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How To Integrate DTIPrep Into Diffusion-Weighted Image Pre- Processing

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References

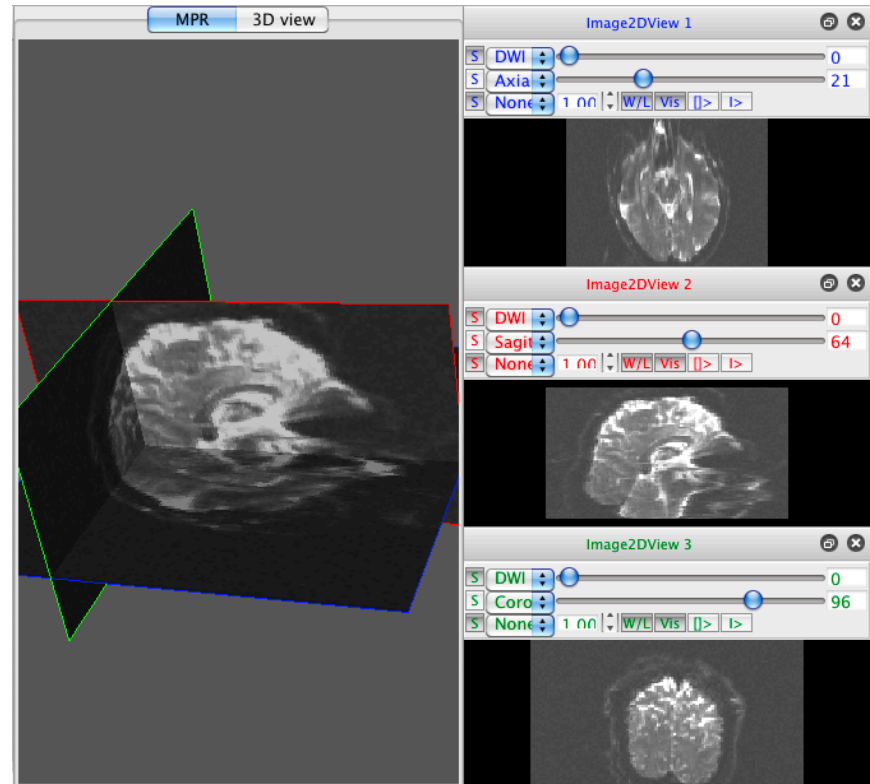
This tutorial is based on information from the following resources:

- http://www.nitrc.org/docman/?group_id=283
- <http://www.nitrc.org/plugins/mwiki/index.php/dtiprep:MainPage>
- <http://www.nitrc.org/plugins/mwiki/index.php/dtiprep:MainPage>
- <http://www.slicer.org/slicerWiki/index.php/Modules:DicomToNRRD-3.6>



Learning Objective

The goal of this tutorial is to demonstrate how to apply DTIPrep to diffusion-weighted imaging (DWI) data as an automatic quality control (QC) step in a DWI data processing pipeline.





Pre-requisite tutorials

- Data Loading & 3D Visualization tutorial

Author: Sonia Pujol, PhD

http://www.slicer.org/slicerWiki/images/2/2e/Slicer3_DataLoadingAndVisualization_UCSF2010_SoniaPujol.pdf

- Diffusion Tensor Imaging tutorial

Author: Sonia Pujol, PhD

http://www.slicer.org/slicerWiki/images/3/35/DiffusionMRITutorial_UCSF2010_SoniaPujol.pdf



Material

This tutorial requires the installation of the Slicer 3.6, DTIPrep, and DicomToNrrdConverter, and the tutorial dataset. They are available at the following locations:

Slicer download page

<http://www.slicer.org/pages/Downloads/>

DicomToNrrdConverter and DTIPrep

<http://www.nitrc.org/plugins/mwiki/index.php/dtiprep:DTIPrepCompilation>

Tutorial dataset: DTIPrep_TutorialContestSummer2011.zip

[\[Add a link to the tutorial dataset\]](#)



Platforms

- Mac Darwin
- Linux 64



Overview of tutorial

- Part 1: Using DicomToNrrdConverter to convert DWI DICOM files to NRRD file format
- Part 2: Initial visual inspection of data
- Part 3: Using the DTIPrep GUI for automatic quality control checking of DWI NRRD file
- Part 4: Visual re-inspection of DTIPrep QC results
- Part 5: Using DTIPrep as a command line tool



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-



DicomToNrrdConverter

DicomToNrrdConverter is used here to create the input NRRD file for DTIPrep. It can be used in Slicer or as a command line tool.

Help can be derived at the command line by typing:

```
DicomToNrrdConverter --help
```

Complete documentation for DicomToNrrdConverter can be found here:

<http://www.slicer.org/slicerWiki/index.php/Modules:DicomToNRRD-3.6>



DicomToNrrdConverter

In general, use of the DicomToNrrdConverter command line tool is recommended since it has options for trouble-shooting problematic DICOM files. The command line tool will be demonstrated in this tutorial.



DicomToNrrdConverter

Change into the
DTIPrep_TutorialContestSummer2011
directory:

```
cd DTIPrep_TutorialContestSummer2011
```

Type the following command to convert the
DICOM directory to a NRRD file:

```
DicomToNrrdConverter --inputDicomDirectory  
DICOM --outputVolume DTIPrepInput.nhdr
```



DicomToNrrdConverter

DicomToNrrdConverter will output the following information about your scan to the terminal:

- Scanner vendor (Siemens, Philips, GE)
- Mosaic or non-mosaic format
- Order of DICOM images (slice or volume interleaving)
- Measurement frame
- Voxel spacing
- Space directions
- Number of 3D volumes and slices per volume



DicomToNrrdConverter

DicomToNrrdConverter will detect baseline images and check if the magnitude of each non-baseline gradient direction coordinate vector is appropriate for its b value.

```
Number of Directions : 3
Directions 0: 0
Directions 1: 0
Directions 2: 0
Image#: 0 BV: 1000 GD: 0 0 0
```

Baseline image
terminal output

```
Number of Directions : 3
Directions 0: -0.203553
Directions 1: -0.520248
Directions 2: -0.829402
DiffusionVector_magnitude_difference 9.47729e-08
gradient_scaling_factor 1
DiffusionVector_magnitude 1
Image#: 1 BV: 1000 GD: -0.203553 -0.520248 -0.829402
```

Non-baseline image terminal
output with b value of 1000



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Visual inspection

The first step in inspecting DicomToNrrdConverter outputs (DTIPreInput.nhdr and DTIPreInput.raw.gz in this case) is to look at the NRRD header file. Check the following features for accuracy:

- Image size
- Slice thickness
- b value(s)
- Number of baseline images
- Gradient direction vector coordinates

```
NRRD0005
content: exists(DTIPreInput.raw,0)
type: short
dimension: 4
space: left-posterior-superior
sizes: 128 128 70 31
thicknesses: NaN NaN 2 NaN
space directions: (2,0,0) (0,2,0) (0,0,2) none
kinds: space space space list
endian: little
encoding: raw
space units: "mm" "mm" "mm"
space origin: (-128,-128,-70)
measurement frame: (1,0,0) (0,1,0) (0,0,1)
modality:=DWMRI
DWMRI b-value:=1000
DWMRI_gradient_0000:=0 0 0
DWMRI_gradient_0001:=-0.203553 -0.520248 -0.829402
DWMRI_gradient_0002:=0.197695 -0.520657 -0.830562
DWMRI_gradient_0003:=0.401955 -0.176658 -0.898457
DWMRI_gradient_0004:=-0.403572 -0.731857 -0.549104
DWMRI_gradient_0005:=-0.201573 -0.941929 -0.268585
DWMRI_gradient_0006:=0.852749 0.519126 0.0576821
DWMRI_gradient_0007:=0.731269 0.520087 0.44131
DWMRI_gradient_0008:=-0.407559 -0.176959 -0.895869
DWMRI_gradient_0009:=0.732625 0.177173 0.657169
DWMRI_gradient_0010:=0.650407 0.730683 -0.207539
DWMRI_gradient_0011:=-0.322134 -0.941099 0.102775
DWMRI_gradient_0012:=-0.324216 -0.520604 0.789845
DWMRI_gradient_0013:=-0.650408 -0.520154 0.553458
DWMRI_gradient_0014:=0.978619 0.176929 -0.104889
DWMRI_gradient_0015:=0.854877 0.177104 -0.487667
DWMRI_gradient_0016:=-0.00073729 0.731961 -0.681346
DWMRI_gradient_0017:=-0.00188675 0.942326 -0.334691
DWMRI_gradient_0018:=0.653997 -0.520151 0.549301
DWMRI_gradient_0019:=0.329525 -0.5206 0.787648
```

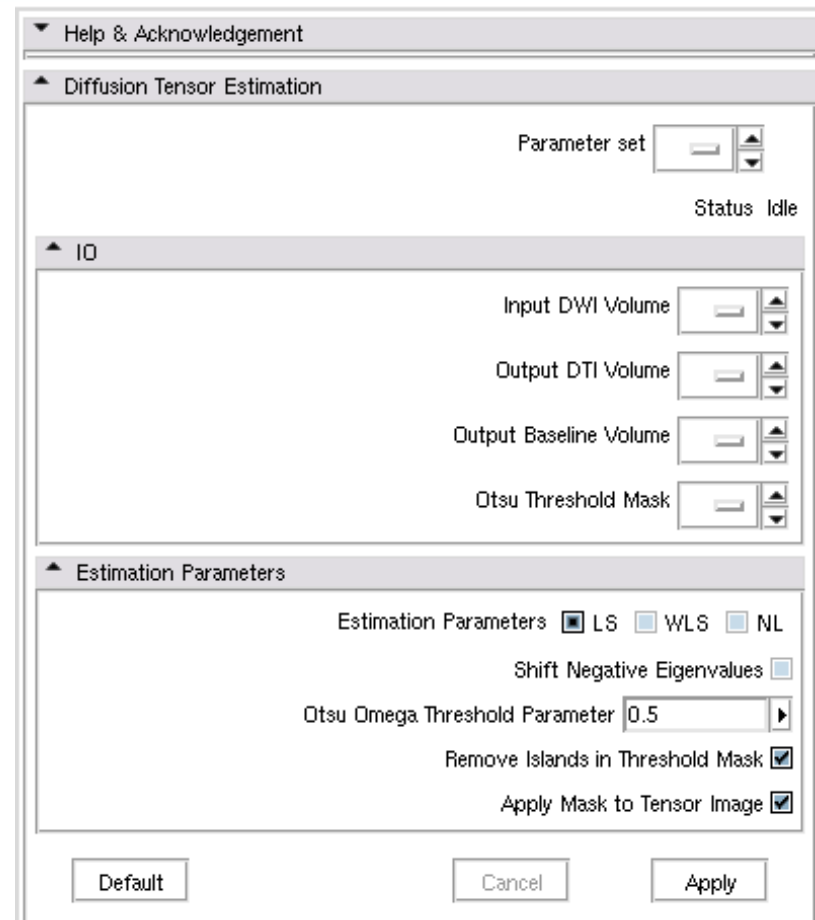



Visual inspection

The next step in inspecting DicomToNrrdConverter outputs is a superficial check of gradient direction orientations via the tensor image.

Load DTIPrepInput.nhdr into Slicer. Use the Diffusion Tensor Estimation module with the following parameters:

- Input DWI Volume: DTIPrepInput.nhdr
- Output DTI Volume: Create New DiffusionTensorVolume
- Output Baseline Volume: Create New Volume
- Otsu Threshold Mask: Create New Volume
- Estimation Parameters: defaults



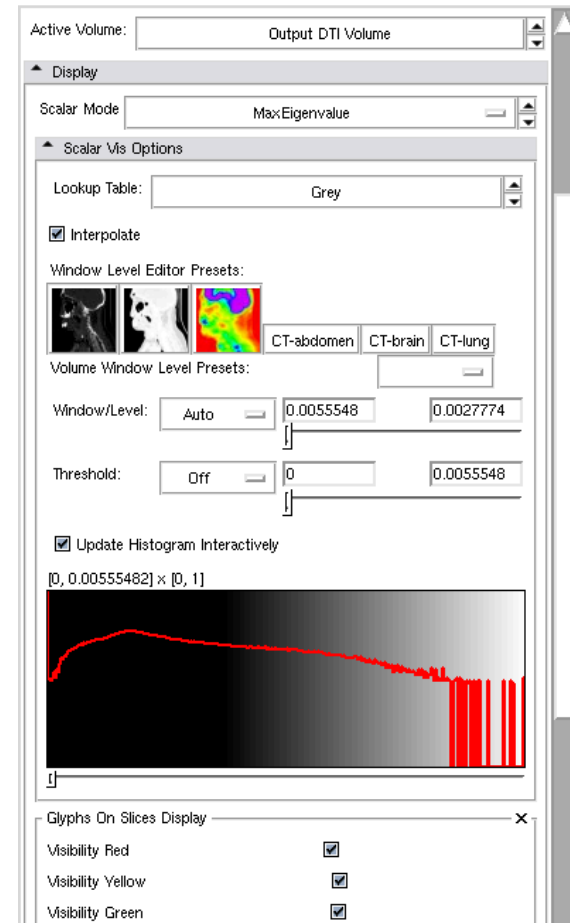


Visual inspection

Once the Diffusion Tensor Estimation module is finished running, change the Volumes module to display the Output DTI Volume as the Active Volume.

Use the following settings:

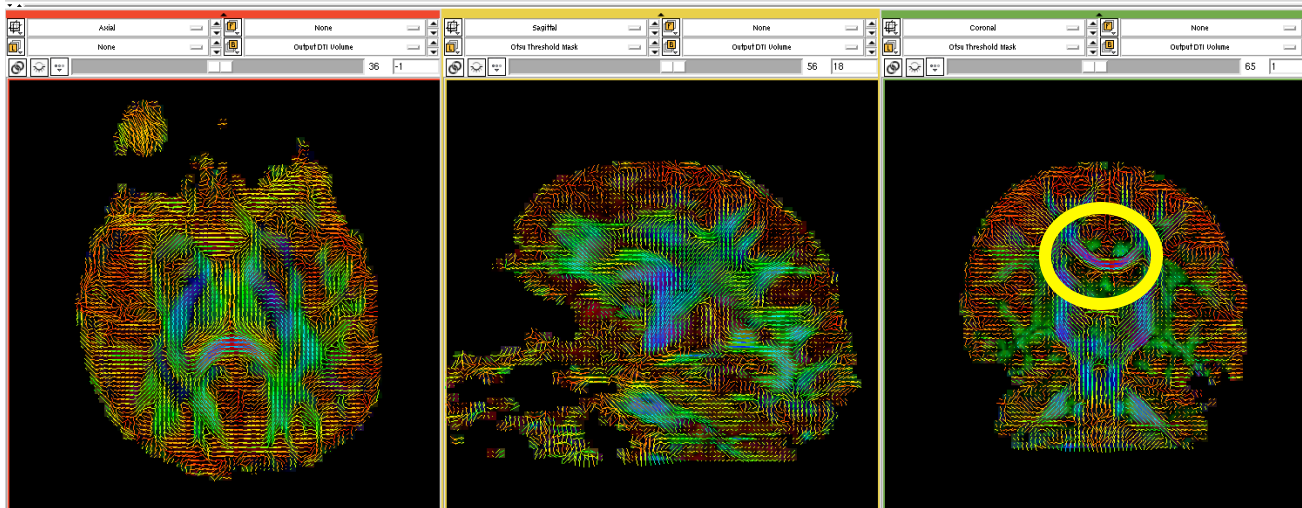
- Scalar Mode: MaxEigenvalue
- Glyphs On Slices Display: check all boxes (Visibility Red, Visibility Yellow, Visibility Green)





Visual inspection

Change viewer bars to display only the Output DTI Volume with the color glyphs.

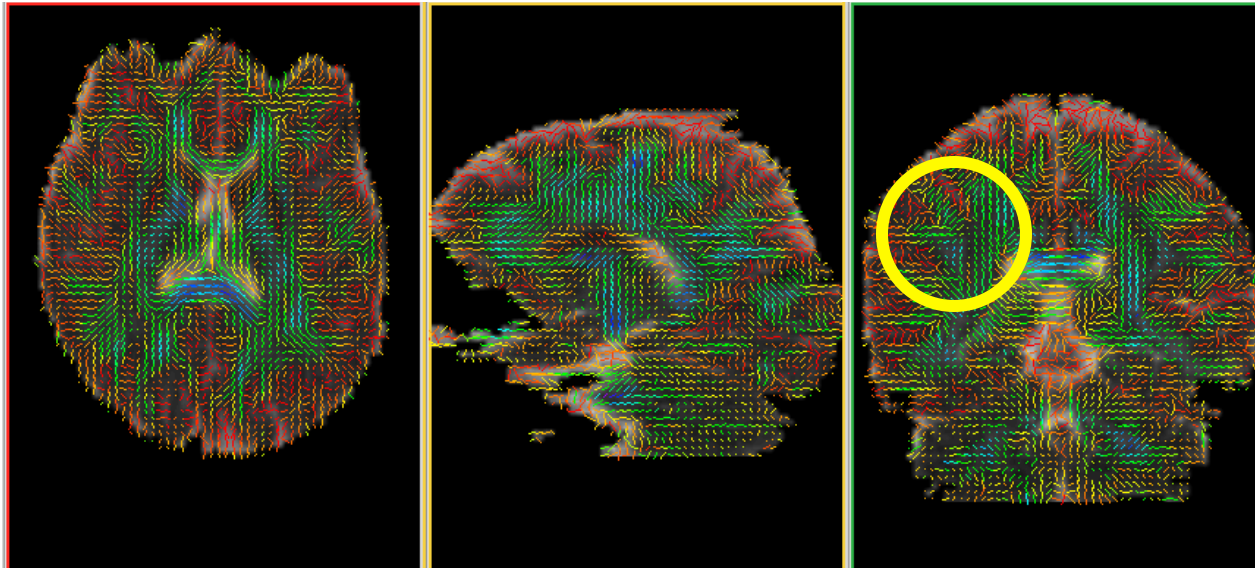


The glyph orientation will reflect the general direction of diffusion at that voxel. To provide a reference point: notice how the corpus callosum contains a large number of blue left-to-right glyphs. We recommend using this maximum eigenvalue view to get a general feel if the diffusion gradient direction coordinates in the NRRD file are correct.



Visual inspection

In the event your diffusion gradient direction coordinates are not accurate, the glyph orientations are generally counterintuitive. Here is an example of a blatantly bad data set, where the green glyphs are oriented perpendicular what they should be. Incorrect diffusion gradient directions in the DICOM element tags are often the cause of this problem.





Visual inspection

Some of the following visual inspection steps can also be done in Slicer. They will instead be done here in the DTIPrep GUI to highlight all of DTIPrep's features.

Full documentation for DTIPrep can be found here:

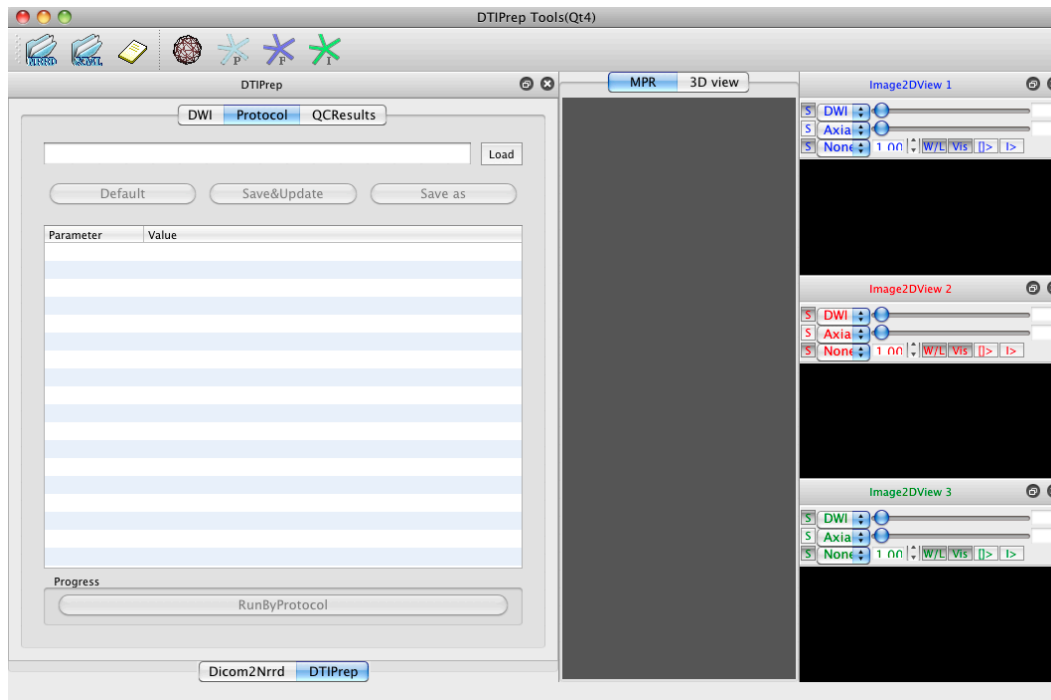
<http://www.nitrc.org/plugins/mwiki/index.php/dtiprep:MainPage>



Visual inspection

Launch the DTIPrep GUI with the following command:

DTIPrep



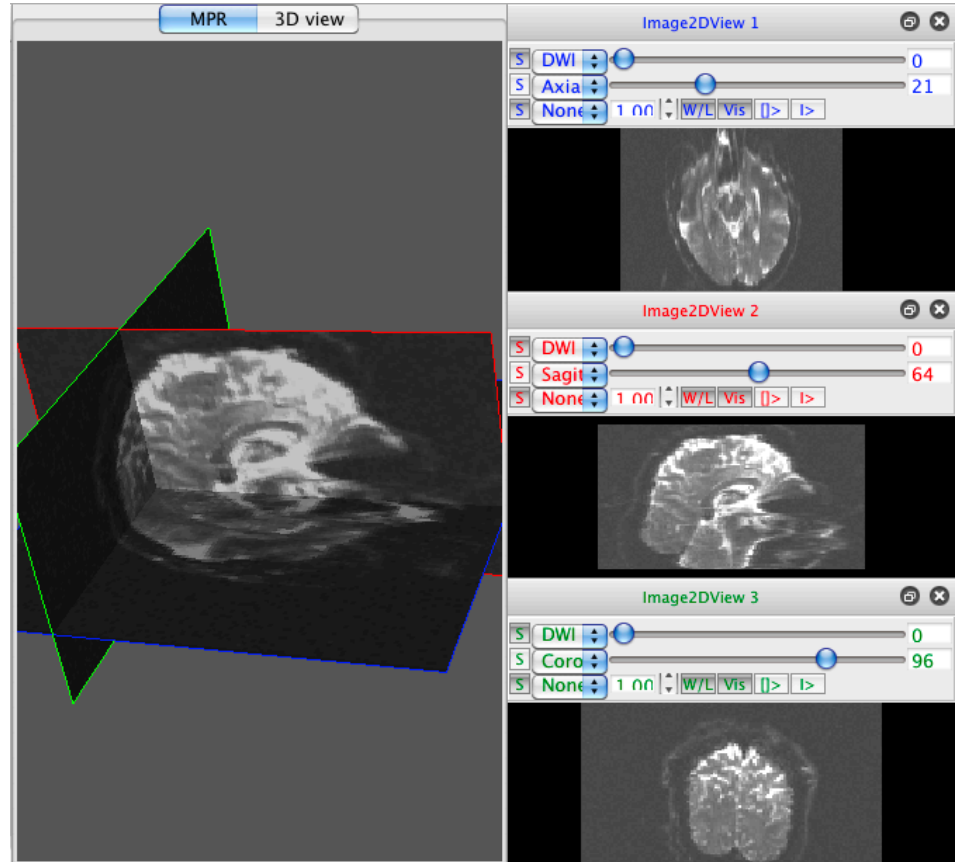


Visual inspection

Load a NRRD file by clicking the NRRD icon in the top left corner.



Select DTIPreInput.nhdr to load the DWI image in the axial, coronal, and sagittal views. Click the MPR tab to turn it blue and bring all views into the main window.





Visual inspection

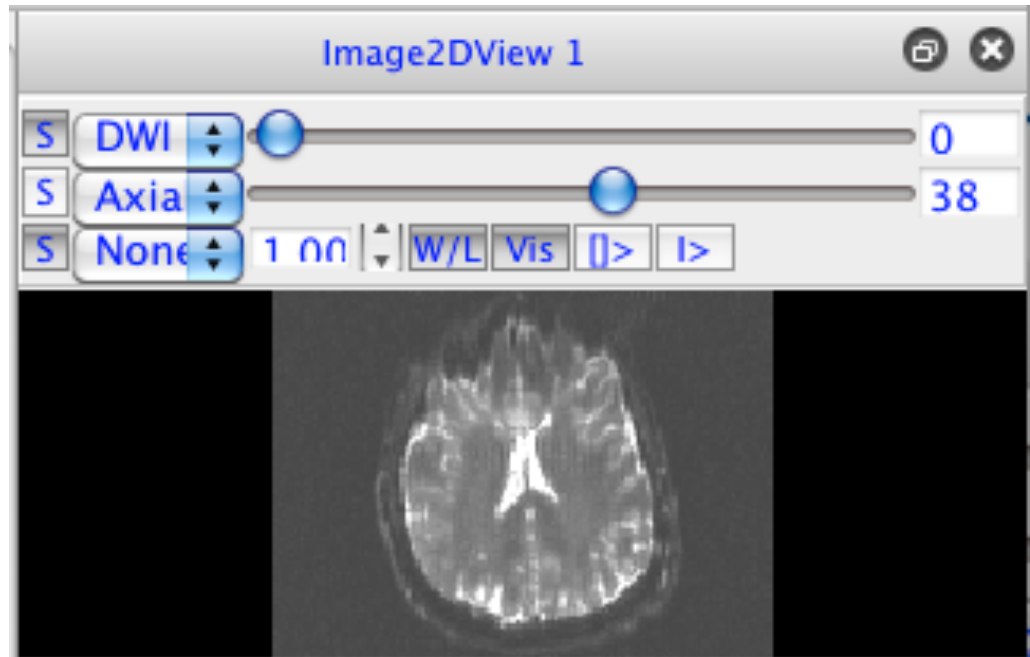
The following are clicks/keys that manipulate the DWI image in the main window view:

- Roll mouse scroll wheel forward/backwards over images to increase/decrease their sizes
- Click mouse, hold click and drag mouse forward/backwards over images to darken/brighten window level
- Click mouse, hold click and drag mouse left/right over images to change contrast
- r - bring 3D view back to center
- f - zoom in on 3D view
- w - remove views from 3D view
- s - bring back views in 3D view



Visual inspection

Use the scrolling circles on each view to scroll through DWI volumes (top scroller) and 3D volume slices (bottom scroller).

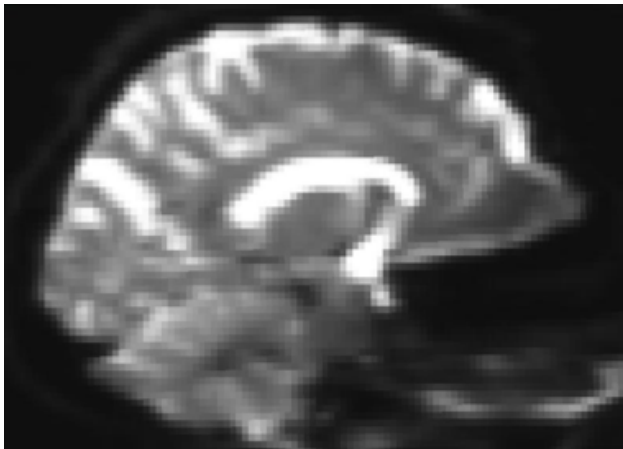




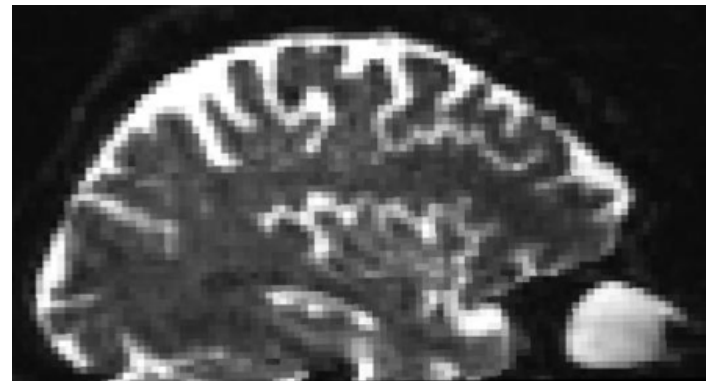
Visual inspection

Inspect degree of brain coverage. Here are examples of good and bad coverage. Degree of coverage will determine the types of analyses that can be done on the data (i.e. full coverage is necessary for atlas building).

Good coverage



Bad coverage



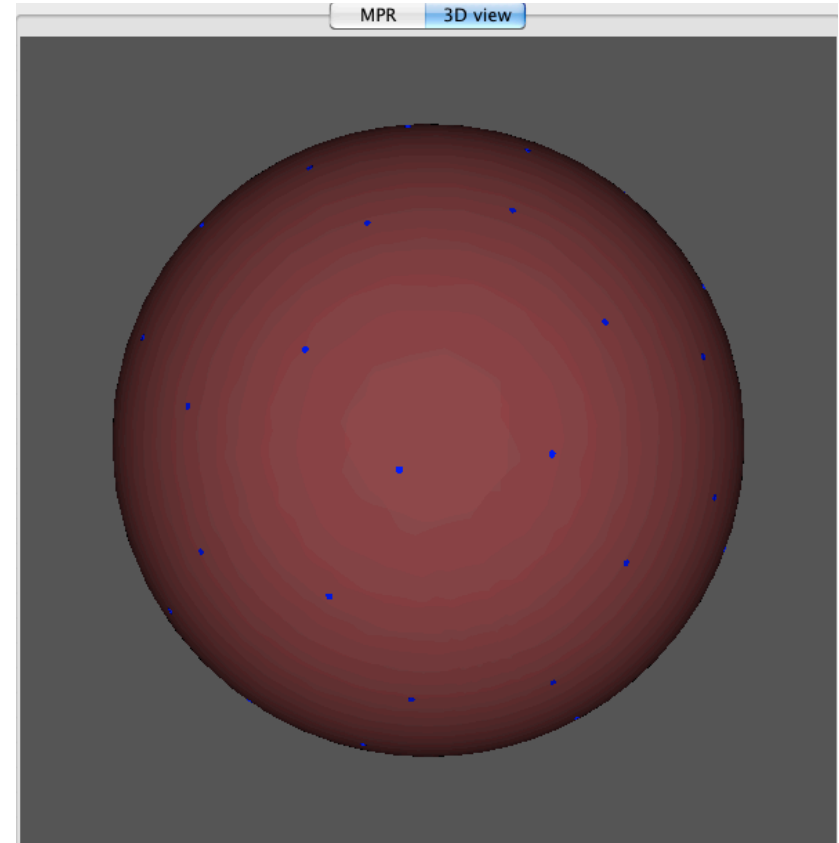


Visual inspection

Inspect the distribution of diffusion directions sampled in the DWI scan to be sure they are homogeneous. Click on the 3D view tab, followed by the sphere and F (blue star) icons.



A sphere with dots (that represent the unit vectors of each diffusion gradient direction projected onto a unit sphere) will appear in the 3D View.





Overview of tutorial

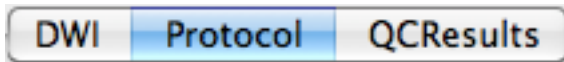
- Part 1: Using DicomToNrrdConverter to convert DWI DICOM files to NRRD file format
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-



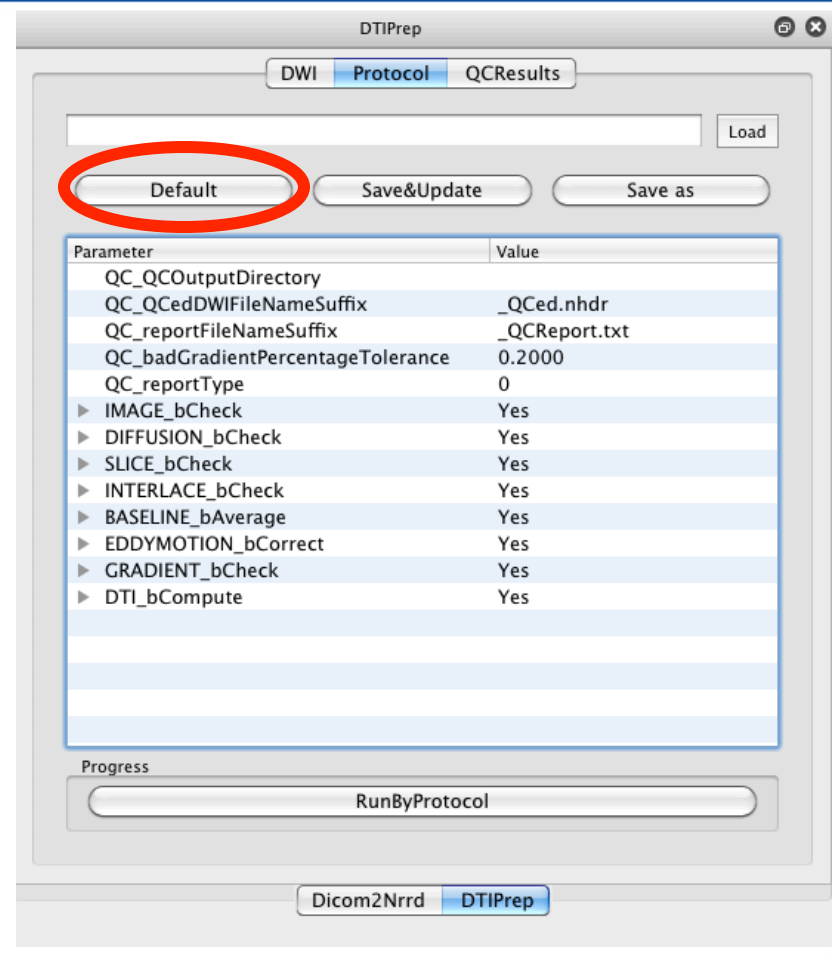
DTIPrep: GUI

Since this is the first time DTIPrepInput.nhdr is being loaded into DTIPrep, a new data acquisition protocol (automatic QC checking parameters) must be defined.

Click the Protocol tab.



Click the Default button to bring up the default automatic QC checking parameters.

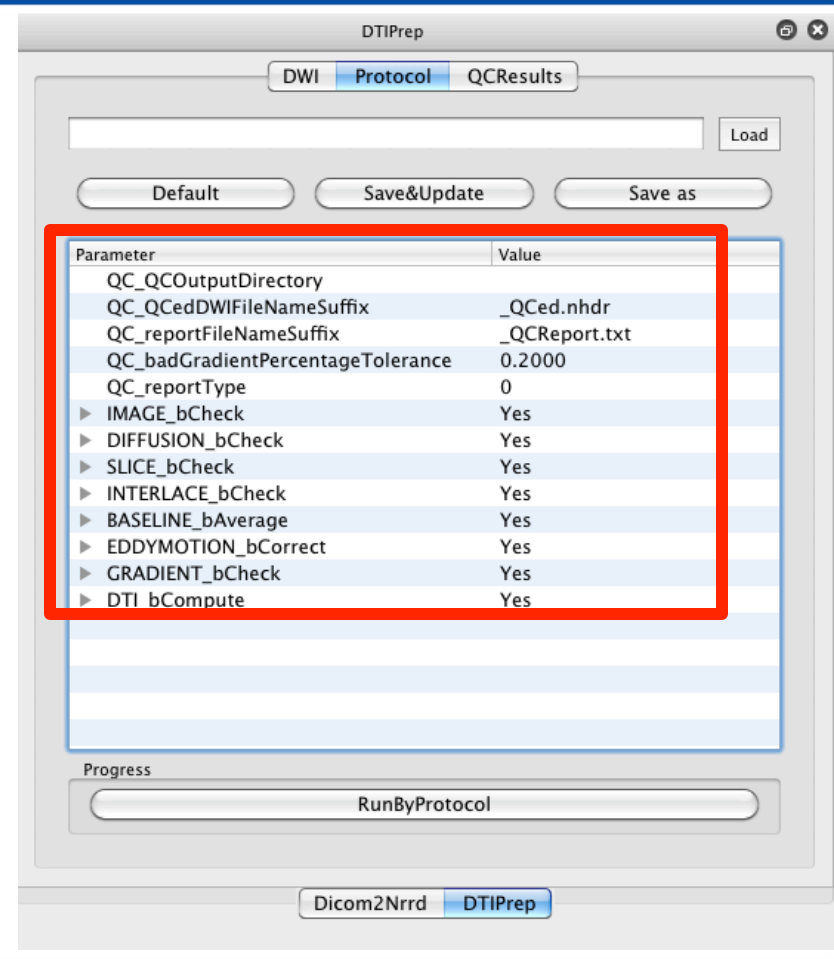




DTIPrep: GUI

Note: The checking parameters used in this tutorial will be the DTIPrep default settings. These default settings were originally designed for neonatal DWI data. It is possible to change the checking parameters by double clicking on the list elements. A complete description of all checking parameters can be found here:

<http://www.nitrc.org/plugins/mwiki/index.php/dtiprep:DTIPrepQCConfigurations>

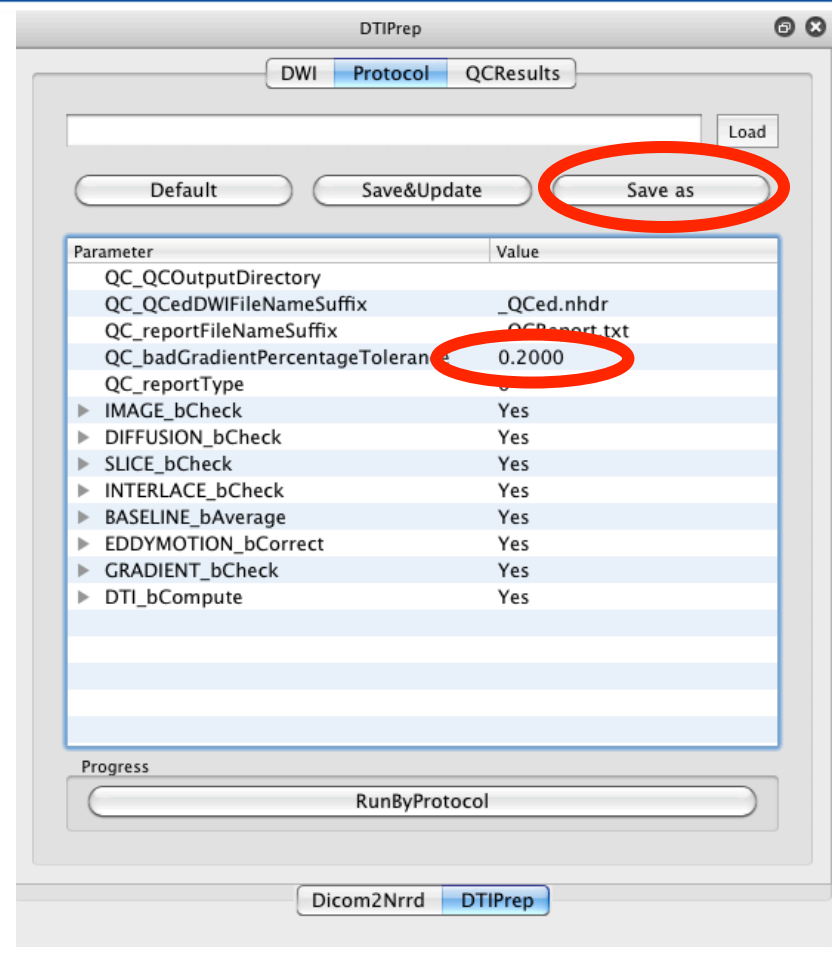




DTIPrep: GUI

Since we want to see how many gradients will be excluded in this scan, double click 0.2000 next to QC_badGradientPercentageTolerance and change it to 0.5000.

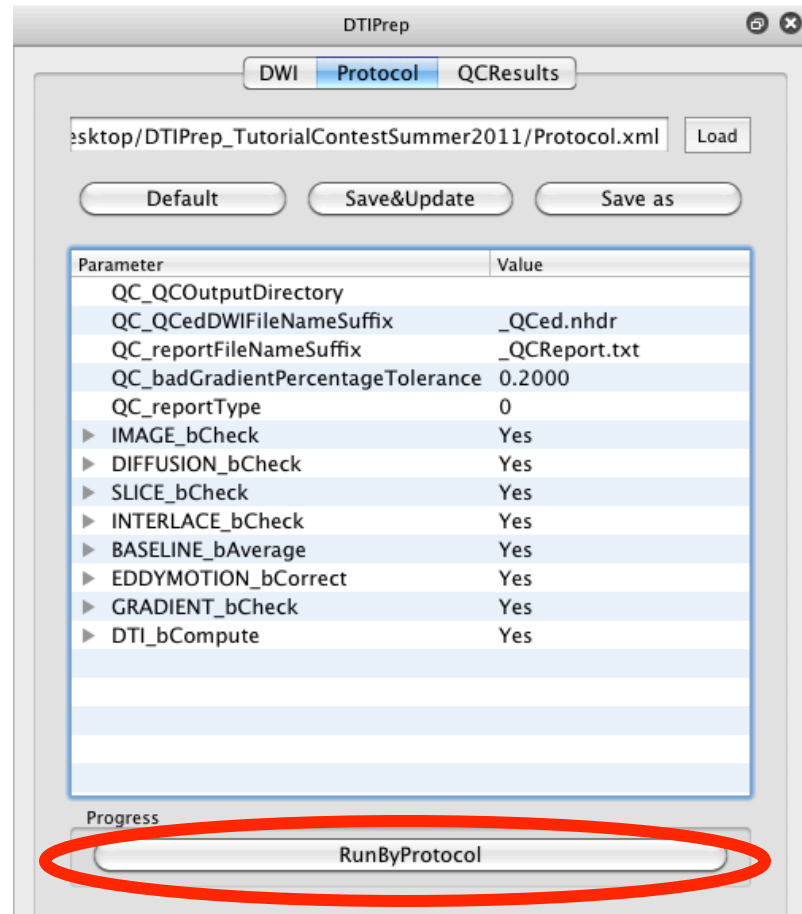
Click the Save as button to bring up the dialog box to save the automatic QC checking parameters to an xml file as "Protocol.xml."





DTIPrep: GUI

The GUI is now ready to begin automatic QC checking. Click RunByProtocol to begin checking.





DTIPrep: GUI

DTIPrep will output its status to the terminal. DTIPrep will proceed through 7 main steps that will PASS or FAIL:

- Image information check
- Diffusion information check
- Slice-wise checking
- Interlace-wise checking
- Baseline averaging
- Eddy-current and head motion artifacts correcting
- Gradient-wise checking



DTIPrep: GUI

When DTIPrep finishes running, it will display a summary report in the terminal listing the checking steps that passed and/or failed.

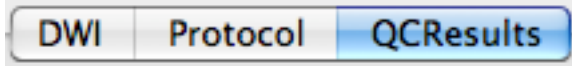
```
Left DWI Diffusion:
baselineLeftNumber: 1
bValueLeftNumber: 1
gradientDirLeftNumber: 23
0      [ 0.000000, 0.000000, 0.000000 ] 1
1      [ 0.401435, -0.181050, -0.897815 ] 1
2      [-0.400872, -0.735869, -0.545710 ] 1
3      [-0.201688, -0.943149, -0.264181 ] 1
4      [ 0.849503, 0.524304, 0.058728 ] 1
5      [ 0.727700, 0.525137, 0.441097 ] 1
6      [-0.405594, -0.179572, -0.896241 ] 1
7      [ 0.730220, 0.182930, 0.658267 ] 1
8      [ 0.647370, 0.733459, -0.207241 ] 1
9      [-0.320629, -0.941399, 0.104717 ] 1
10     [-0.327449, -0.520418, 0.780633 ] 1
11     [-0.650200, -0.521709, 0.552322 ] 1
12     [ 0.977828, 0.181324, -0.104756 ] 1
13     [ 0.854234, 0.181206, -0.487286 ] 1
14     [-0.000120, 0.731385, -0.681965 ] 1
15     [-0.000665, 0.942392, -0.334511 ] 1
16     [ 0.651537, -0.518627, 0.553647 ] 1
17     [ 0.325899, -0.518037, 0.790840 ] 1
18     [ 0.201024, -0.174253, 0.963964 ] 1
19     [-0.651503, 0.729780, -0.207278 ] 1
20     [ 0.322608, -0.940534, 0.106398 ] 1
21     [ 0.198576, -0.943672, -0.264673 ] 1
22     [ 0.857436, -0.179059, 0.482433 ] 1
23     [ 0.979122, -0.177245, 0.099521 ] 1

=====
QC result summary:
=====
Image information check:    PASS
Diffusion information check: PASS
Slice-wise check:         PASS
Interlace-wise check:     PASS
Gradient-wise check:      PASS
```



DTIPrep: GUI

The results of the automatic QC checking are now ready for viewing. Click on the QCResults tab to display the results table.



The QCResults will list which gradients failed QC and at what step. Gradients that passed QC are also listed, along with their alterations (i.e. coregistration to baseline)

type	result	processing
▼ ImageInformation		
origin	Pass	
size	Pass	
space	Pass	
spacedirection	Pass	
spacing	Pass	
▼ DiffusionInformation		
b value	Pass	
gradient	Pass	
measurementFrame	Pass	
▼ IntensityMotion		
▶ gradient_0000		BASELINE_AVER...
▶ gradient_0001		EXCLUDE_SLICE...
▼ gradient_0002		EXCLUDE_SLICE...
OriginalDir	0.197695 -0....	
ReplacedDir	0.197695 -0....	
CorrectedDir	0.197695 -0....	
▼ SliceWiseCheck		EXCLUDE
Slice#	14	
Correlation	0.878637	
Slice#	15	
Correlation	0.877339	
Slice#	16	
Correlation	0.819039	
Slice#	18	
Correlation	0.852367	
Slice#	19	
Correlation	0.834914	
Slice#	20	
Correlation	0.85037	
▶ InterlaceWiseCheck		NA
▶ GradientWiseCheck		NA
▶ gradient_0003		EDDY_MOTION...
▶ gradient_0004		EDDY_MOTION...
▶ gradient_0005		EDDY_MOTION...
▶ gradient_0006		INCLUDE
▶ gradient_0007		EDDY_MOTION...
▶ gradient_0008		EDDY_MOTION...
▶ gradient_0009		EDDY_MOTION...
▶ gradient_0010		EDDY_MOTION...
▶ gradient_0011		EDDY_MOTION...
▶ gradient_0012		EDDY_MOTION...

Manual Checking

Default Result Save DWI



DTIPrep: GUI

One of the gradients removed from the sample data set was Gradient #2 by the Slicewise checking step. That is indicated in the GUI report on the left and the image that was excluded can be inspected on the right. In this case, slices 14 through 20 in gradient 2 did not pass QC and were thus excluded.

The screenshot displays the DTIPrep GUI with the 'QCResults' tab selected. The report shows the following data for the 'measurementFrame' section:

type	result	processing
ImageInformation	Pass	
origin	Pass	
size	Pass	
space	Pass	
spacedirection	Pass	
spacing	Pass	
DiffusionInformation	Pass	
b value	Pass	
measurementFrame	Pass	
IntensityMotion		
gradient_0000	BASELINE_AVER...	
gradient_0001	EXCLUDE_SLICE...	
gradient_0002	EXCLUDE_SLICE...	
OriginalDir	0.197695 -0...	
ReplacedDir	0.197695 -0...	
CorrectedDir	0.197695 -0...	
SliceWiseCheck	EXCLUDE	
Slice#	14	
Correlation	0.878637	
Slice#	15	
Correlation	0.877339	
Slice#	16	
Correlation	0.819039	
Slice#	18	
Correlation	0.852367	
Slice#	19	
Correlation	0.834914	
Slice#	20	
Correlation	0.85037	
InterlaceWiseCheck	NA	
GradientWiseCheck	NA	
gradient_0003	EDDY_MOTION...	
gradient_0004	EDDY_MOTION...	
gradient_0005	EDDY_MOTION...	
gradient_0006	INCLUDE	
gradient_0007	EDDY_MOTION...	
gradient_0008	EDDY_MOTION...	
gradient_0009	EDDY_MOTION...	
gradient_0010	EDDY_MOTION...	
gradient_0011	EDDY_MOTION...	
gradient_0012	EDDY_MOTION...	

The GUI also shows a 3D view of the brain data and two 2D image views (Image2DView 2 and Image2DView 3) displaying the excluded slice. The 'Manual Checking' section at the bottom includes buttons for 'Default Result' and 'Save DWI'.

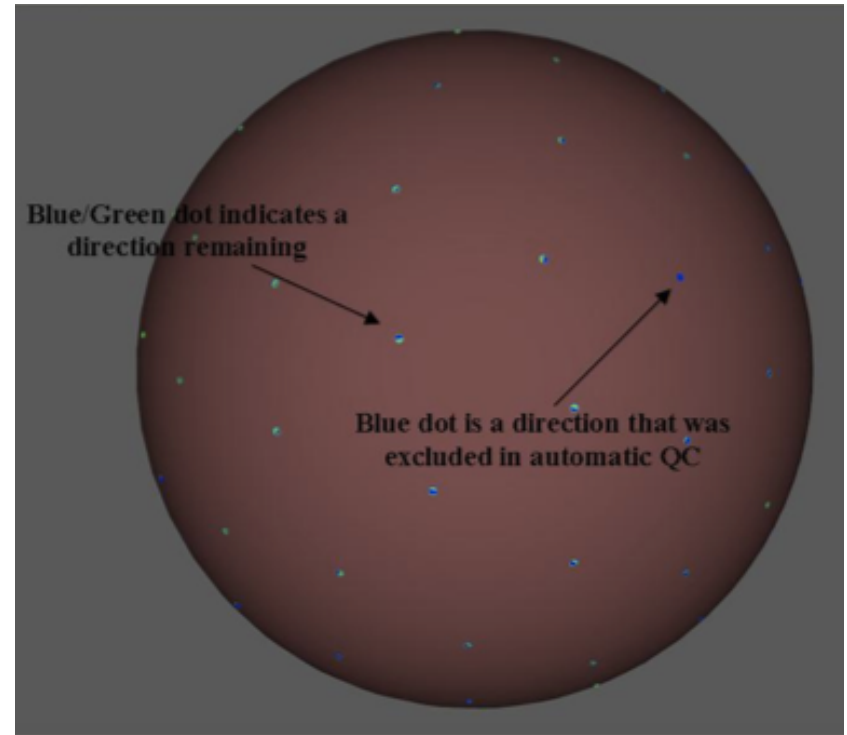


DTIPrep: GUI

Switch to 3D View to view how the gradient direction projections on a unit sphere changed. Click the sphere, F, and I icons.



The F (blue) represents gradients before QC and I (green) represents gradients left after QC. Note any unevenness in spatial distribution.





DTIPrep: GUI

The QCResults obtained in the GUI are outputted to an xml file:

- DTIPrepInput.nhdr_XMLQCResult.xml

DTIPrep also outputs a new NRRD file that only contains gradients that passed QC and a text file report describing the actions DTIPrep took during the QC process:

- DTIPrepInput_QCed.nhdr
- DTIPrepInput_QCed.raw.gz
- DTIPrepInput_QCReport.txt



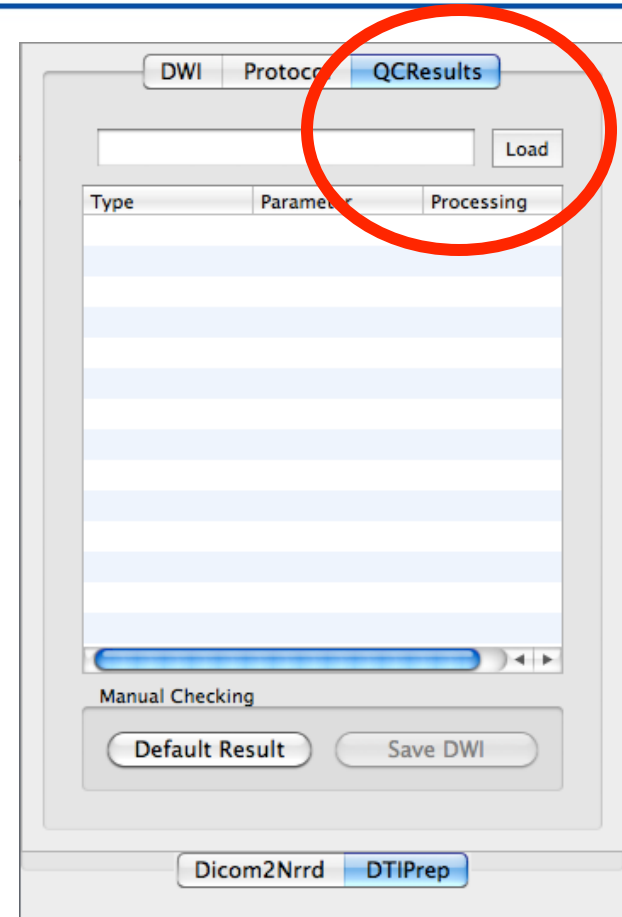
DTIPrep: GUI

The QCResults.xml file (DTIPrepInput.nhdr_XMLQCResult.xml) can be reloaded into the GUI re-review via one of two ways:

- 1) Click the yellow icon in the upper left corner and choose the QCResult.xml file



- 2) Click the QCResults tab, followed by the Load icon to bring up a dialog box to select the QCResult.xml file





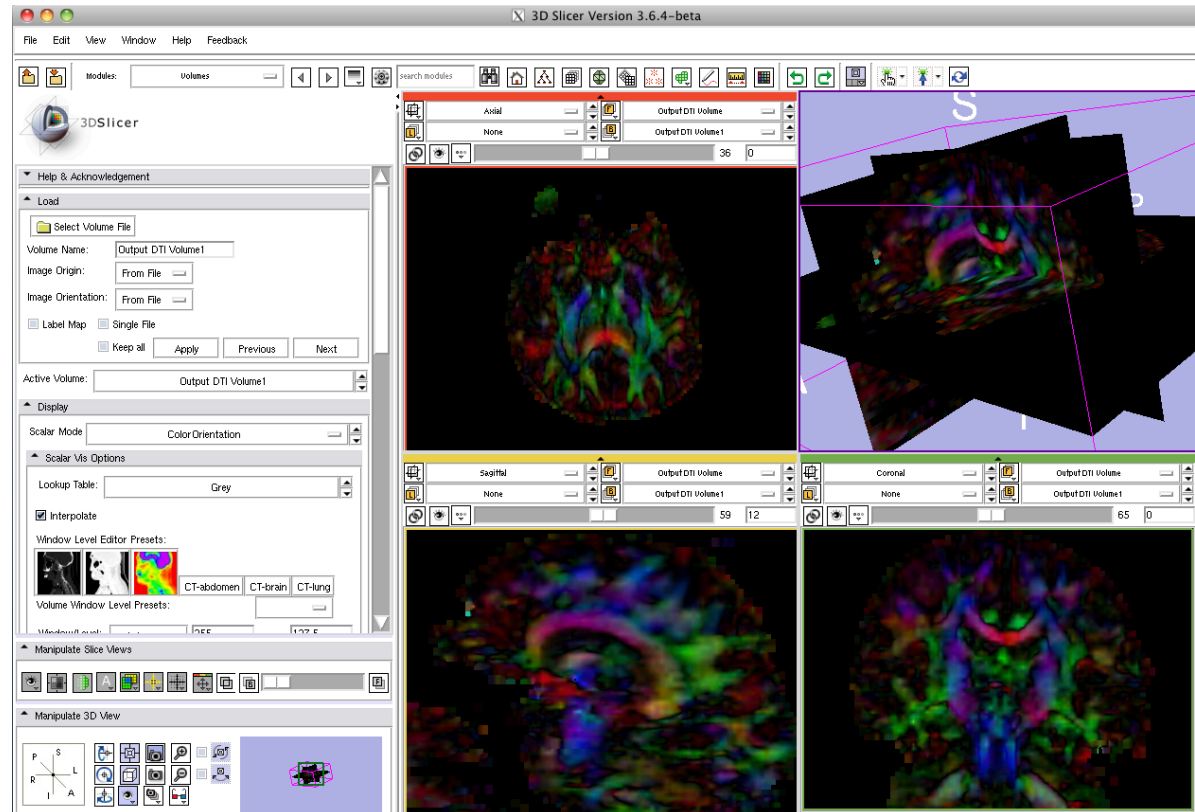
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Visual re-inspection

Load both DTIPrepInput.nhdr and DTIPrepInput_QCed.nhdr files into Slicer. Compute tensor images for each image and set the Scalar Mode to ColorOrientation for both in the Volumes module. Compare color orientation maps derived from NRRD files before and after using DTIPrep.

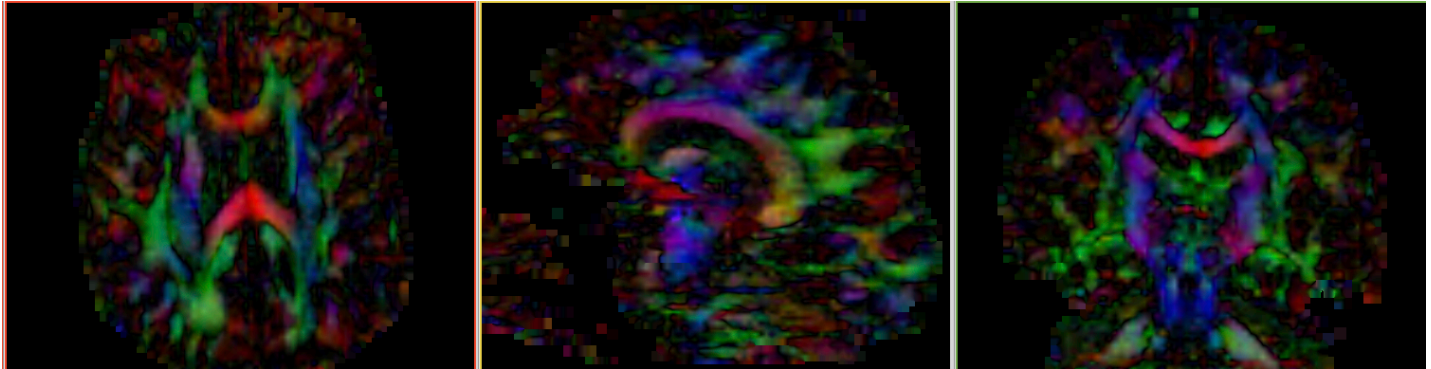




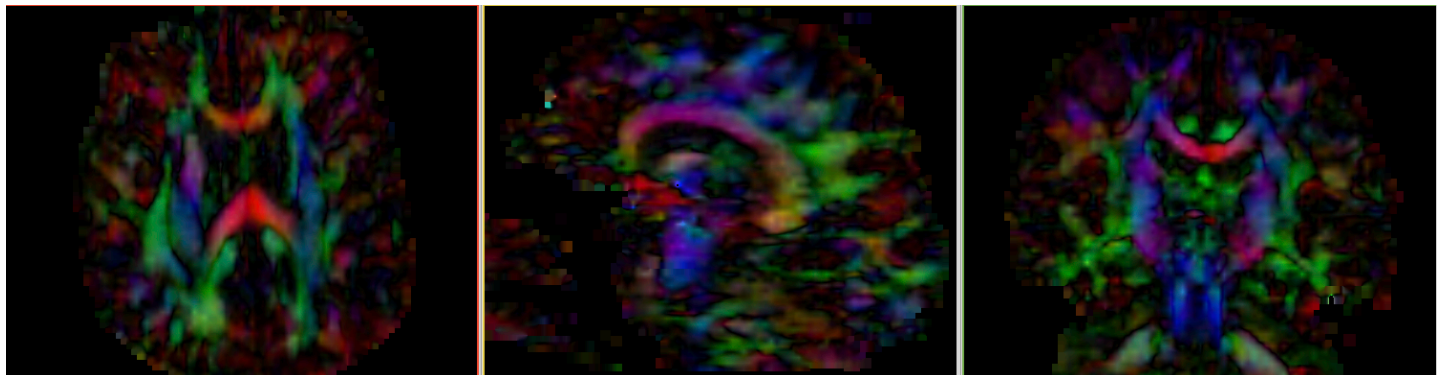
Visual re-inspection

One can note the difference in color orientation maps before and after processing with DTIPrep.

Before
DTIPrep



After
DTIPrep





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DTIPrep: Command line

Running DTIPrep from the command line (validating against a previously created data acquisition protocol file)

```
DTIPrep --DWINrrdFile < DWIFilename > --xmlProtocol < xmlFileName > --check --outputFolder < OutputFolder >
```

Running DTIPrep from the command line (generate a new data acquisition protocol file based on input NRRD file)

```
DTIPrep --DWINrrdFile < DWIFilename > --xmlProtocol < xmlFileName > --default --outputFolder < OutputFolder >
```

Running DTIPrep from the command line (generate a new data acquisition protocol file from the input NRRD file AND begin validation)

```
DTIPrep --DWINrrdFile < DWIFilename > --xmlProtocol < xmlFileName > --default --outputFolder < OutputFolder >
```



Conclusion

DTIPrep can be a useful tool for automated quality control of diffusion-weighted images.



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