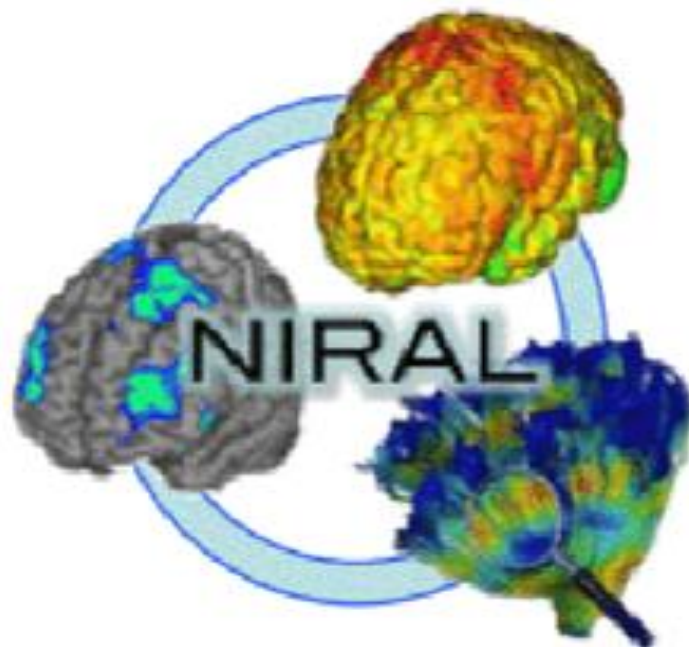


Quality Control Tutorial for DTI



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There are three main steps to Quality Control protocol for DTI

- 1.) DICOM conversion – Download and conversion of files to .nhdr files for use in programs
- 2.) DTIPrep Automatic QC – Execution of a protocol script to automatically QC scans
- 3.) Visual DWI & DTI QC – Visual recheck of DTIPrep QC results, preliminary fiber tracking, and visual check of signal loss and anomalies

I. DICOM conversion

A. Checking for and preparation of incoming data

Step	Description	Action
1	Go into the CHDI directory	<code>cd /projects4/CHDI_TrackHD/</code>
2	Check recent downloads	<code>tail -40 downloadlog.txt</code>
3	go into the Data repository	<code>cd Data</code>
4	unzip corresponding tar file	<code>gtar -xzf <tar.gz file></code>
5	move subject folder into HDNI folder	<code>mv HDNI/<xxxx> ../HDNI</code>
6	Update Wiki table	http://pandora.ia.unc.edu/wiki/index.php/HDNI:General

B. Conversion of Dicom to NHDR

Step	Description	Action
1	Go to subject folder	<code>cd /projects4/CHDI_TrackHD/HDNI/<subjectID></code>
2a.	Run Dicom conversion	<code>DicomConv_HDNI.script <subjectID> <fullpath to DICOMfolder></code>
2b.	Run Dicom conversion for two Dicom folders	<code>DicomConv_HDNI_MergeTwo.script <subjectID> <fullpathtoDICOMfolder1> <fullpathtoDICOMfolder2></code>
2c.	Add option Phillips for all Philips datasets	<code>DicomConv_HDNI.script <subjectID> <fullpath to DICOMfolder> Phillips</code>
2d.	Add option Zoltan at the end for all zoltan datasets (only works for 2 Dicom folder present)	<code>DicomConv_HDNI_MergeTwo.script <subjectID> <fullpathtoDICOMfolder1> <fullpathtoDICOMfolder2> Zoltan</code>
3	Verify correct conversion with DTIPrep	DTIPrep - In DTIPrep GUI, click on “File” and then “Open DWI” to open the .nhdr file
4	Update Wiki table	http://pandora.ia.unc.edu/wiki/index.php/HDNI:General

II. DTIPrep Automatic QC

A. Initial Visual QC

- i. In DTIPrep, review baseline images in axial, sagittal, and coronal views. Note any issues of coverage, i.e. inferior axial slices missing such as the cerebellum and temporal lobe, and/or superior slices missing. Second, notice any artifacts or motion in these scans, i.e. “venetian blind” effect, checks, etc. DTIPrep will automatically detect and extract most of these artifacts. For more details on these artifacts see section III - “Visual DWI & DTI QC”

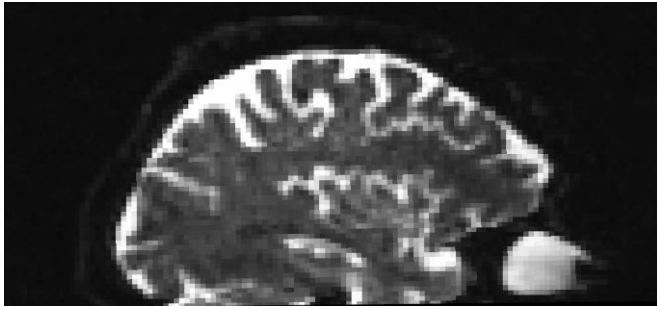


Figure 1.1

“Bad coverage (severe)” a scan missing nearly all of the cerebellum and a large portion of the temporal lobe

B. Run Protocol

- Click on the “Protocol” tab on the left side of the screen. Select “Load” and choose the appropriate protocol script. Click on RunByProtocol button on the bottom of the DTIPrep box.
- The results for each gradient check read Pass or Fail in the command line, depending on the parameters and threshold set in the protocol. [For this study the first two checks, the Image information check and Diffusion check, are inconsequential. As well, the failure threshold is set at 30% for all scans except merged Philips data from two scans, which is 60%]

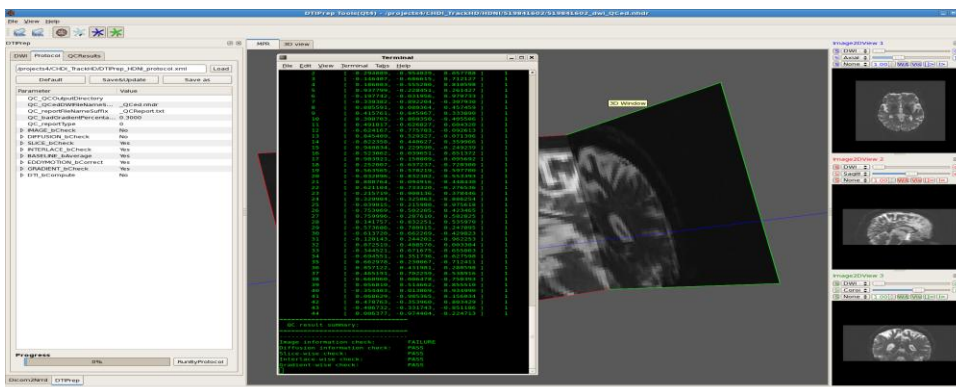
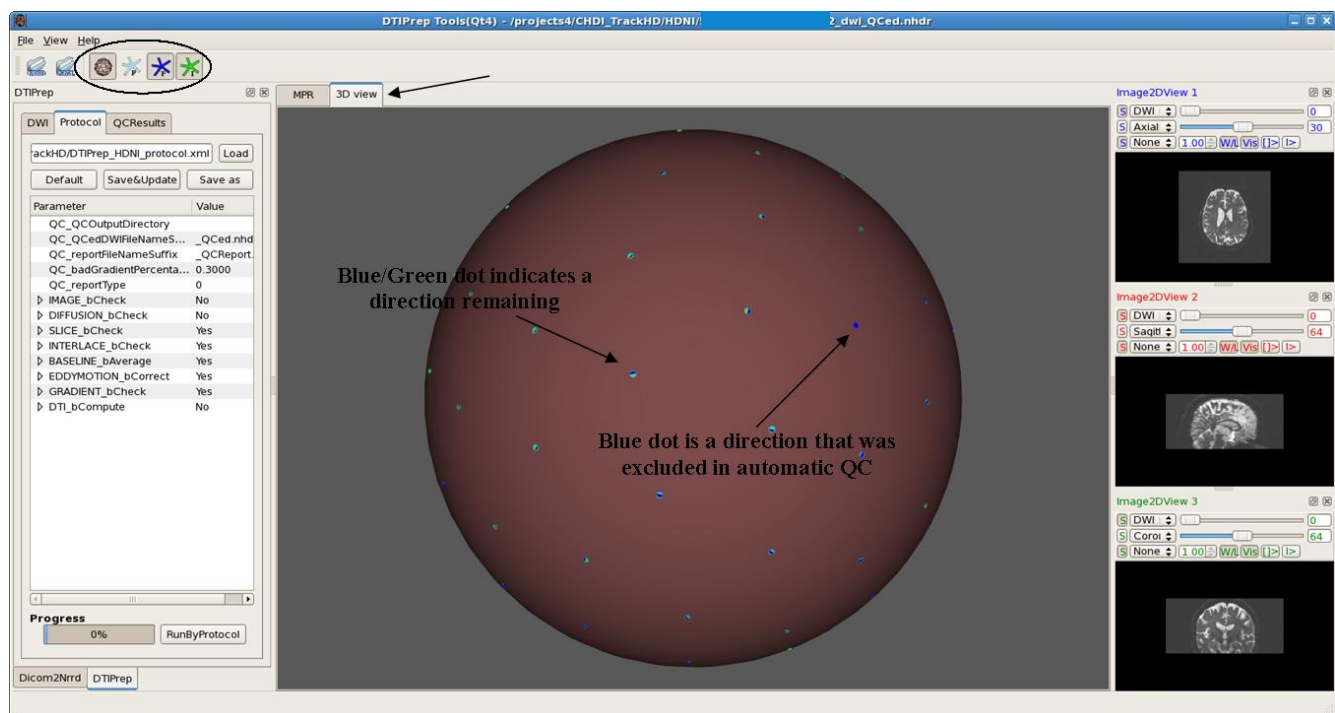


Figure 1.2

Command line showing results overlaying DTIPrep GUI with protocol loaded

- After the protocol runs, select 3D view tab and click on the sphere icon as well as the F and I icons to view distribution of directionality. The F represents the directions before automatic QC. These directions are represented in blue. The I represents the directions left after the automatic QC, labeled in green. Note any major unevenness in spatial distribution. [For the purposes of this study, “major unevenness in spatial distribution” is defined generously. For example, no documentation of spatial gaps occurs unless a visual estimation equals approximately 40% or more of the sphere.]
- As a reconfirmation of the Pass/Fail results from DTIPrep based on the set threshold percentage, view the QC Report and note the number of excluded gradients over the total number of directions in the dataset. [Consider that the number of DWIs showing in the ~QCed.nhdr file may not add up to the original total minus the exclusions due to baseline averaging]



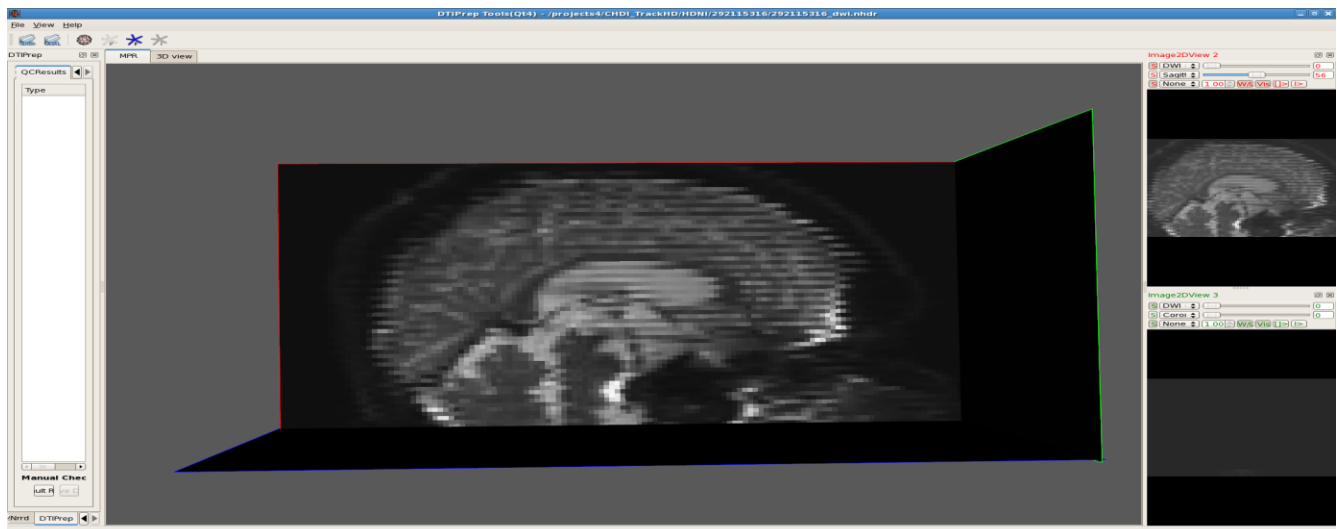


Figure 1.4 “Venetian Blind” Effect A clear example of the “venetian blind” artifact as seen in DTIPrep

- v. Record the amount and gradient numbers of manually excluded directions on wiki page:
<http://pandora.ia.unc.edu/wiki/index.php/HDNI:General>

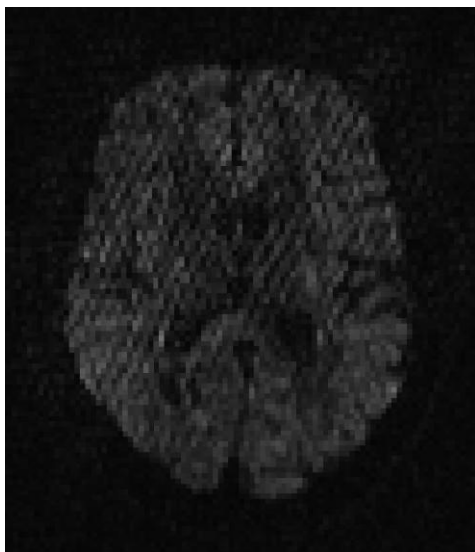


Figure 1.5 (left) “Checkers” artifact shown in an axial slice in a DWI gradient

This artifact occurs most commonly in scans that also have a three-stripe blurring effect. In this study, some of the Siemens protocol dataset contained these three-stripe blur artifacts as shown below in Fig. 1.6

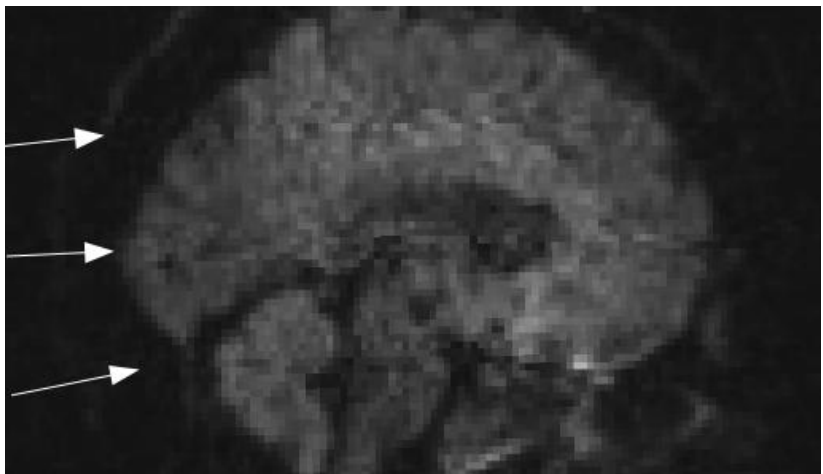


Figure 1.6 (right) “Three-stripe blur” artifact in sagittal view of DWI gradients

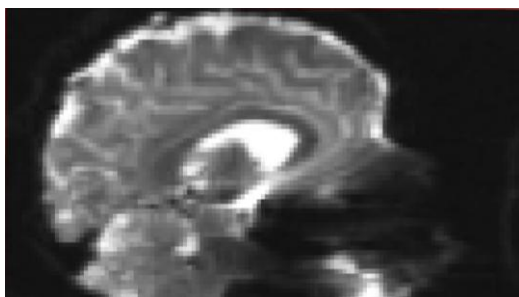


Figure 1.7 (left) Frontal Distortions Distortion clearly visible in a baseline image from a Zoltan-protocol dataset

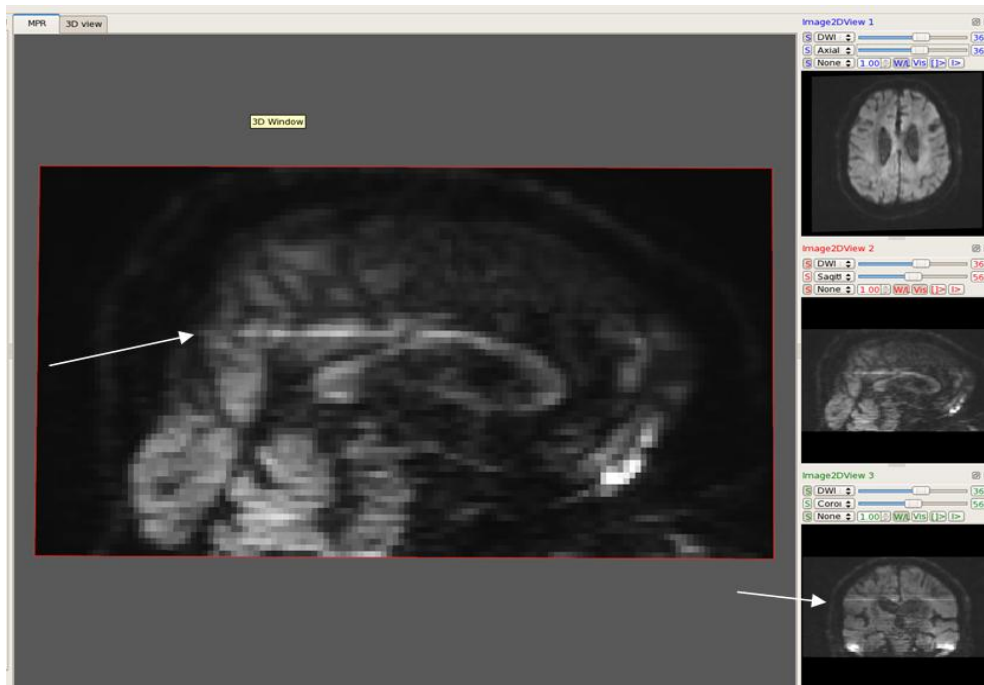


Figure 1.8 DWI with a high-intensity axial slice as displayed in DTIPrep
Although in the sagittal view this slice appears only halfway bright, both the axial and coronal views show a consistent difference in intensity compared to the surrounding slices

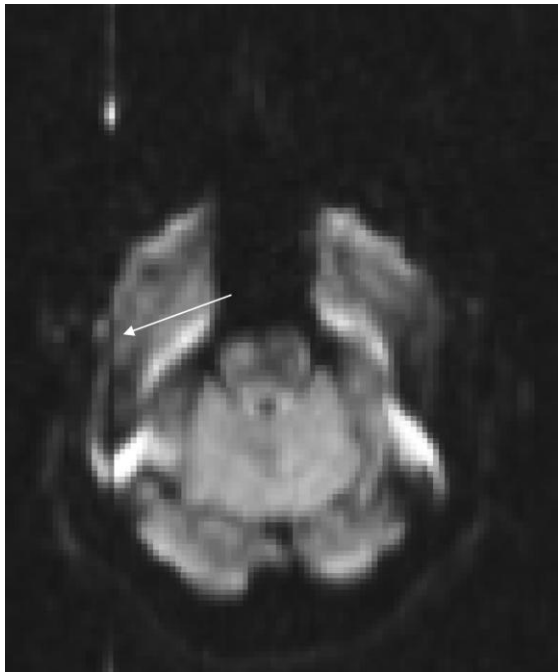


Figure 1.9 Distortion-related artifact “Z stripe” running in the anterior/posterior direction and visible in axial slices and occasionally in sagittal view. Prominent in Zoltan protocol.

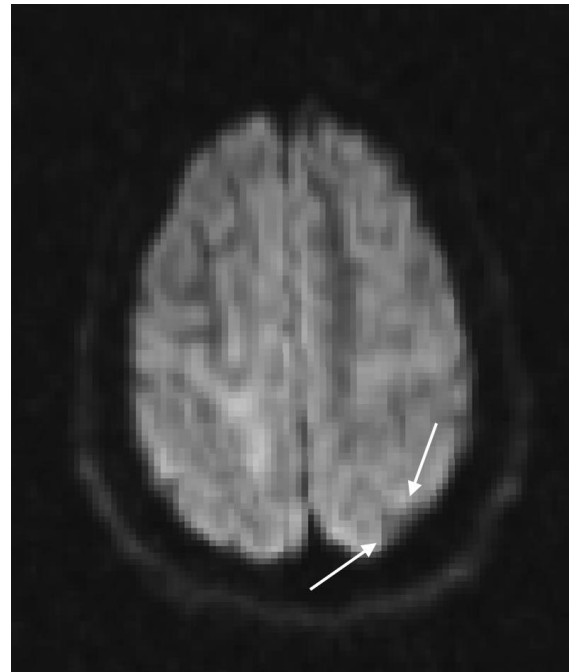


Figure 1.10 One type of geometric artifact, triangular in shape, possibly caused by eddy current motion

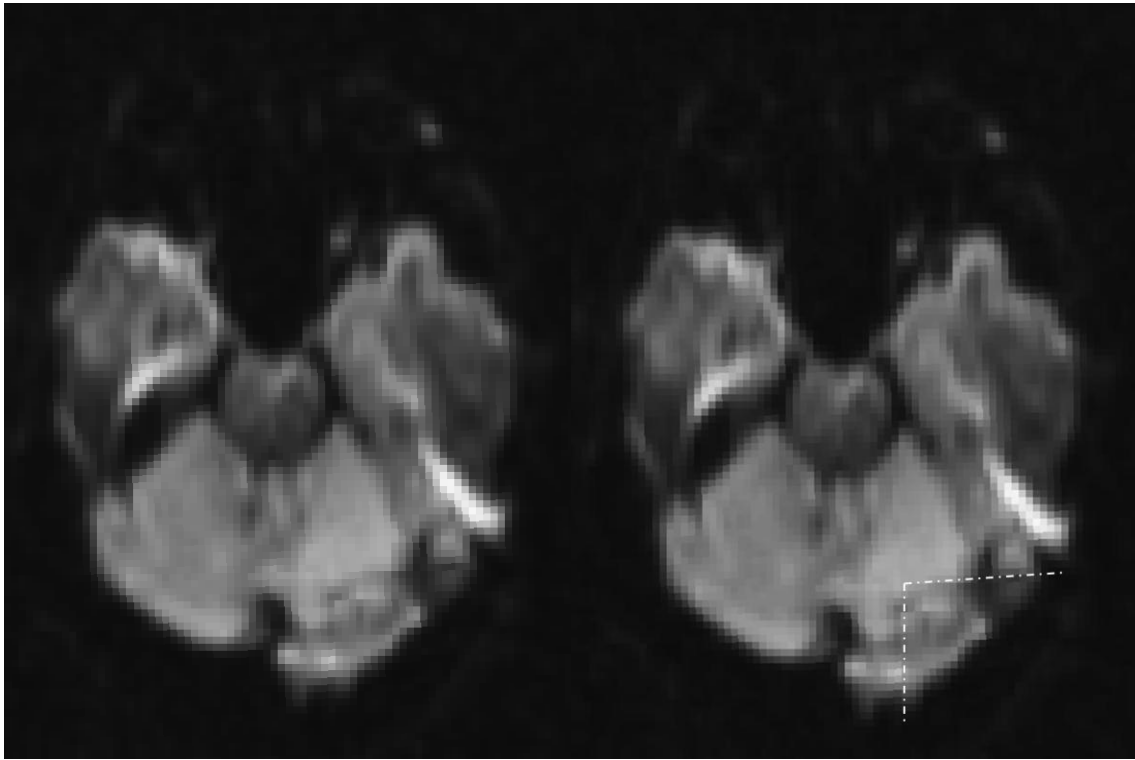


Figure 1.11 Another type of triangle-shaped geometric artifact, outlined on the right

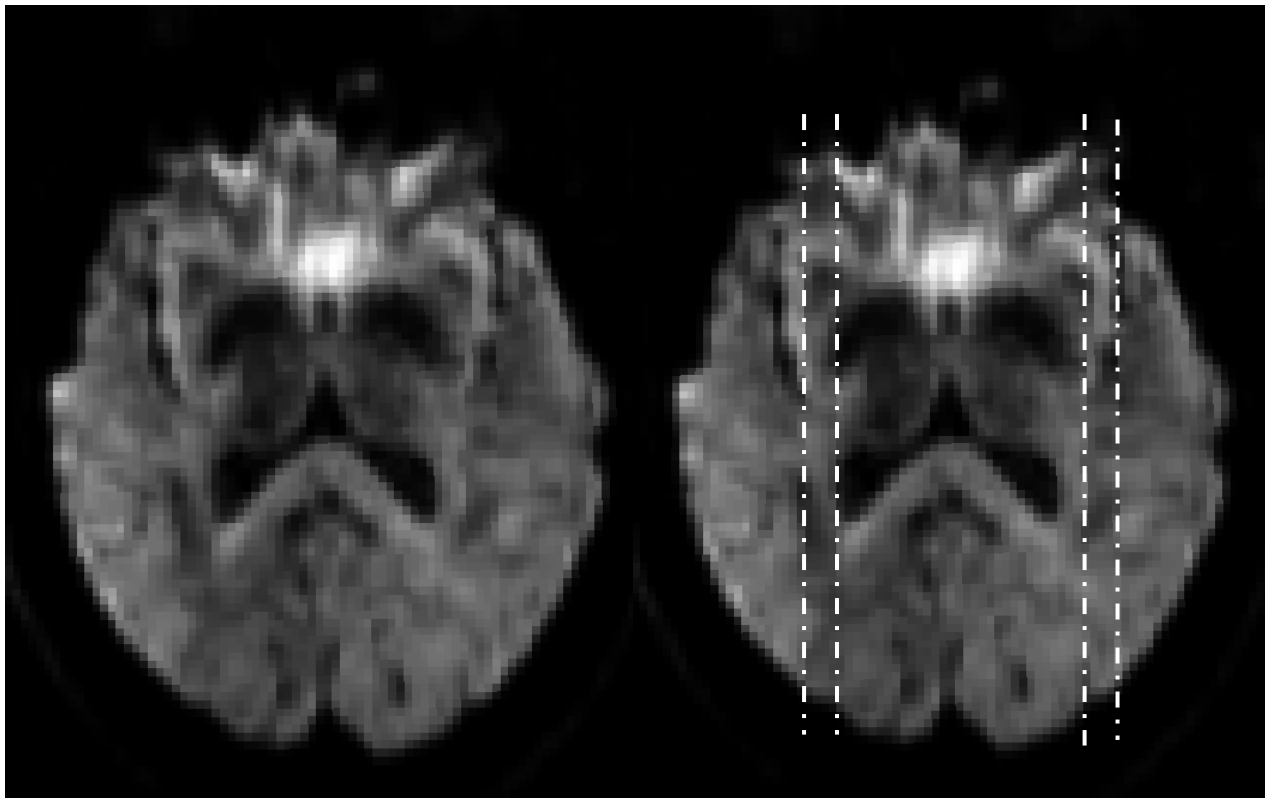


Figure 1.12 “Double-bar artifact” outlined on the right, there are other “bar artifacts” visible in this figure, seen in conjunction with distortion particularly in Zoltan protocol.

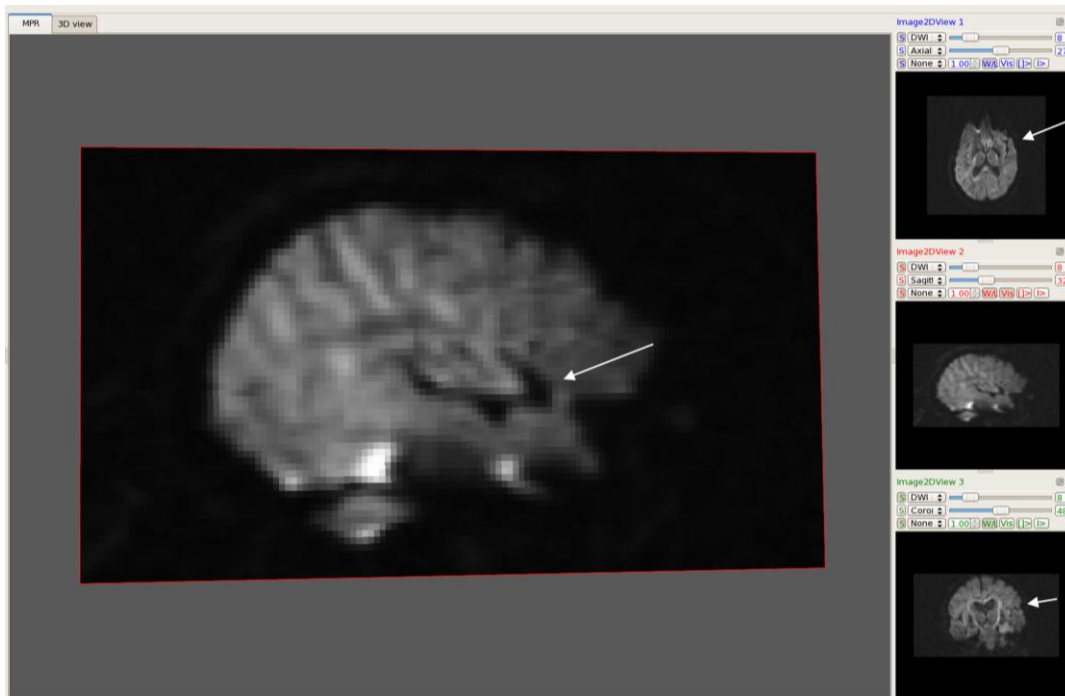


Figure 1.13 Lateral sulcus anomaly present in all protocols, but more consistently in Zoltan dataset

B. Preliminary DTI QC (glyphs and fiducial seeding)

- vi. Convert ~QCed_extracted.nhdr (or ~QCed.nhdr if there are no manual extractions) files into ~.nrrd files using CreateDTIImages.script [for Zoltan cases, use HackZoltanBvalue.script before CreateDTIImages.script]. Open ~float.nrrd file in Slicer under File>Add Volumes>Apply
- vii. Glyph check
 - a) Under the “Volumes” module, select the “Display” drop down menu and change the Scalar Mode to “Color Orientation”
 - b) Select all three boxes in the “Glyphs Visibility Display” area
 - c) Adjust spacing setting as necessary to clearly see the individual glyphs
 - d) Look at the directionality of the glyphs in the Axial window, examine the Corpus Callosum, genu and splenium, to ensure that the glyphs are following the tract
 - e) Do the same with the coronal section of the CC, which can be seen in the Coronal slices. After QC check, deselect the three glyph visibility boxes

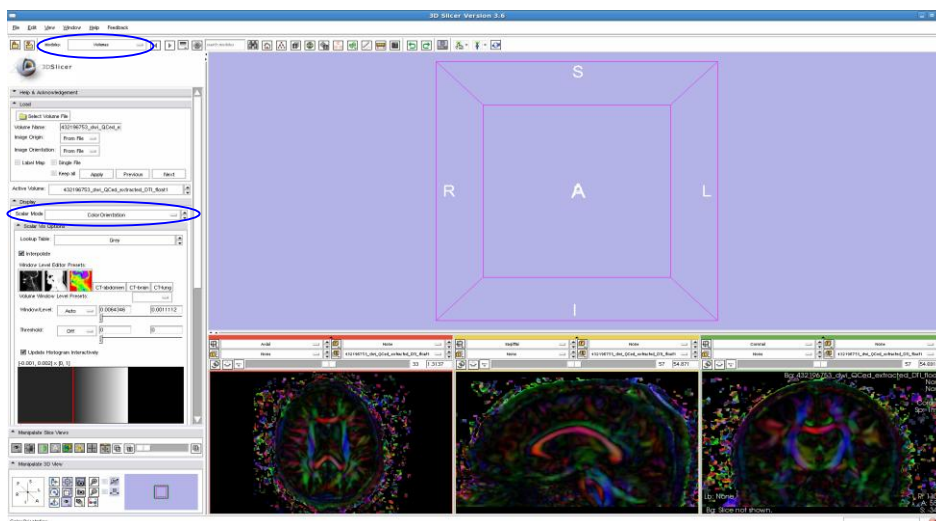


Figure 2.1
Selecting
“Color
Orientation”
in the Scalar
Mode

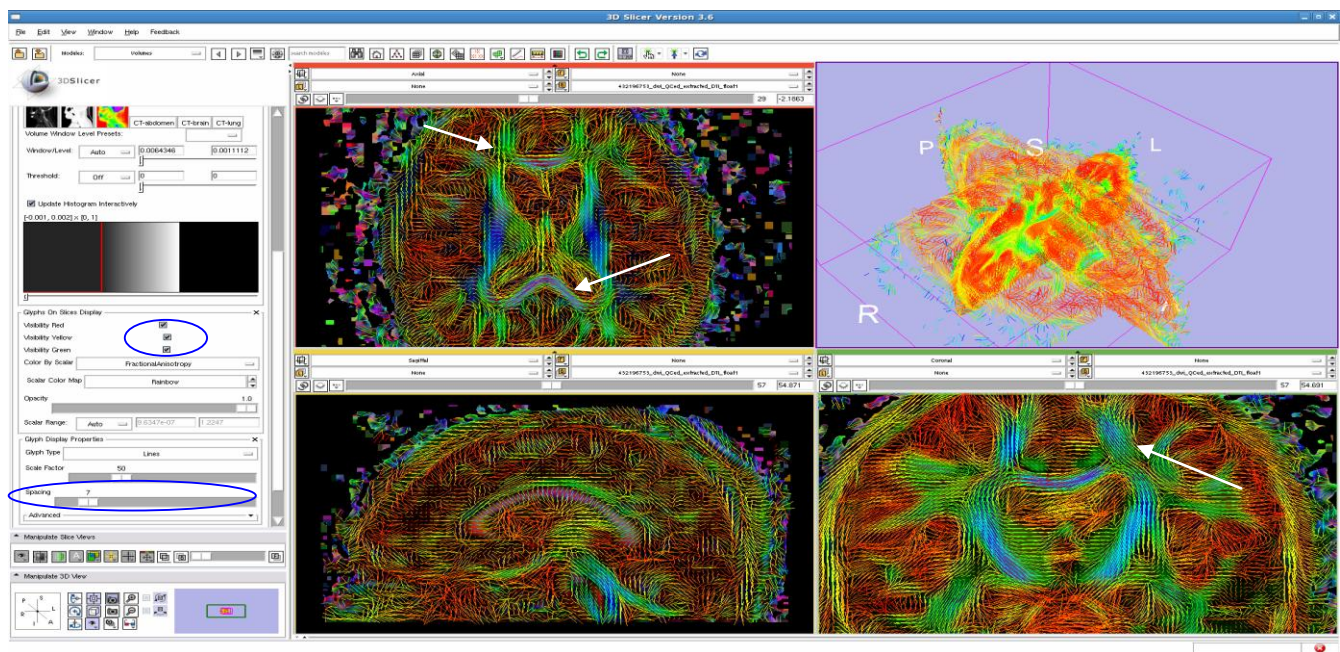


Figure 2.2 Viewing Glyph Directions in Slicer – Selecting “glyph visibility” and changing the spacing

viii. Tracking using Fiducial Seeding

- a) Select the “Fiducials” Module and click on the arrow icon in the top icon toolbar, selecting “Use mouse to create-and-place persistently” to place seeds for five tracts: Corpus Callosum (genu, splenium, coronal); Cingulum, Uncinate, Arcuate, and Internal Capsule
- b) Directionalities are demonstrated in the color map along the following orientations: red is left/right, green is anterior/posterior, and blue is inferior/superior
- c) Seedmap labeling of tracts
 - CC – Starting in the Sagittal plane, identify the CC, which typically appears red in DTI Color Orientation maps. It is bounded superiorly by the cingulum and inferiorly by the lateral ventricles. Place a fiducial in the most anterior part to mark the genu. Place another label in the posterior section of the CC, to mark the splenium. In the coronal view, mark the CC at its vertex to track the coronal fiber bundles of the CC.
 - Cingulum – In the Coronal view, superior to the CC, is the cingulum appearing normally as two green “teardrop” shaped bodies. Mark the left side cingulum.
 - Uncinate – In the axial view, move inferiorly through the slices. Lateral to the brainstem, the anterior tip of the inferior longitudinal fasciculus appears blue/purple. Place a fiducial on the right side to mark the uncinate.
 - Arcuate (2 fiducials) – In the axial view, locate the arcuate. Lateral to the inferior fronto-occipital fasciculus/inferior longitudinal fasciculus, and at the temporo-parietal junction towards the posterior direction of the brain, lies a blue/purple portion of the arcuate. Place a fiducial here. “The fronto-parietal portion of the arcuate fasciculus encompasses a group of fibers with antero-posterior direction (green)” that can be found lateral to the corticospinal tract a few axial slices superior from the last fiducial, place a second marker here. (Catani et. al., 2008, “A diffusion tensor imaging tractography atlas for virtual in vivo dissections”)

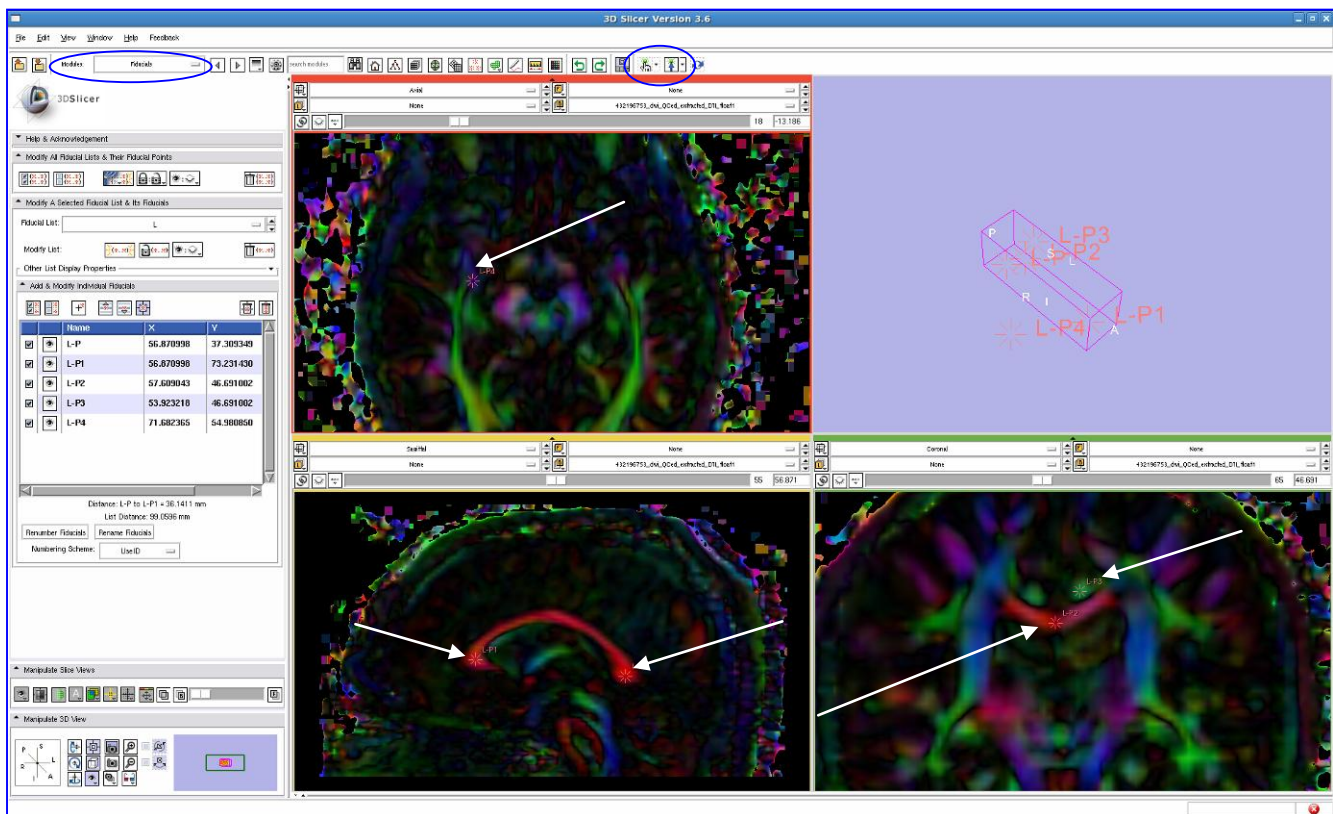
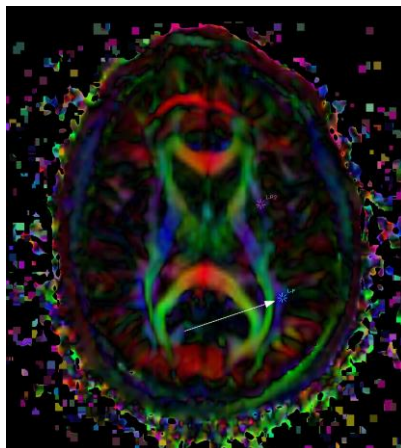
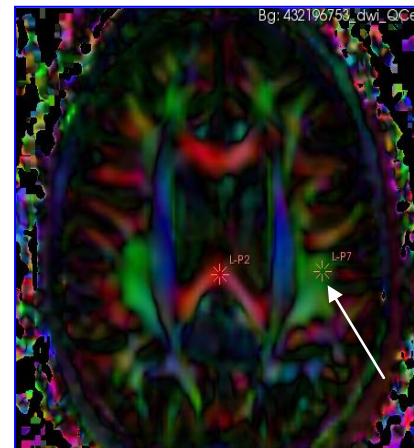


Figure 3.1 Placing Fiducial Label Seeds to track the Uncinate, Cingulum and Corpus Callosum (genu, splenium, and coronal section)



- Place one fiducial in posterior portion (normally blue/purple) of the arcuate. (see left)
Place another several slices up in the superior direction next to corticospinal tract, the arcuate is usually green here. (see right)



- Internal Capsule – In the coronal view, medial to the arcuate and inferior longitudinal fasciculus and lateral to the CC is the internal capsule. Usually, it is mostly blue/purple. Place 2-3 fiducials in the internal capsule, particularly, in the most inferior part of the IC that is blue/purple

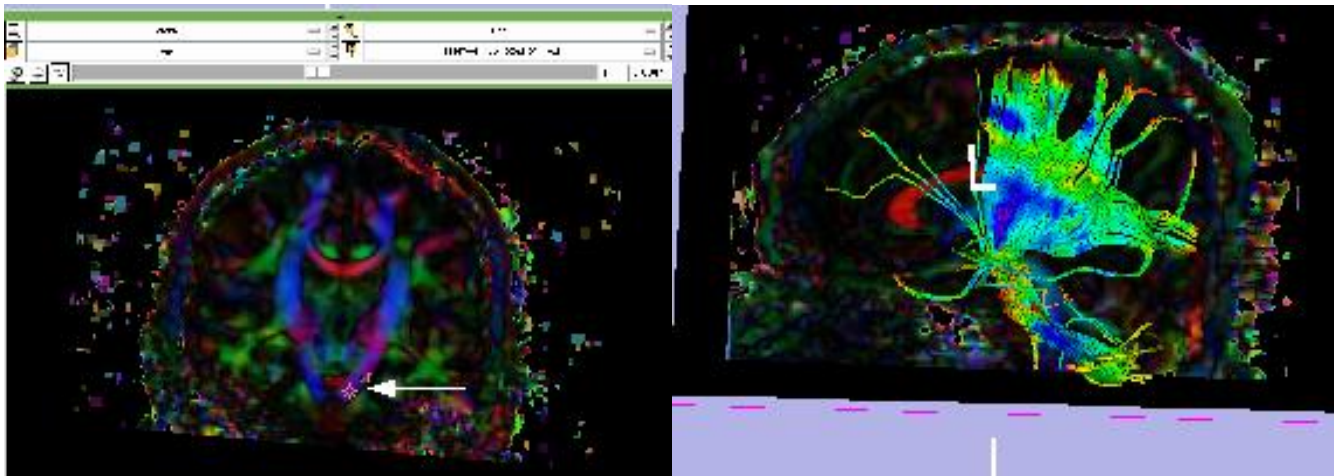


Figure 3.2 Placing Fiducial Label Seeds to track the Internal Capsule (IC) in Slicer

d) Diffusion Tractography for preliminary QC

- Under “Modules”, go to Diffusion > Tractography> Fiducial Seeding; Choose “L” from the “Select FiducialList or Model” drop down menu, then “Create New Fiber Bundle” from the “Output Fiber Bundle Node” drop down menu.
- Set the Stopping Value to 0.10, the Fiducial Seeding Region (mm) to 6.0 mm, and the Fiducial Seeding Step Size (mm) to 1.0 mm.

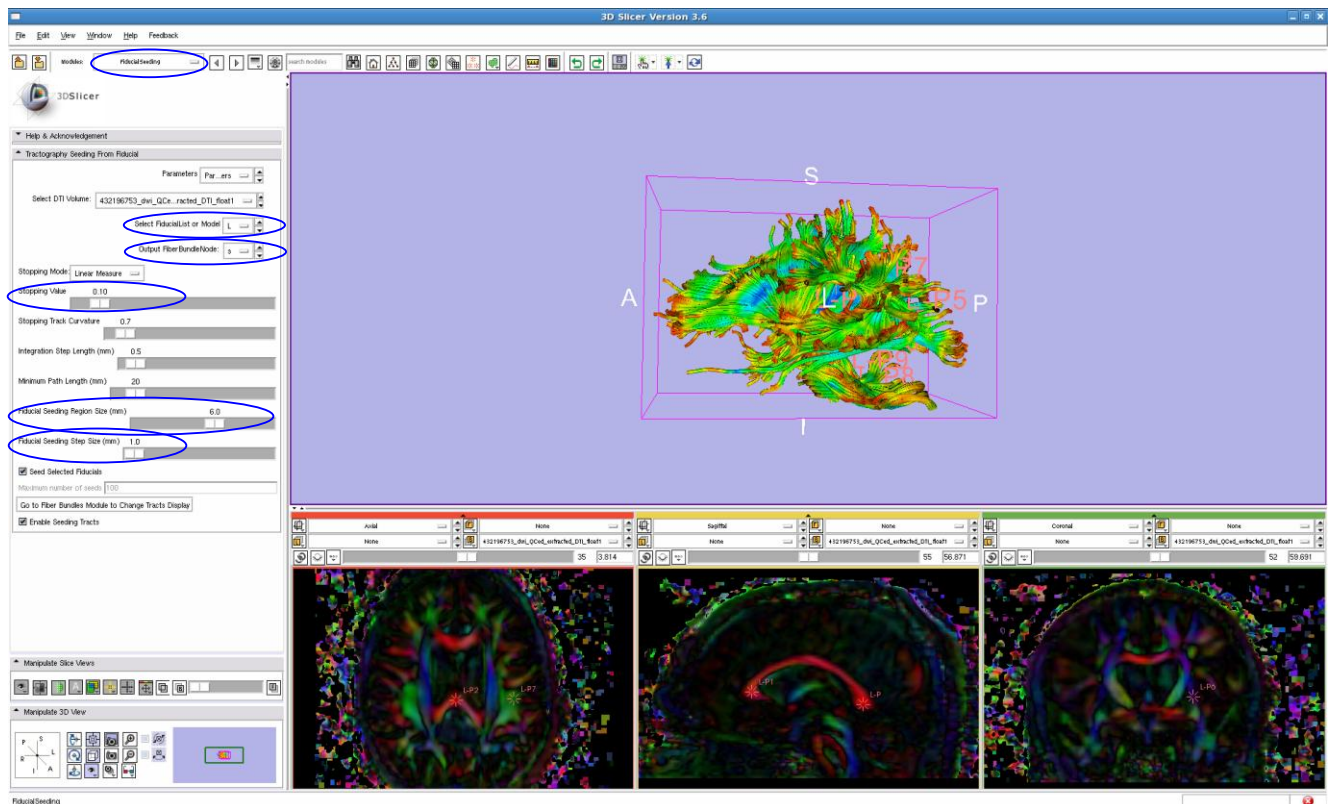


Figure 3.3 Diffusion Tractography of Fiducial Labels

- [Optional] To increase speed and performance, it is possible to change the display of tubes to lines. Go to Diffusion > Tractography > Fiber Bundles. Click on the “Lines” tab and select the “Visibility” box. Click on the “Tubes” tab and deselect the “Visibility” box.

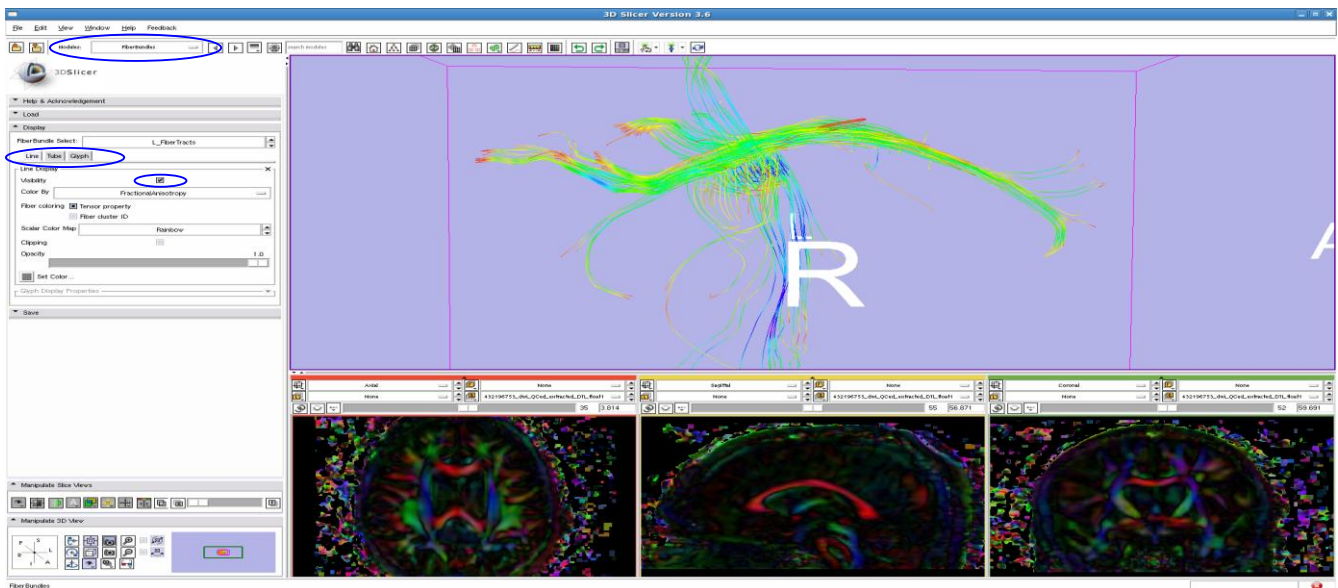


Figure 3.4 Cingulum fiber bundle tractography viewed with Line display

- Return to the Fiducials module, deselect any labels that are undesired to appear in the 3D Viewing pane. Look to ensure that all tracts are present. If they are incomplete, add more fiducial seeds in areas that are lacking. Or, move the existing labels using the “Use mouse to Pick-and-Manipulate persistently” option under the hand icon. If this is not successful, note any incomplete or missing tracts.

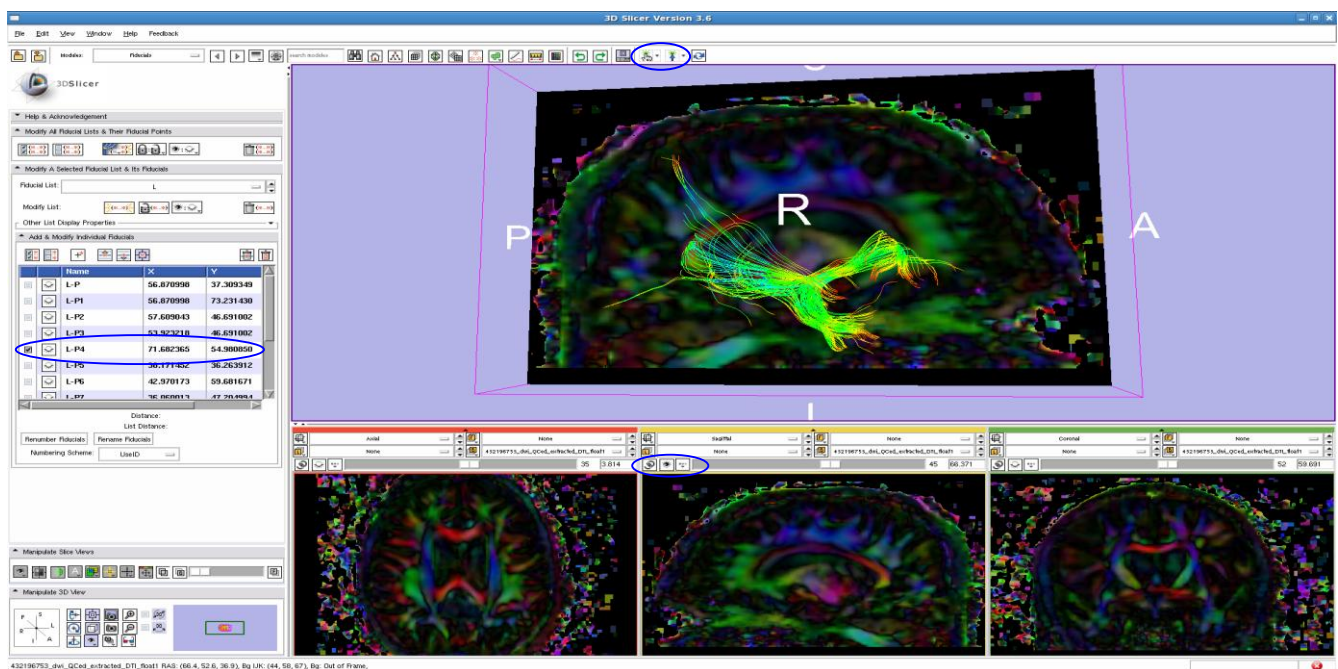


Figure 3.5 Uncinate label only selected, shown with Sagittal slice in 3D window

C. Visual QC for Signal Loss and Anomalies in the Scalar Diffusion Parameters

- ix. CreatedDTIImages.script created the last of the separate scalar diffusion parameter files
- x. In ITK SNAP, open each scalar diffusion parameter ~.nrrd file – either reviewing them individually or using the “multisession cursor” option to scroll through the multiple images at once. Fractional Anisotropy – FA; Mean Diffusivity – MD; Axial Diffusivity – AD; Radial Diffusivity – RD

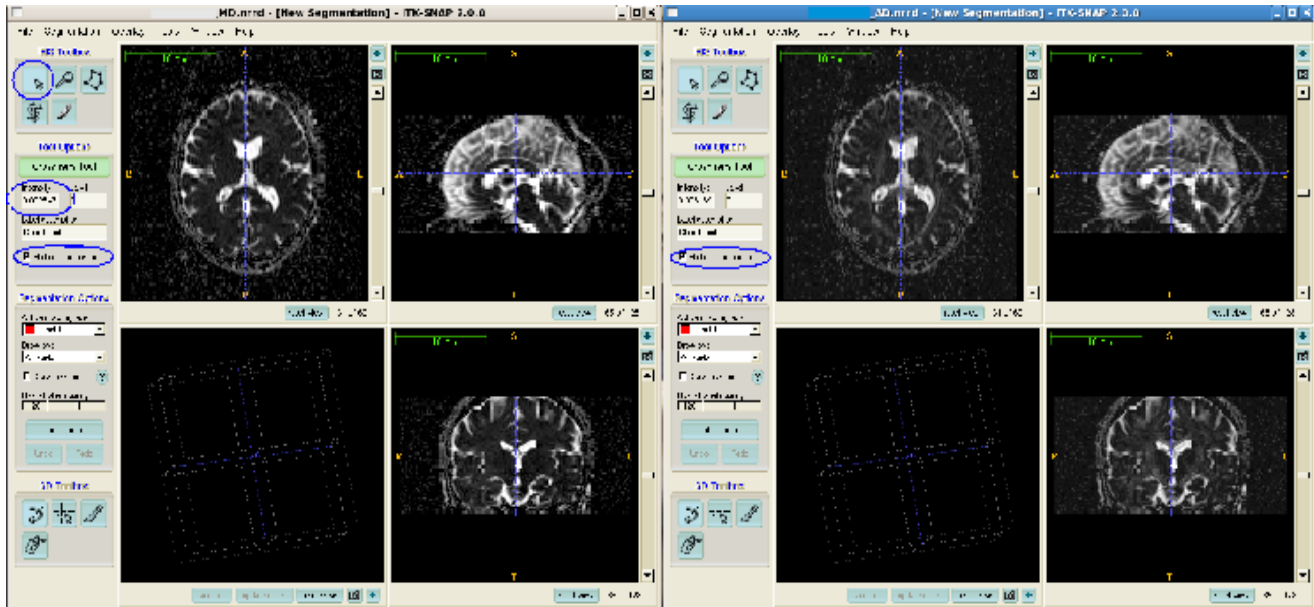


Figure 4.1 “Multisession Cursor and Crosshairs tool on AD and MD NRRD files”

- a) Adjust the contrast as necessary in Tools>Image Contrast, manipulate the graph to change the darkness and brightness of the images
- b) Visually check all slices for signal loss/noise represented by pixelated bright spots in the FA file and dark spots in the MD, AD, and RD files.

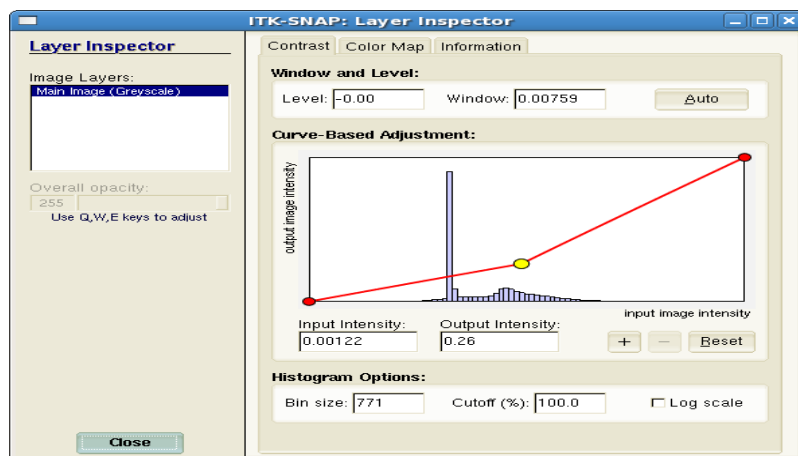


Figure 4.2 Adjusting Image Contrast in ITK SNAP

- Look for clusters of this perceived signal loss. If present, click the Crosshairs tool in the area and review the intensity information. In the FA, anatomy should not equal more than 1.0.

In the MD, RD, and AD files, it should not be less than zero. If these intensities are more than 1.0 and less than 0, note the area for signal loss.

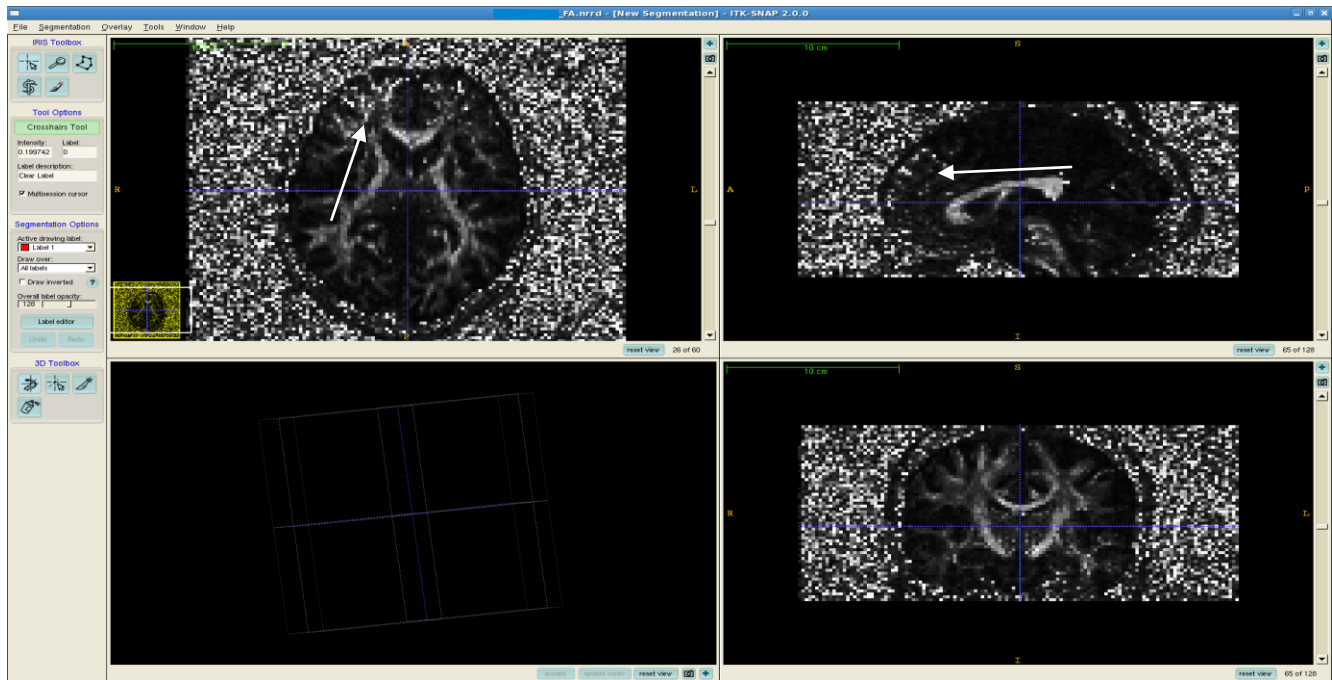


Figure 4.3 Signal Loss demonstrated in FA image in Right Pre-Frontal Lobe

- Observe that some signal loss in the orbital regions is typical

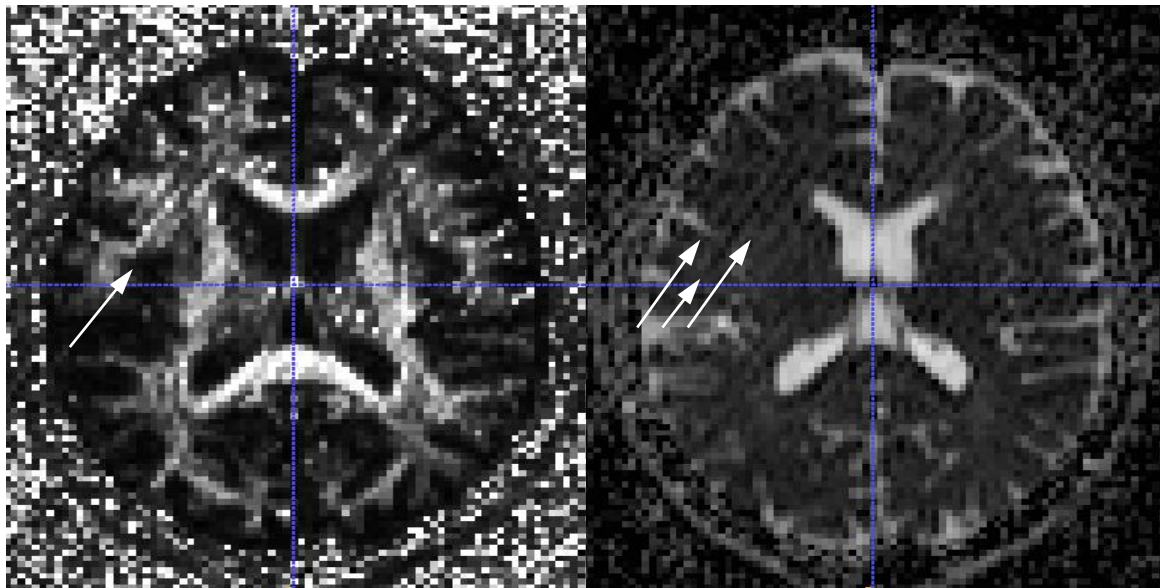


Figure 4.4 Diagonal NRRD artifact displayed in ITK SNAP, FA and MD images respectively
This case was subsequently failed as a result of this issue with image-acquisition

- c) During the visual check, also note any anomalous regions that may be due to anatomical lesions or problems in image acquisition. In this study, five types of artifacts were identified in the scalar diffusion files: diagonal NRRD artifact, possible motion artifacts, wrapping artifacts, a pre-frontal anomaly traced to the Philips protocol, and distortion-related signal loss artifacts.

- Diagonal NRRD artifact, Figure 4.4 demonstrates this diagonal striping artifact. The MD image reveals the large extent of the brain area affected by this issue.

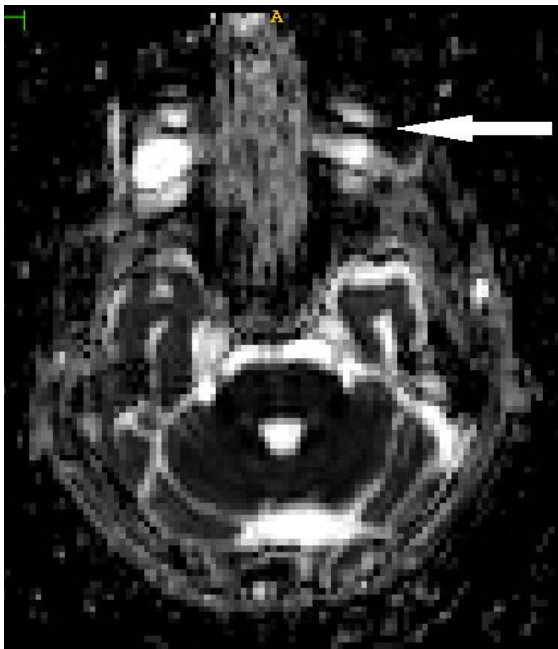


Figure 4.5
(left)
Possible
motion artifacts
in the NRRD
files



Figure 4.6
(right)
Wrapping
artifacts in the
NRRD files

- Possible motion artifacts such as the one displayed in Figure 4.5 are often apparent in inferior axial slices up through the eye area. Like all visually detected artifacts, these are noted in the Visual QC notes on the wiki.
- Wrapping artifacts contain one or several “shadow” images that may or may not be inverted. In Figure 4.6, the eyes clearly mark this artifact.

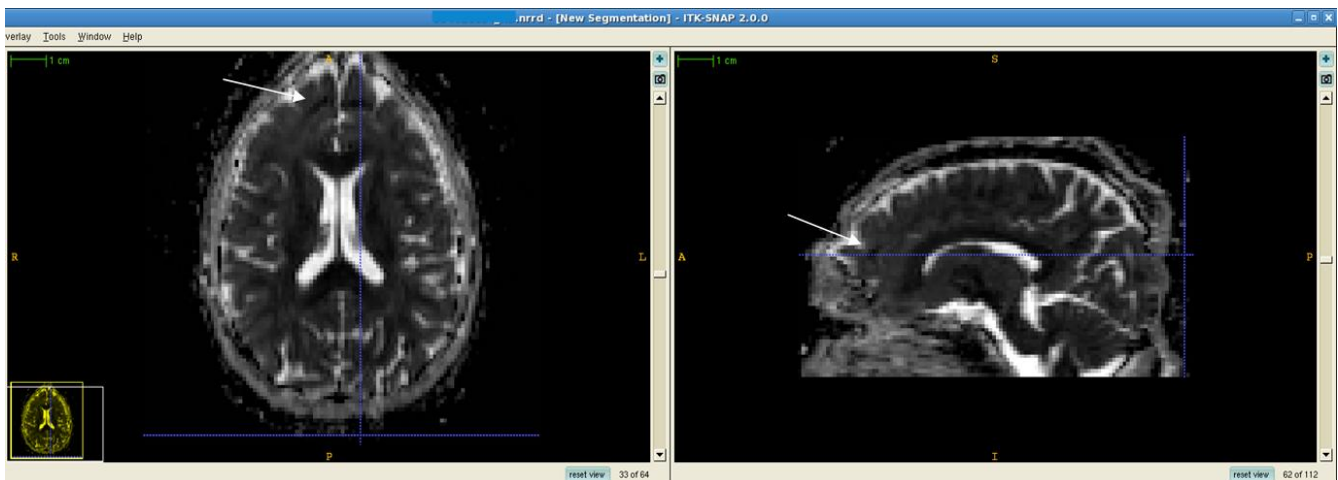


Figure 4.7 Pre-frontal anomaly in RD ~.nrrd file, axial and sagittal views

- Figure 4.7 demonstrates a pre-frontal anomaly in ~50% of a dataset from a Philips protocol. It is mostly visible in axial views, but is occasionally visible in the sagittal view as well.
- If available, the color FA can be loaded on top of the FA ~.nrrd file in ITK SNAP for closer examination of such anomalies. Go to File>Open RGB Image. Click “Browse” to find the appropriate color FA ~.nrrd file

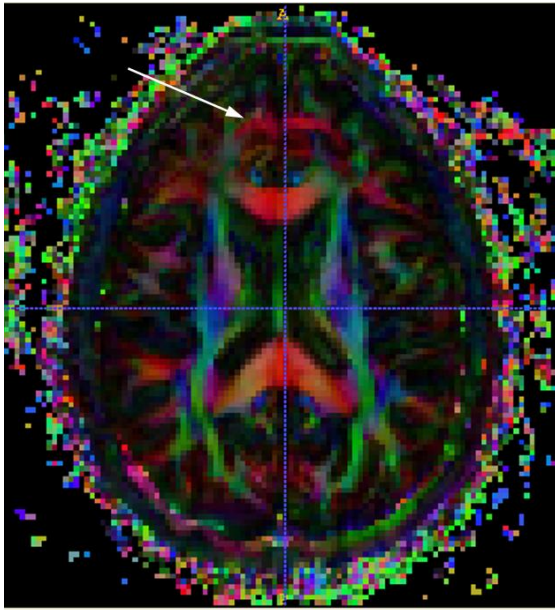


Figure 4.8 Pre-frontal anomaly in FA_color ~.nrrd file, Axial view in ITK SNAP

This is the same case and anomaly as in Figure 4.7, but viewed in the FA color file. The red arc showing in the pre-frontal area is not a result of anatomy and may be examined in Slicer for further evidence in determining whether the anomaly is anatomical or acquisition-based.

- Figure 4.9 displays evidence of both wrapping artifacts and pre-frontal distortion-related signal loss. A similar type of artifact is shown in the posterior part of the occipital lobe in Figure 4.10

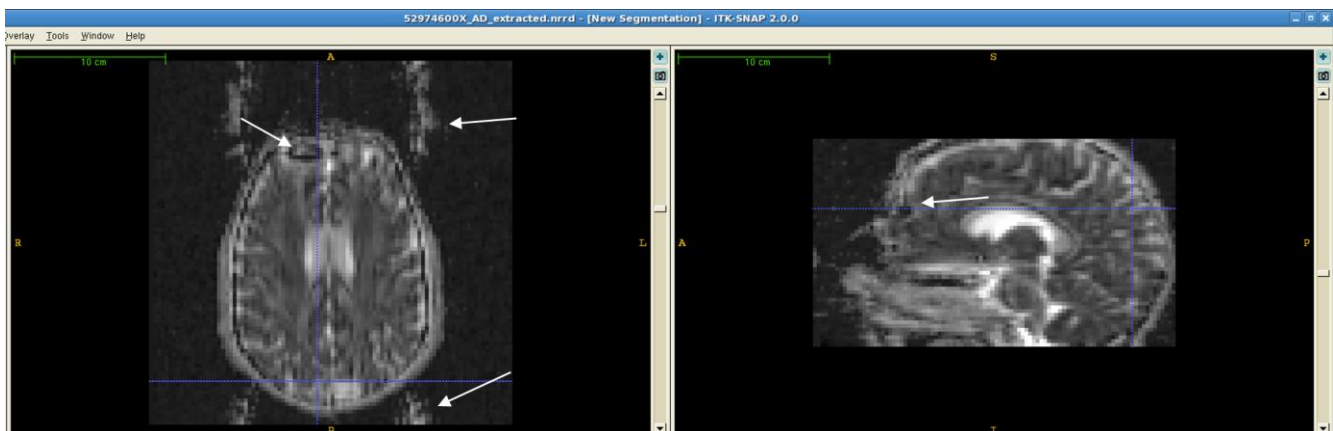


Figure 4.9 Wrapping artifacts, anterior pre-frontal signal loss, and frontal distortion shown in AD

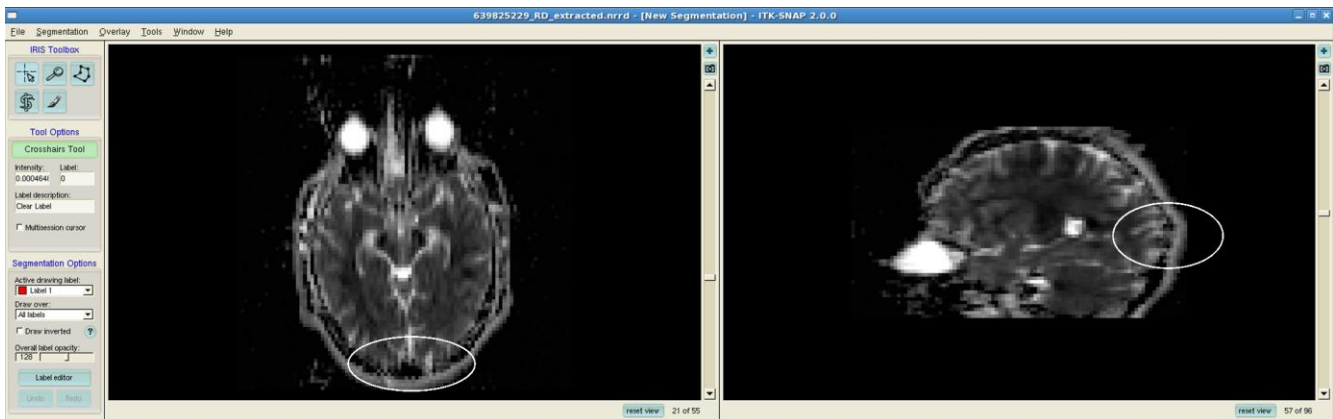


Figure 4.10 Posterior occipital signal loss

IV. Upload of Report to TrackHD

A. Login to the TrackHD website: <https://www.track-hd.net/html/login>

- i. Under the individual subject's page, go to V3 and then click on the MRI DTI QC bar to go to the QC page.
- ii. After selecting the appropriate Quality Control Result (pass, fail, or borderline), upload a PDF version of the ~QCReport.txt created by the DTIPrep QC protocol.
- iii. In the Quality Control Comment box, record all QC notes that should already be on the wiki page, including coverage issues, percentage of gradients automatically excluded by DTIPrep, gradient numbers of manual exclusions, and Visual QC notes in the QC note field before submitting the report

