the fibers that you want to exclude, and double-click to complete the ROI.
5. Right-click the ROI and click **Exclude**.
6. Click **Track** in the task guidance panel to track the fiber bundle.

⇨ All fibers in the new ROI are excluded from the tracked fiber bundle.

Save Fiber Bundles

In this step of the FiberTrak process you can save fiber bundles with the series for review in MultiModality Viewer.

1. Ensure that the fiber bundles that you want to save are displayed.

2. Click **Save Fiber Bundles**.

Fiber Statistics

1. To show statistics about fibers and ROIs that you have created, click **Show Statistics**.

⇨ The statistics panel is displayed below the main viewport.

2. Click **Show Fiber Statistics** to display details of fibers.

3. Click **Show ROI Statistics** to display details of ROIs.

4. To export the statistics for fibers and ROIs, click **Export**, and then save the statistics file using the **Save As** dialog box..

⇨ The statistics file is saved in CSV format, which can be opened in a spreadsheet application.

5. To close the statistics panel, click the **Close** button in the panel's title bar.

3000063387791_A/881 * 2021-06-30

Co-Registration Inspection

When co-registration is performed, you should verify the accuracy of the registration. You can inspect and edit the registration using the **Inspect/Correct Data Alignment** step.

NOTICE

If you edit the registration and save your adjustments, all computed results are deleted.

1. Click **Manual Alignment** in the toolbar to open the **Inspect/Correct Data Alignment** step.
   ⇨ The input series and the reference series are displayed as fusion views in three orthogonal orientations. You can change the orientation of the view, if desired.
   ⇨ The initial alignment is calculated using the **Normalized Mutual Information** algorithm.
2. To change the alignment algorithm, select an option from the drop-down list in the task guidance panel.
3. You can make the following manual adjustments to the registration using tools in the task guidance panel:
   - **Translation Tools**: Click an arrow to nudge the registration in the corresponding direction, or use the **Translate** tool  to move the registration manually.
   - **Rotation Tools**: Click an arrow to rotate the registration clockwise or counter-clockwise, or use the **Rotate** tool  to rotate the registration manually.

4. To undo an adjustment, click **Undo**.

5. To reapply an adjustment that you have undone, click **Redo**.

6. To reset the registration to the original position, click **Reset All Alignment**.
7. To save the registration and continue with the analysis, click **Save**.
8. To ignore the changes, click **Cancel**.

WARNING

Alignment between functional and anatomical series should be inspected and corrected using the registration inspection step in IViewBOLD and FiberTrack.

Creating and Saving Batches/Saving in Surgical Navigation Format

You can create a batch of images and export to surgical navigation from a volume using the Batch/export to surgical navigation option in the Task panel.

The following batch types can be created:

Parallel: Creates a set of parallel slabs, in the current orientation of the slab displayed in the main image.

Freestyle: Creates a freestyle batch based on user-defined key-frames.

Creating a parallel batch

1. Select the **Batch/export to surgical navigation** icon (or via the **Batch** dropdown in the Task guidance panel.)

2. Select viewport in the viewing area and click **Parallel**.

3. Navigate to the start point in the view and click **Start**.

4. Navigate to the end point in the view and click **End**.
5. If desired, select **Axial**, **Sagittal** or **Coronal** batch preset to create a parallel batch covering the entire volume.
6. If desired, modify the batch properties:
   - **Nr Images**: Number of images to be generated.
   - **Increment**: The incremental step size in terms of the distance between the centers of the slabs. Initially this is equal to the current slab thickness of the image in the viewport.
   - **Thickness**: The slab thickness of the images to be generated. This is always equal to the current slab thickness of the image in the view. This helps in previewing the quality of the final result.

⇨ The effect of the selected range is visible by means of reference lines in the reference images indicating the positions of the images that are to be generated.

⇨ The number of images and the incremental step size are linked. For example, increasing the number of images decreases the incremental step size, keeping the distance between the center of the first slab and the last slab constant.

7. To preview the batch, do one of the following:
   -  Click **Play/Stop** to preview the batch automatically.
   -  Click **Batch scroll interactor** to scroll through the batch manually.
   - **Clear batch** is used for resetting the parameters for all kinds of batches, including parallel, radial and freestyle.

300006338791_A/881 * 2021-06-30

Creating a freestyle batch

1. Select the **Batch/export to surgical navigation** icon (or via the **Batch** dropdown in the Task guidance panel.)

2. Click **Freestyle**.

3. Navigate to the start point in the view and click **Add Key-frame**.

4. Manipulate the view to display the next point that you want to capture in the batch and click **Add Key-frame** again.

5. Optional step: To remove the last Key-frame that you added, click **Remove last Key-frame**.
6. Continue to add Key-frames as desired.

7. To remove all Key-frames and start over, click **Remove all Key-frames**.

NOTICE

When creating a freestyle batch, reference lines of batch image positions are not displayed.

8. To preview the batch, do one of the following:
   -  Click **Play/Stop** to preview the batch automatically.
   -  Click **Batch scroll interactor** to scroll through the batch manually.
9. To adjust the speed of the move, drag the slider between **Slow** and **Fast**.
10. Enter a number in the **Playing time** box (measured in seconds) to set the duration of the movie.
11. Choose between setting a number of frames per second, or setting a total number of frames for the movie.

NOTICE

The speed and duration of the movie, and the number of images used are linked, and as you change one parameter, the other parameters are adjusted to achieve the requested result. Select one parameter that you wish to define and allow the application to configure the other parameters.

3000063879l_A/881 * 2021-06-30

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Saving a batch

1. To save the batch, click **Save Batch As** in the Common tools panel.
2. The **Save Batch As** dialog is displayed, allowing you to select a file name, file format, and destination. You can save the series in DICOM format, or in non-DICOM format. If you select a non-DICOM format, you can additionally select a file system destination for exporting.
3. When saving the batch in Movie format, the following settings are available:
   - **Quality**: drag the slider between **Low** or **High**. The higher the quality, the larger the size of the saved movie file.
   - **De-identify**: When selected, the De-identify Patient dialog box is displayed, allowing you to manually typing new patient details (this function removes patient information before saving the movie).
4. Click **Save**.

⇨ The batch is automatically previewed once in the main display area before it is saved.

Saving to Surgical Nav. Format for MR Data

You can save 3D anatomical volumes, fibers and SPM's (Statistical Parameter Maps) from the MR FiberTrak application in surgical nav. format for surgery systems for review, preparation, and navigation during surgical interventions.

The following MR data types can be saved to surgical nav. format:

- Routine MR anatomical data (DICOM data)
- fMRI results (activation areas) as generated by the iViewBOLD package in IntelliSpace Portal
- White matter tracts (also called "fibers") as generated by the Diffusion Package in IntelliSpace Portal

NOTICE

Saving images in ‘Surgical navigation format’ is possible only if the source DTI sequence is aligned / registered with the selected (Anatomical) underlay.

1. Select the data that you want to save to surgical nav. format.

⇨ If a user-defined batch is not available, a parallel batch covering the entire volume is automatically generated. The number of slices, the slice thickness and the orientation of the batch are the same as the anatomical data.

⇨ Alternatively, you can create a batch and define the parameters according to your needs.

2. Click to **Save to Surgical Nav. Format** in the Common tools panel to display the **Save to Surgical Nav. Format** dialog box.
3. Enter a **Description** for the saved data, if desired (to a maximum of 64 characters).

3000063387791_A/881 * 2021-06-30

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⇨ A description is provided by default based on the type of data being saved.

4. Select the Options to apply to the saved data:
   - **Combine Data**: Results are combined (for example, underlay, overlay, maps, and fibers). This option is useful if the surgery system that you are exporting to does not support fusion. (Fused images can be saved if they meet the export requirements, for example: an MR series overlaid with another MR series.)
     - **Apply Transparency**: Selecting this option saves fibers and fMRI activation areas with transparency, so that they can be used as overlays on corresponding (co-registered) anatomical images on the surgery system. If this option is not selected, overlay data is opaque.
   - **Separate Data**: Results are saved as separate series. Gray values for fMRI are preserved (but they are converted to standard MR data). For fibers and segmentations, the maximum gray value is used. This option is useful if the surgery system that you are exporting to supports fusion. Each object is stored with a different gray value, which maps to a specific color during fusion. Additionally, positive and negative activation (if available) in the SPM map are saved as separate objects, so that they can be easily distinguished on the surgery system.

⇨ The saved data can be exported to the following surgery systems:

- Stealth Navigation (Medtronic)
- iNtellect Cranial (Stryker)
- VectorVision (BrainLAB)

3000063879l_A/881 * 2021-06-30

WARNING

When using the “Saving to Surgical Nav. Format for MR Data” option, there is a remote possibility that even with all registration steps being performed on the fused images (fMRI maps or Fiber Tracks aligned to anatomical images), there is still a residual misalignment which may be introduced due to small patient motion during the acquisition of the images. This may result in inaccurate information for surgical planning and it is recommended for the surgery planning review board to inspect the results.

Click **Back to MR FiberTrack** to return to **Track Fibers** stage.

300006338791_A/881 * 2021-06-30

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