

DTI Pre-processor User Guide

INTRODUCTION

OVERVIEW

The DTI Pre-processor is a graphical user interface (GUI) intended for basic pre-processing of diffusion MRI data.

The processing steps available are based on FSL's recommended DTI processing pipeline and call on FSL functions for execution. These steps are brain extraction (*bet*), artifact correction (*topup*, *eddy*), Bayesian estimation of diffusion parameters (*bedpostx*), creation of registration matrices (*flirt*, *covert_xfm*), diffusion tensor fitting (*dtifit*), binary mask creation, and probabilistic tractography (*probtrackx*).

The results of brain extraction, artifact correction, diffusion tensor fitting, mask creation, and probabilistic tractography are loaded into a viewer upon completion. This viewer facilitates visualization of three and four-dimensional images. The user can interact immediately with the results of each pre-processing step, viewed in consistent display orientations, and proceed easily from one step to the next.

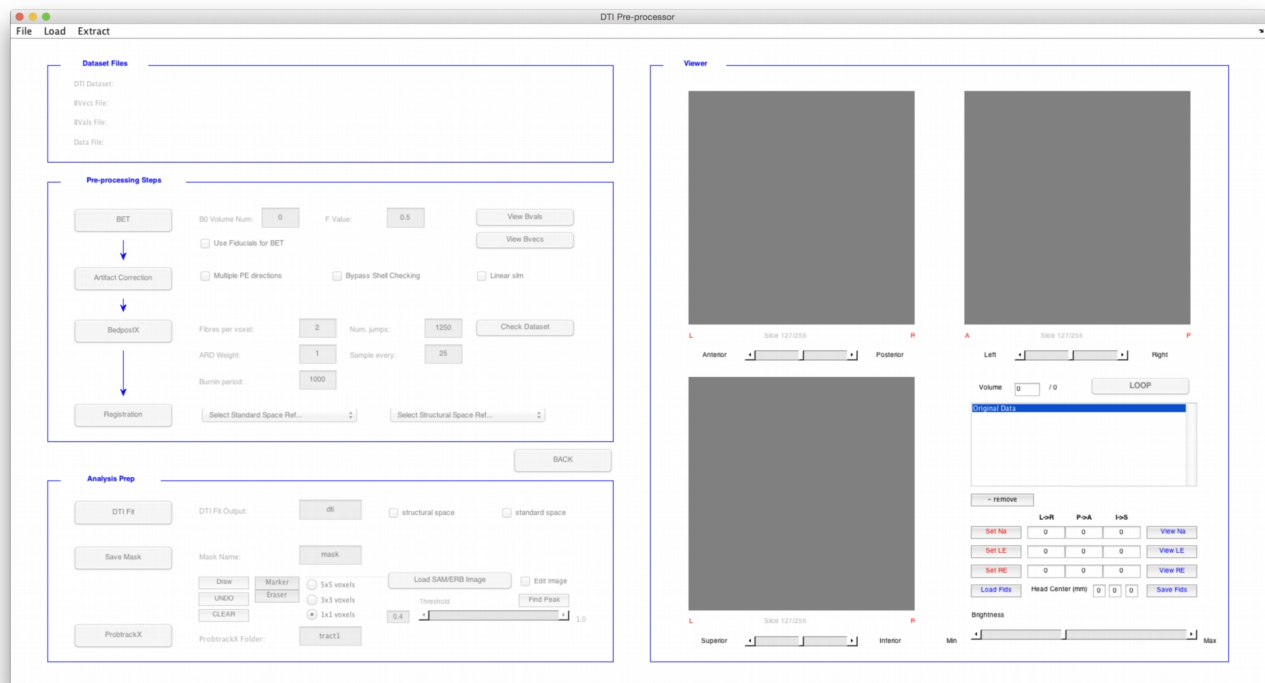
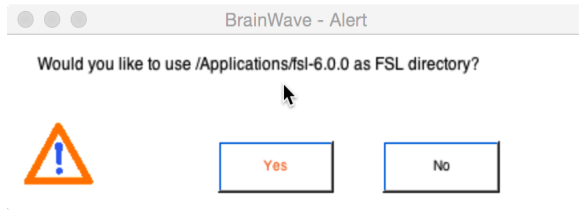


TABLE OF CONTENTS

Introduction.....	0
FSL Versions.....	3
Getting Started.....	3
Pre-processing Steps.....	4
Brain Extraction.....	4
Artifact Correction.....	5
BedpostX.....	7
Registration.....	8
Analysis Prep.....	9
DTI Fit.....	9
Mask Creation.....	10
Probabilistic Tractography.....	12
Viewer.....	14
3-Slice Viewer.....	14
Volume Editor & Loop Button.....	15
File Listbox.....	15
Fiducial Editor.....	15
Expanded Slice Viewer.....	16
Other Capabilities.....	17
Back Button.....	17
Load Menu.....	17
Extract Menu.....	17
FSL Referencing Note.....	18
References.....	18

FSL VERSIONS



Before the DTI Pre-processor opens, the user is prompted to locate FSL's installation location. The version of FSL used affects the options available for artifact correction.

Version 5.0.10 and earlier:

- *Eddy_correct* is used for eddy current and subject motion artifact correction.

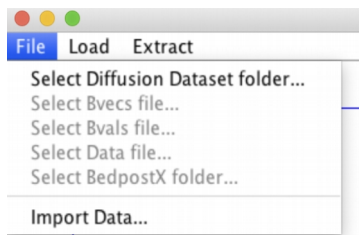
Version 5.0.11 and later:

- *Eddy* is used for eddy current and subject motion artifact correction.
- Shell checking can be bypassed when *eddy* is run (see Pre-processing Steps).
- Linear second level model can be used in *eddy* (see Pre-processing Steps).

Version 6.0.0 and later:

- *Topup* is available for susceptibility-induced artifact correction.

GETTING STARTED



The DTI Pre-processor takes input in either of two ways:

- 1) A diffusion dataset folder containing a diffusion-weighted image file (NIfTI format), a diffusion direction (b-vector) text file, and a b-value text file.
- 2) A folder containing diffusion weighted images in DICOM format (*.dcm or *.IMA files).

DICOM images must be imported into the Pre-processor first (**File -> Import Data**). Importing converts the images to NIfTI format and saves b-vectors, b-values, and acquisition parameters in separate text files. If the images are unsorted, importing the data will sort them and prompt the user to select the diffusion series.

If *bedpostx* was already run on the selected data, there is an option to skip brain extraction, artifact correction, and bedpostX by loading the *bedpostx* output folder (**File -> Select BedpostX folder**).

PRE-PROCESSING STEPS

Pre-processing Steps

BET

↓

Artifact Correction

↓

BedpostX

↓

Registration

B0 Volume Num: 0

F Value: 0.5

☐ Use Fiducials for BET

☐ Multiple PE directions

☐ Bypass Shell Checking

☐ Linear slm

Fibres per voxel: 2

Num. jumps: 1250

ARD Weight: 1

Sample every: 25

Burnin period: 1000

Select Standard Space Ref...

Select Structural Space Ref...

Check Dataset

View Bvals

View Bvecs

BACK

BRAIN EXTRACTION

BET

↓

B0 Volume Num: 0

F Value: 0.5

☐ Use Fiducials for BET

View Bvals

View Bvecs

Brain extraction is executed by FSL's *bet* function, and is run on a b0 volume selected by the user. The result is used in later processing steps.

After *bet* has run, the extracted brain outline is shown in the Viewer. A few attempts may be required to achieve a satisfactory brain extraction.

Options

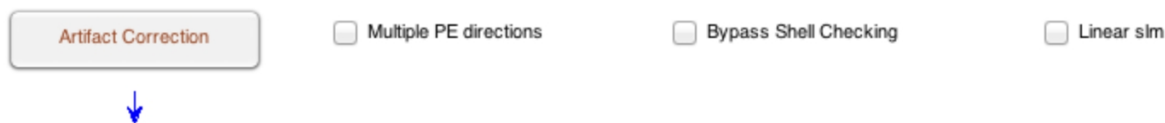
- **B0 Volume Num:** volume number of a b-value=0 image from the original diffusion-weighted data. *bet* is run on this volume.
B0 volumes can be identified visually in the original data or by viewing the b-values (**View Bvals** button).
- **F Value:** fractional intensity threshold. Default is 0.5. Values greater than 0.5 decrease the size of the extracted brain and smaller values increase the size.
- **Use Fiducials for BET:** if selected, the fiducials specified in the Viewer section (see Viewer) are used to calculate a center-of-gravity value used in brain extraction.

- View Bvals: if button is pressed, the b-values of each diffusion-weighted image are displayed under the corresponding volume numbers.
- View Bvecs: if button is pressed, the end points of all b-vectors are plotted in a rotating 3D figure. This figure allows visualization of the diffusion-weighting directions used during acquisition.

Required Files

- Diffusion-weighted images containing the specified b0 volume ('Original Data')
- B-value file and b-vector file

ARTIFACT CORRECTION



During Artifact Correction, eddy current, subject motion, and susceptibility-induced artifacts can be corrected using FSL's *eddy* (or *eddy_correct*) and *topup* functions.

The artifact-corrected images are loaded into the Viewer.

Options

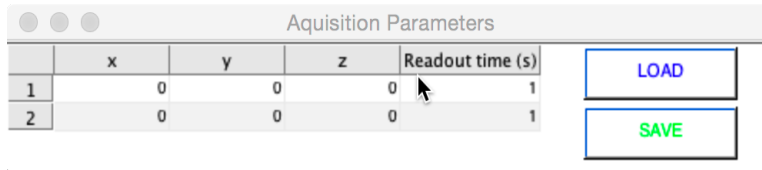
- Multiple PE directions: if selected, *topup* is run before *eddy* to help correct susceptibility-induced distortions. Diffusion-weighted images must have been acquired with multiple phase-encoding directions. Enabled for FSL versions 6.0.0 and greater only.
- Bypass Shell Checking: if selected, *eddy* does not verify whether the data is shelled. This is occasionally necessary for data collected with small b-values and few diffusion directions. Enabled for FSL versions 5.0.11 and greater only.
- Linear slm: if selected, *eddy* uses a linear second level model. This is recommended when data was collected with few directions or not on a whole sphere.

Required Files

- Diffusion-weighted images to be corrected ('Original Data')
- Brain mask (output of BET step)
- B-vector file and b-value file

- If FSL version is 5.0.11 or greater:

- Acquisition parameters file. Can be created or loaded from a previously created file (e.g. If imported DICOM images). The following prompt appears when Artifact Correction is run.

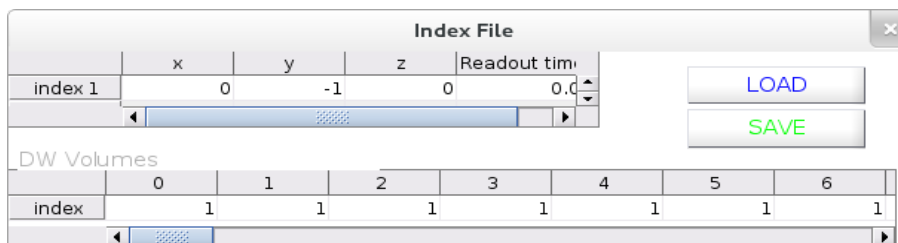


	x	y	z	Readout time (s)
1	0	0	0	1
2	0	0	0	1

Each row in the file describes the acquisition parameters used for at least one volume of the diffusion images. The parameters included are phase-encoding direction (x,y,z) and total readout time.

If more than two rows are necessary, create file beforehand and load it in when prompted.

- Index file. Maps each volume of the diffusion-weighted images (columns in the index file) to a row of the acquisition parameters file (value in each column). The following prompt appears when Artifact Correction is run. The acquisition parameters file is displayed as well for reference.



	x	y	z	Readout time
index 1	0	-1	0	0.0

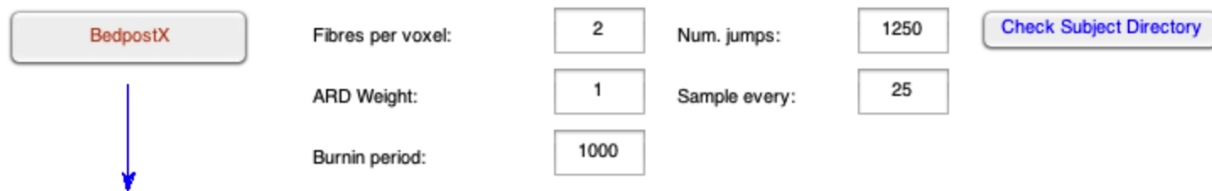
	0	1	2	3	4	5	6
index	1	1	1	1	1	1	1

Can be created or loaded from a previously created file (e.g. If imported DICOM images).

- If **Multiple PE directions** is selected:

- B0 image(s) collected with different acquisition parameters than the b0 volume used in brain extraction step. User is prompted to select image(s) when Artifact Correction is run.
- Text file with chosen *topup* parameters (default is FSLDIR/etc/flirtsch/b02b0.cnf). User is prompted to select file when Artifact Correction is run.
- Acquisition parameters file (as described above).

BEDPOSTX



BedpostX

Fibres per voxel: 2

ARD Weight: 1

Burnin period: 1000

Num. jumps: 1250

Sample every: 25

Check Subject Directory

A Bayesian estimation of diffusion parameters at each voxel is executed by FSL's *bedpostx* function. This step prepares diffusion data for probabilistic tractography.

Options

- Check Subject Directory: pressing this button runs a check on whether the chosen diffusion dataset folder conforms to *bedpostx* naming requirements. If not, a warning describing the discrepancies appears (see Required Files for naming requirements). If requirements are met, the BedpostX step becomes available.
- Fibres per voxel: the number of fibres modeled per voxel. Default is 2.
- ARD Weight: automatic relevance determination weight. Default is 1. Values smaller than 1 correspond with increased weighting on additional fibres per voxel, larger values correspond with less weighting on secondary fibres.
- Burnin period: number of iterations completed before sampling starts. Default is 1000. Longer burnin may be required for noisy data.
- Num. Jumps: number of jumps. Default is 1250.
- Sample every: sample every _ jumps. Default is every 25 jumps

Required Files

- Artifact-corrected data file named 'data.nii.gz' (output of Artifact Correction step)
- B-vector file named 'bvecs' (no extension)
- B-value file named 'bvals' (no extension)
- Brain extracted mask named 'nodif_brain_mask.nii.gz' (output of BET step)

REGISTRATION



Registration matrices for transformations between diffusion, structural, and standard space are created using FSL's *flirt* and *covert_xfm* functions.

Options

- Select Standard Space Reference: prompts selection of standard space reference file (brain extracted).

If a file is selected, registration matrices for conversion between standard space and diffusion space are generated and saved in a sub-folder of the subject's bedpostX directory, named 'xfms'.

- Select Structural Space Reference: prompts selection of brain extracted structural space reference file.

If a file is selected, registration matrices for conversion between structural space and diffusion space are generated and saved in a sub-folder of the subject's bedpostX directory, named 'xfms'.

If both standard and structural space references are selected, registration matrices between standard and structural space are also generated.

Required Files

- Bedpostx directory for current data set (output of BedpostX step)
- At least one brain extracted reference file (standard or structural).

ANALYSIS PREP

The screenshot shows the 'Analysis Prep' window with the following settings:

- DTI Fit** button is highlighted.
- DTI Fit Output:** ☐ structural space ☐ standard space
- Save Mask** button.
- Mask Name:**
- Draw** button.
- Marker** button (selected).
- Eraser** button.
- ☐ 5x5 voxels
- ☐ 3x3 voxels
- ☒ 1x1 voxels
- Load SAM/ERB Image** button.
- ☐ Edit Image
- Threshold** slider: 0.4 to 1.0
- Find Peak** button.
- ProtrackX Folder:**
- ProtrackX** button.

DTI FIT

The screenshot shows the 'DTI FIT' window with the following settings:

- DTI Fit** button is highlighted.
- DTI Fit Output:** ☒ structural space ☐ standard space

A diffusion tensor model is fit to the diffusion data at every voxel by FSL's *dtifit* function. DTI Fit can be run before Artifact Correction to check whether principle eigenvector (V1) directions look logical. If V1 directions look off, the b-vector file may be formatted improperly.

After *dtifit* has run, the V1 image is displayed in the Viewer with its transparency modulated by the FA image. If the results were registered to standard and/or structural space, the registered images are displayed in the same manor and overlaid on the appropriate reference images.

Options

- DTI Fit Output: name of the sub-folder created within the dataset folder to contain *dtifit* output files. Also used as the prefix for each *dtifit* output file.
- Structural space: option to register *dtifit* output to structural space. Images registered to structural space are saved with the suffix '_str'.
- Standard space: option to register *dtifit* output to standard space. Images registered to structural space are saved with the suffix '_mni'.

Required Files

- Diffusion-weighted data to run diffusion tensor fitting on

- Brain mask (output of BET step)
- B-vector file and b-value file

MASK CREATION



The user can create binary masks, either by hand-drawing them or by thresholding/editing an MEG source image (SAM/ERB volume).

When hand-drawn, saving the mask will create a binary image where only voxels that were selected by the marker (shown in red) have a value of 1. When a SAM/ERB volume is loaded, saving the mask will create a binary image where only the remaining SAM/ERB volume overlay voxels (shown in warm colours), after thresholding and editing with the marker/eraser, have a value of 1. Any hand-drawn voxels on the SAM/ERB image will also be included in the mask. The created mask is loaded into the Viewer after it is saved.

The save mask can be used as a seed, waypoint, target, exclusion, or termination mask in probabilistic tractography.

Options

- Mask Name: name mask will be saved under in the diffusion dataset folder.
- Hand-drawing:



- Draw/Pause: enables/disables the hand-drawing function. When **Draw** is pressed, the button name switches to **Pause** and the cursor becomes a marker or eraser, depending on the marker/eraser toggle. The marker/eraser can be used by clicking and dragging the cursor on any of the images displayed in the slice viewers.

When **Pause** is pressed, the button name switches to **Draw** and the hand-drawing function stops. Regular use of the cursor is restored.

- Undo: removes the marker's previous click-and-drag.

- Clear: removes all marker from image and the mask is reset to zeros.
- Marker/Eraser toggle: allows user to choose either a red marker cursor or an eraser that removes whatever marked voxels it encounters (including SAM/ERB image voxels if viewing SAM/ERB image and **Edit Image** is selected).
- Marker size toggle: allows user to choose a marker/eraser size. Options are 1x1 voxel, 3x3 voxels, or 5x5 voxels.
- MEG source image:



- Load SAM/ERB image: if button is pressed, the user is first prompted to select an MRI to overlay the SAM/ERB image onto and then the SAM/ERB image itself. The user is asked to confirm whether the current fiducials (shown below the file listbox) are appropriate for the chosen MRI. If not, the user can load a *.mat file with the appropriate fiducials or cancel and set them by hand before loading the SAM/ERB image (see Viewer).

If the SAM/ERB image contains both positive and negative data, the user is prompted to select which of these to display.

Either .svl files or .nii (normalized SAM/ERB images) can be loaded. Normalized images are only properly displayed when overlaid on an image that is also in standard MNI space.

- Threshold Slider/Editor: allows control over how much of the SAM/ERB image is visible. At the highest threshold only the very peak of the image (voxels with max values) will be visible.
- Find Peak: when this button is clicked, the 3D viewer shows the absolute peak of the SAM/ERB image displayed.
- Edit Image: when selected, use of the eraser will edit the SAM/ERB image displayed as well as any marker applied. When unselected, use of the eraser will not affect the SAM/ERB image.

PROBABILISTIC TRACTOGRAPHY

ProbtrackX

ProbtrackX Folder: tract1

↓

Probabilistic Tractography

Seed Mask(s): - remove ADD

Waypoint Mask(s): - remove ADD

Target Mask(s): - remove ADD

Exclusion Mask: None

Termination Mask: None

Mask Space: ☒ Diffusion ☐ Structural ☐ Standard

Num. Samples: 5000 Step Length: 0.5 ☐ Use Modified Euler Streamlining

Curv. Thresh.: 0.2 ☒ Loopcheck ☐ Use Anisotropy to Constrain Tracking

Max. Num. Steps: 2000 ☐ Verbose ☒ Use Distance Correction

RUN

Probabilistic tractography is run by FSL's *probtrackx*. *Bedpostx* must have been run beforehand.

After completion, the generated tractography map is loaded into the Viewer by itself as a maximum intensity projection, as well as overlaid on a reference image in the appropriate space.

Options

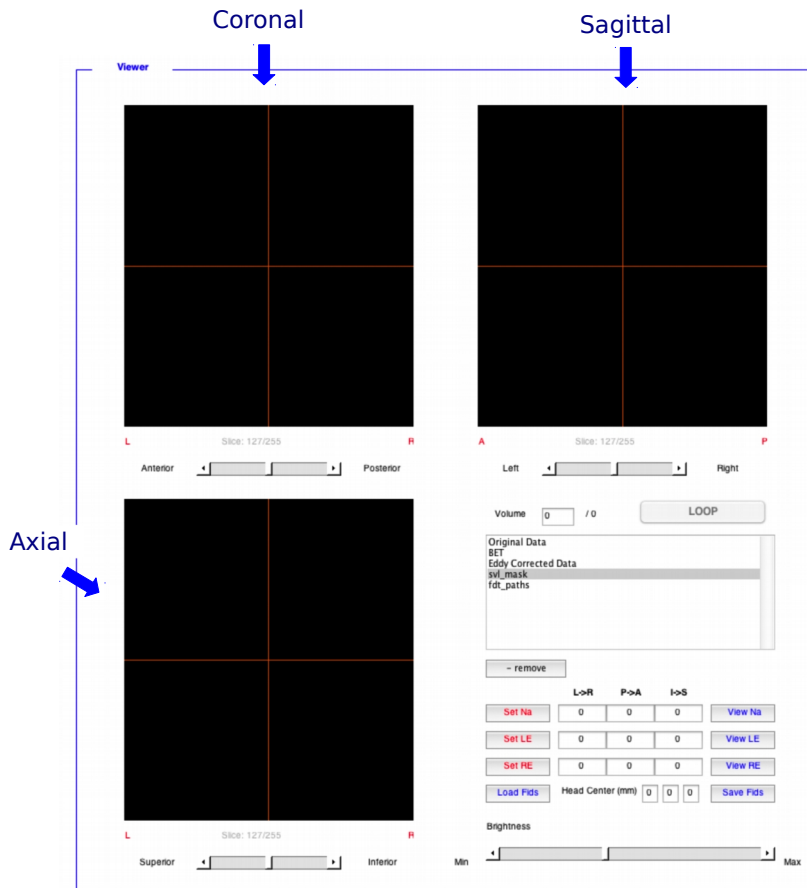
- ProbtrackX Folder: name of the output folder that is created in the diffusion dataset directory to contain the *probtrackx* output.
- Seed Mask(s): list of chosen seed masks for tractography. Masks can be added from the file listbox or the file directory. The **Remove** button removes the selected mask from the list.
- Waypoint Mask(s): list of chosen waypoint masks. Optional. Masks can be added from the file listbox or the file directory. The **Remove** button removes the selected mask from the list.
- Target Mask(s): list of chosen target masks. Optional. Masks can be added from the file listbox or the file directory. The **Remove** button removes the selected mask from the list. Only available when exactly one seed mask is chosen. If selected, seed-to-targets will be output as volume(s) and a text file, automatically.

- Exclusion Mask: chosen exclusion mask. Optional. Can be selected from the file listbox or the file directory.
- Termination Mask: chosen termination mask. Optional. Can be selected from the file listbox or the file directory.
- Mask Space: the coordinate space that all selected masks are in, as well as the space the tractography output will be in.
- Num. Samples: number of samples (tracts) that are taken to build the posterior distribution on the streamline. Default is 5000.
- Curv. Thresh: curvature threshold determining the angle of curvature between the preceding and current fibre direction beyond which paths are discarded. Default 0.2 (80 degrees).
- Max. Num. Steps: maximum number of steps per sample tract. Default 2000.
- Step Length: length of each step. Default 0.5 mm.
- Loopcheck: option to terminate paths that return to a point they have previously encountered.
- Verbose: option to output additional information to the command-line as tractography is run.
- Use Modified Euler Streamlining: option to use modified Euler streamlining, which is more accurate and slower than default streamlining.
- Use Anisotropy to Constrain Tracking: option to stop tracts that encounter an anisotropy value lower than a randomly chosen threshold.
- Use Distance Correction: option to correct for the decrease in connection probability further from the seed mask.

Required Files

- Subject's bedpostX directory (output of BedpostX step)
- Seed mask
- Brain mask (output of BET step)
- If mask space is structural or standard: transformation matrices between diffusion space and chosen mask space (located in 'xfms' folder of subject's bedpostX directory)

VIEWER



3-SLICE VIEWER

Any loaded volumes can be displayed by the 3-Slice Viewer, which shows three intersecting slices of a volume. Each of the three images shows slices of the volume in a specific plane: coronal (top left), sagittal (top right), and axial (bottom left).

- Sliders: allow scrolling through the slices in a plane. Labels on either side of the sliders indicate the direction of scrolling (e.g. anterior – posterior).
- Red labels: L (left), R (right), A (anterior), and P (posterior). Indicate the orientation of the displayed slice.
- Slice labels: indicate the slice number currently being viewed in each image.
- Orange crosshairs: indicate the position in the volume currently being viewed. Clicking on any of the images will relocate the orange crosshairs and the slices viewed to the location of the cursor.

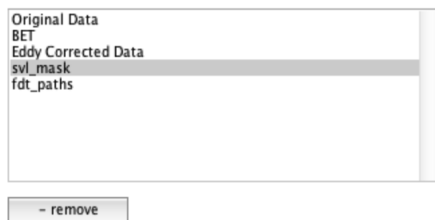
VOLUME EDITOR & LOOP BUTTON



The volume editor and loop button allow the user to view different volumes of a 4-dimensional image.

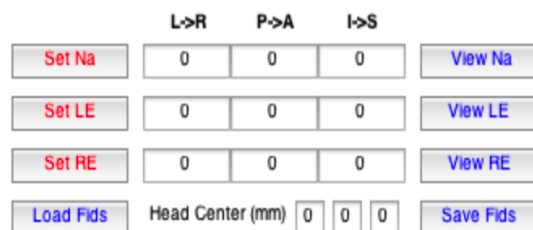
- Volume editor: user can select a volume from the currently loaded image to view. Range of volume indices is 0 to number of volumes-1. The maximum index value is displayed to the right of the volume editor box.
- Loop button: user can view all the volumes of a 4D image one after the other.

FILE LISTBOX



All loaded files are added to the listbox. Selecting a file from the list loads it into the 3-Slice Viewer. Pressing the - **remove** button will remove the currently selected file from the list and viewer.

FIDUCIALS EDITOR

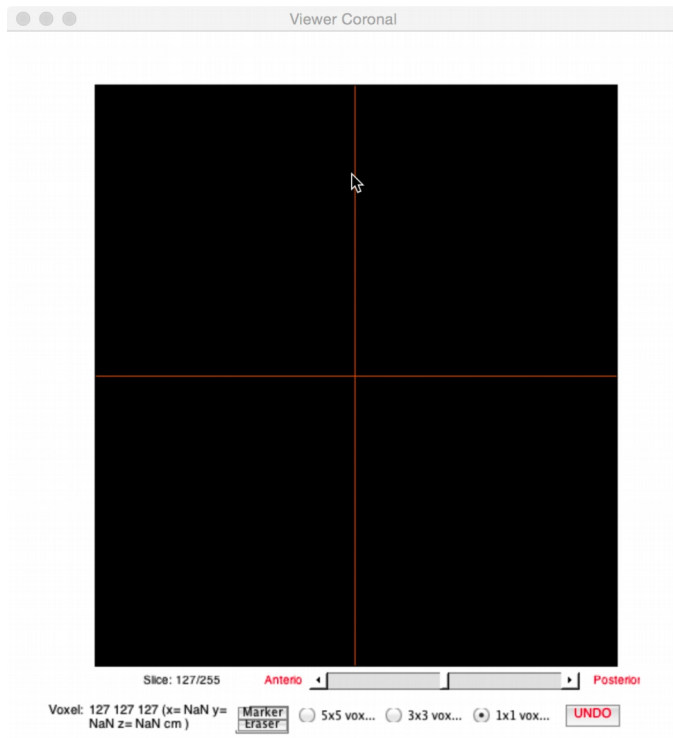


Nasion, left ear, and right ear fiducials can be set, viewed, saved, and loaded. Fiducials are indicated in the 3-Slice Viewer by orange circles.

- Set buttons: set fiducial (Na, LE, or RE) to current location (shown by crosshairs).
- View buttons: view fiducial (Na, LE, or RE) in slice viewers.
- Load Fids: load a previously created Matlab fiducial file.

- Save Fids: save fiducials in a Matlab file.
- Head Center: estimated head center coordinates in mm (x, y, z).

EXPANDED SLICE VIEWER



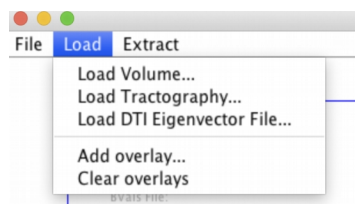
Double clicking on any of the slice viewers (coronal, sagittal, or axial) will open a larger figure for easier viewing. Fiducials can be set, and drawing can continue from this larger viewer. The coordinates of the cross hair position are shown in slice numbers and MEG coordinates (if fiducials are set) on the bottom left.

OTHER CAPABILITIES

Back Button: reverses most recently completed Pre-processing Step. All output files and folders from the previous step are deleted, files produced from the previous step are removed from the Viewer, and the previous step is enabled again.

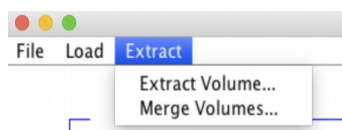


Load Menu:



- Load Volume: any NIfTI image can be loaded into the Viewer and file listbox.
- Load Tractography: a probabilistic tractography file (NIfTI format) can be loaded into the Viewer and file listbox. It can be viewed by itself as a projection or overlaid onto a NIfTI volume in the same space (i.e. diffusion, structural, or standard).
- Load DTI Eigenvector File: an eigenvector file can be viewed by itself, modulated by another diffusion tensor image (e.g. FA), and/or overlaid on another NIfTI volume (e.g. Subject's T1, if the eigenvector file is registered to structural space). Eigenvectors are displayed with RGB coding: x-axis values are red, y-axis values are green, and z-axis values are blue.
- Add overlay: add NIfTI image overlay to current image (each overlay is displayed in a new colormap). Max 5 overlays per image.
- Clear overlays: discard all overlays on currently viewed image.

Extract Menu:



- Extract Volume: a single volume from a 4D image can be saved in its own file. Specify image and then volume number (first vol = 0). Executed by FSL's *fslroi*.
- Merge Volumes: multiple NIfTI volumes can be concatenated (in the 4th dimension) and saved as a single 4D image. Executed by FSL's *fslmerge*.

FSL REFERENCING NOTE

Please refer to FSL's referencing policy for use of their programs in research (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FDT>)

REFERENCES

Cottaar, M. (2019, October 2). *FDT/UserGuide*. Retrieved from

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FDT/UserGuide>

Hanayik, T. (2019, September 25). *eddy/UserGuide*. Retrieved from

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/eddy/UsersGuide>

Jenkinson, M. (2018, January 5). *BET/UserGuide*. Retrieved from

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/BET/UserGuide>

Webster, M. (2012, September 4). *topup/TopupUsersGuide*. Retrieved from

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/topup/TopupUsersGuide>