Quality Control of Diffusion Weighted Images

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ABSTRACT

Diffusion Tensor Imaging (DTI) has become an important MRI procedure to investigate the integrity of white matter in brain in vivo. DTI is estimated from a series of acquired Diffusion Weighted Imaging (DWI) volumes. DWI data suffers from inherent low SNR, overall long scanning time of multiple directional encoding with correspondingly large risk to encounter several kinds of artifacts. These artifacts can be too severe for a correct and stable estimation of the diffusion tensor. Thus, a quality control (QC) procedure is absolutely necessary for DTI studies. Currently, routine DTI QC procedures are conducted manually by visually checking the DWI data set in a gradient by gradient and slice by slice way. The results often suffer from low consistence across different data sets, lack of agreement of different experts, and difficulty to judge motion artifacts by qualitative inspection. Additionally considerable manpower is needed for this step due to the large number of images to QC, which is common for group comparison and longitudinal studies, especially with increasing number of diffusion gradient directions. We present a framework for automatic DWI QC. We developed a tool called DTIPrep which pipelines the QC steps with a detailed protocoling and reporting facility. And it is fully open source. This framework/tool has been successfully applied to several DTI studies with several hundred DWIs in our lab as well as collaborating labs in Utah and Iowa. In our studies, the tool provides a crucial piece for robust DTI analysis in brain white matter study.

Keywords: Diffusion Weighted Imaging, Diffusion Tensor Imaging, Quality Control, Intensity Artifact, Eddy Current Artifact, Motion Artifact

1. INTRODUCTION

Diffusion Tensor Imaging (DTI) has become an important MRI procedure to image tissues with micro fabric structures in vivo, especially to investigate the integrity of brain white matter. DTI is increasingly applied to brain studies of normal development, aging and pathological changes from various diseases. DTI is estimated from a series of Diffusion Weighted Imaging (DWI) volumes collected by using (at least 6) non-collinear diffusion sensitizing gradients (Basser et al., 1994).

An image artifact in MRI is a structure or imperfection which is not normally present but visible as a result of either a limitation or malfunction in the hardware or software of the scanning device, or a consequence of the subject scanned. Many types of artifacts may occur in MRI. Changes in patient position, different pulse sequences, metallic artifacts, or other imaging variables can cause image distortion during image acquisition. Although techniques are developed to reduce the artifacts, sometimes these artifacts can still be very noticeable, especially in DWI.

Due to the inherent low signal to noise ratio (SNR) and relatively long scanning time of the multi-direction DWI acquisition compared to common MRI modalities, DWI always suffers from several kinds of artifacts, including eddy-current artifact, head motion artifact, bed vibration artifact, etc. These artifacts show up as slice-wise intensity abnormalities and/or motion between different gradients and interleaved parts within one gradient image volume.

Even if the artifact in DWI is just a few pixels out of balance, artifacts in DWI result in estimation errors of tensors and give confusing artifactual appearances further in tensor-derived scalar maps such as fractional anisotropy (FA), mean diffusivity (MD), Frobenius Norm, Eigen values and Eigen vectors. While doing tractography, this leads to fibers with wrong orientation or premature fiber tracking termination. In short, artifacts in DWI will finally produce bias in any form of DTI analysis. Sometimes, these artifacts are so severe that it is impossible to get good fidelity in estimating the DTI

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information of the brain under investigation. Thus, a quality control procedure is a key preprocessing to detect and correct the artifacts in DWI, or to exclude one or more gradients bearing strong artifacts that cannot be corrected, providing there are enough diffusion gradient volumes left for a reasonably stable estimation of tensor fields. In addition, for collaborative multi-site studies, data is collected at different institutions and may be even collected with different scanners or with same scanners but different versions of software. Although routine scanner QC at each site and phantom scans are conducted, inconsistencies w.r.t. DWI quality and consistency might occur.

Despite rapid progress in DTI processing and application, the problem of quality control (QC) in DTI remains to be elusive. There are some papers addressing this problem. (Gallichan et al., 2009) studied the systematic vibration artifact, suggesting extending the TR and using a full k-space acquisition. However, these methods are not always clinically acceptable. (Hasan, 2007) proposed a framework for quality control and parameter optimization in DTI. The approach is based on the analytical error propagation of the MD and provided simple analytical quality control measures for optimization of diffusion parameter space in an isotropic medium. (Mangin et al., 2002) proposed a robust DTI estimation approach, in which after eddy-current artifact correction, the weight of each data point is set to a function of the residuals of the previous iteration while doing iteratively reweighted least-squares fitting. Their method ensures that potentially artifactual data points having large residuals are given lower weights in the estimation of the tensor parameters. (Chang et al., 2005) proposed an approach for robust diffusion tensor estimation by outlier rejection. Their method uses iteratively reweighted least-squares regression to identify potential outliers and subsequently exclude them while estimating the tensor. Head motion artifact is common in DWI. For the motion between gradients induced artifact, we can correct them easily and the data should not be excluded as outliers. Chang's method will also result in a DTI map in which not all the voxel tensors are estimated from the same number of data points.

Currently, most of the DWI quality control procedures are conducted manually by visually checking the DWI data set in a gradient by gradient and slice by slice way, or by examining the DTI itself. The results often suffer from low consistency across different data sets and insufficient inter-rater reliability of different expert QC raters. Further, it is very difficult to judge motion artifacts across DWI scans by qualitative inspection only. Also, considerable manpower is needed for this step due to the increasing number of gradients used in the data collecting protocol, especially for those studies with large number of subjects.

We extend our work (Liu et al., 2009) in DTI preprocessing and present a full DWI preprocessing framework for automatic DWI quality control. The QC pipeline has been implemented in a tool called DTIPrep, which pipelines information checking, artifacts checking and correction, and DTI computation functionalities with a detailed protocoling and reporting facility. DTIPrep is fully open source and can run in both GUI and command line modes.

2. PIPLINE

Usually, for the convenience of image processing, analysis and most importantly, not to bring unexpected influence and bias to the final results, a data acquisition protocol needs to be defined for the whole study or for each of the subgroups before collecting the data. And for the whole subjects or with a subgroup of them, their image properties are usually similar, because of the controlling of the subjects' attributes. This allows us to set up a unified checking protocol for the DWI QC for a study or for a group of similar individuals.

The QC framework proposed here is composed of several steps. Each step conducts a specific checking of the DWI data against a group of parameters preset. These steps are streamed to makeup a QC pipeline and all the parameters of all the steps are formulated into a tree structure and stored in an xml formatted file for easy manipulation.

DWI data for one study or one subgroup should be collected using acquisition settings for both the image and diffusion as similar as possible, or ideally, identical. But this cannot always be insured due to various situations, such as mis-manipulation of the scanner, using wrong scan protocol file, and limitation of the subjects. This tends to happen especially in multi-site collaborated large studies. DWI QC should be functioned to find and report such mismatches. It is common to find some intensity related artifacts in some of the directional gradient volumes, most often shown as dark slices. While examining the other orthogonal views of the gradients volumes, venetian blind-like artifacts sometimes can be seen. This kind of artifact comes from the motion occurred during the acquisition of the odd and even fields of the same gradient volume. Eddy currents can cause artifacts in images and may seriously degrade overall magnet performance. Because additional diffusion sensitizing gradient are used, this kind of artifact in DWIs is very common. This kind of artifact is represented in the phase coding direction. If subject moves during the scanning procedure, all the gradient and baseline volumes will not aligned to each other. Both the eddy-current and head motion artifacts destroy the

voxel-wise correspondence across all the DWIs and baselines. To make a good DTI estimation, these two kinds of artifacts need to be detected and corrected before DTI computing. This is usually done by registering each of the gradient volumes to the baseline image followed by an update of the original sensitizing direction vectors. If several baseline volumes are acquired, they need to be aligned and averaged first. The implemented pipeline is described in detail as follows.

2.1 Dicom to NRRD conversion

Currently, there is not a unified format to store DWI data. Different institution and laboratories use different formats to store DWI images. NRRD (teem.sourceforge.net/nrrd/), Nifty and separate files are being used to store DW images. Here we choose to use NRRD format for both DWI and DTI storage. This is because that the NRRD file format, combined with a particular convention for using key/value pairs in the format, can be used to completely represent the necessary information about a DWI image volume, its anatomical orientation, and all the DWI-specific acquisition parameters that determine how the image values are used to estimate diffusion tensors. This is also the choice of National Alliance of Medical Image Computing (NAMIC).

We use DicomToNrrdConverter which comes with Slicer (www.slicer.org) to convert the DWI dicom files into a NRRD formatted file. There is also a module in Slicer to load DWI dicom files and then the data can be saved out as NRRD format. Direct use of DicomToNrrdConverter in scripts is efficient for batch processing.

2.2 Image information checking

In this step, common image information, such as sizes, origin, voxel spacing, space and space directional cosines is checked against the values in the DWI acquisition protocol and any mismatch will be reported.

Among all this parameters, the most important one is the spacing which defines the size of the voxels. Usually, within a study, all the individuals' DWIs are collected with the same voxel sizes. If spacing mismatch is reported, user should decide whether to exclude the subject or to resample the original data (this is not preferable usually). Group analysis of DTI usually requires same image sizes. If image sizes are found to be mismatched, the user can choose to turn on the cropping/padding option to crop or pad the DWIs to the desired sizes defined in the protocol. Although all the images are not required with the same space and space directional cosines, mismatches on these fields are also reported.

2.3 Diffusion information checking

This includes checking the b-value(s), diffusion sensitizing direction vectors and measurement frame. Due to the poor compliant situation of diffusion information storage in dicom files, close attention should be paid to the diffusion related information. This information contained in dicom files is not always the same as in the designed scanning protocol, or even missing, especially in studies with novel or experimental acquisition sequences.

Although usually exact diffusion settings are preferred, sometime we have some obliquely scanned data sets, in which elements of the measurement frame are not equal to 0 or ±1. So, instead of directly comparing the sensitizing vector list and measurement frame separately, we compare the cosine of the angle between the corresponding pairs of vectors from the checking protocol and nrrd file after a transformation as $(\text{measurement frame})^{-1} \times (\text{gradient directions})$. If there is no diffusion sensitizing direction vectors found in the dicom files, the nrrd file contains zero vectors for all the directions. In such situations, choice can be made to replace the diffusion direction vector list with those in the check protocol.

2.4 Slice-wise intensity related artifacts checking

A slice-wise check is designed to examine each slice of a DWI data set to find out if any of them bears any intensity related artifacts. In DWI data set, each gradient volume contains different diffusion information in different direction, and different slices contain different parts of the brain. There exists intensity variance across gradients and slices. This makes it unreasonable to directly compare the intensity of volxel and slices. We propose to use Normalized Correlation (NC) between successive slices across all the diffusion gradients for screening the intensity related artifacts. The NC computes pixel-wise cross correlation and normalizes it by the square root of the autocorrelation of the images:

$$\mathrm{NC}(A, B) = \frac{\sum_{i=1}^{N}(A_i \cdot B_i)}{\sqrt{\sum_{i=1}^{N} A_i \cdot \sum_{i=1}^{N} B_i}}$$

In the equation, A_i is the i-th pixel of Image A, B_i is the i-th pixel of Image B and N is the number of pixels considered.

Intensity artifacts between images result in small measure values. The metric is relatively sensitive to slice by slice motions and quick intensity changes while insensitive to small motions among gradient volumes. We tried to collect all the NCs at the same slice location from all the gradients and plot them, and they looked very much likely normally distributed. We did normal distribution tests at different slice positions from a number of DWIs of several studies with different subject attributions and diffusion acquisition protocols. For almost all of them, the Gaussian distributions are not rejected. So we just assume here that the NCs between the same pair of successive slices across all the diffusion gradients are normally distributed. So we can define the outliers as smaller than $NC_{mean} - \alpha \cdot \sigma$. For normal distributions, α can be calculated such that given the gradient number n, the number of the values lying away from the mean μ outside α time(s) standard deviations is much less than 1 to include all the "good" points. Here, α is the most important parameter to be set. For most clinical DTI study data nowadays, the number of diffusion gradients is typically less than 50. To make constrains looser, we set it to be 3.5 by default and recommend adjusting this parameter slightly (from 3 to 4) according to the data itself of the underlying study. After examining all the slice positions, we can figure out the outlier slice positions (according to adjacent slices) of each gradient volume. If any outlier is detected, the corresponding gradient volume is marked as bad and is excluded in the final output. For most of the time, we can skip the beginning and ending part of the volume slices, because the slices do not contain much brain tissue and the variations between adjacent slices are so large that the distribution are not always so normally distributed.

In short, a slice-wise intensity checking computes the correlations between successive slices in each gradient and examines them at each slice position across all the diffusion gradients volumes. Large deviation from the mean of all the gradients indicates a dramatic intensity change or an intensity artifact. If the DWI is multiple b-valued, the correlations can be configured to be fitted against the b-values using a quadratic model. If multiple baselines are acquired, they are either checked in the same way as DWIs where a single b-value is used, or checked together with all the DWIs if multiple b-values are used to collect the data.

2.5 Interlace-wise Venetian blind artifact checking

An interlace-wise checking detects Venetian blind like artifacts via correlations and motion parameters between the interleaved parts for each gradient volume. Checking of the correlations is the same as what is done in the slice-wise checking. The normalized correlations between the interlaced parts of each of the gradients are assumed to be normally distributed to find outliers caused by any artifacts existing in the interleaved sub-volume. The NCs can also be configured to be fit for multiple b-valued DWIs with a quadratic model. Motion parameters are found by rigidly registering the interleaved sub-volumes. Translation threshold is by default set equal to the average of the voxel sizes $((spacing_x + spacing_y + spacing_z)/3)$ and rotation threshold to 0.5 degree. All detected outliers are marked as "bad" and excluded before streamed into the next step.

2.6 Baseline averaging

State of the art DTI protocols usually use more than 6 diffusion sensitizing directions. A non-diffusion weighted baseline image is advised to get acquired for every 6-8 gradients. Thus the resulting DWI scans usually consist of more than 1 baselines image. These baseline images need to be averaged in order to be used as a registration template during the eddy-current artifact and head motion correction procedure. If there is motion between the baseline scans, 3 strategies can be used to calculate the averaged baseline. The first method is to directly average them. This is definitely not the optimized one in case motions occurred among them although this is the fastest method. A second way is to iteratively register all of them to the average of them followed by updating the average with the newest registration result until the average gets stable and does not dramatically change anymore. This will ending at an optimized position such that the averaged baseline is not bias to any specific one of them. The computation of this method is somewhat moderate. The third method is to average all the baselines to a DWIs-optimized position so that the average position is close to the most possible number of diffusion weighted volumes. This is accomplished by first finding the DWIs optimized position and then registering all the baselines to that position and averaging them. Because the number of the diffusion weighted volumes is much larger than that of the baselines, the computation costs much more to use this method. The default choice is the baseline optimized method.

2.7 Eddy-current and head motion artifacts correction

For eddy-current and head motion artifact detect and correction, we integrate 2 tools developed in University of Utah (gforge.sci.utah.edu/gf/project/dwi-processing) and University of Iowa (www.nitrc.org/svn/vmagnotta) in our tool. They

have the same functionalities and are all able to detect and correct this kind of artifact. In both o the tools, all diffusion gradients are first affinely registered to the baseline and then transformed and re-sampled. The corresponding diffusion sensitizing direction vectors are updated using the affine transformation. User can choose to use either of them.

2.8 Gradient-wise checking

This is designed to detect the residual motion artifacts after eddy-current and head motion corrections. Sometimes, the eddy-current and motion correction tools fail to correct the artifact. Occasionally, they even "produce" some motion artifacts while the registration procedure fails to find the correct transformation parameters. Both can leave obvious motion artifacts in DWI. We need to capture them if this is the case.

2.9 DTI estimation and computation

Last step of the pipeline is to do the DTI computing. DTI is estimated from the QC'ed output of the previous steps and DTI scalar indices (FA, MD, IDWI, Frobenius Norm) and principle eigen-vector coded colorized FA are computed. The user can choose estimation via standard least squares, weighted least squares, non-linear least squares or maximum likelihood. The DTI computation is done by calling a DTIProcess toolkit developed in UNC and University of Utah, which is open sourced and is formerly in UNC NeuroLib (www.niral.unc.edu).

3. DWI QC TOOL: DTIPREP

DTIPrep is the tool we developed to implement the DWI QC pipeline (from step 2.2 to 2.9) we proposed in section 2. It is based on ITK, VTK and Qt 4. DTIPrep oversees graphical user interface handling, protocoling and reporting facilities. The tool allows a "study-specific protocol" based execution via an xml formatted parameter file. Parameter files can be created and edited using the tool's GUI. For each study, a default protocol file can be automatically created, containing all the data collecting parameters and artifacts detection and correction settings from a template data. The parameters can be finely tuned to make the protocol more adaptive to the study data under investigation.

In the GUI, user can browse the whole DWI NRRD file header information and image contents gradient by gradient and slice by slice. This allows DTIPrep to be used as a tool for visually inspecting and manually QC'ing DWI data sets. Although it is hard to find and correct small motion artifacts during a manual QC procedure, for some well controlled studies, eliminating the gradients with intensity and motion artifacts between interleaved fields is sufficient to get a good DTI estimation. Figure 1 shows the GUI and a manual QC example. In this example, the gradient #4 contains intensity artifacts in several slices. This can be easily found by viewing each of the axial slices or by examining the orthogonal sagittal and coronal views. The steps to do a manual QC in DTIPrep's GUI is as follows.

a) Load a DWI NRRD file into DTIPrep.
b) Create a default QC result table. By default, all the gradient volumes are initially marked as *INCLUDE*.
c) Browse the images and gradients, and mark those bearing visually noticeable intensity-related and venetian blind-like artifacts as *EXCLUDE* in the default QC result table, indicating that they are to be excluded.
d) Save the QC'ed DWI out in a NRRD file containing all the gradient volumes with *INCLUDE* markers.

While DTIPrep can be run in standard interactive mode, a command line mode is available too for standard automatic scripting. The tool thus provides the user with the ability to do the QC both in an automatic and manual mode. And it is also easy to edit the automatic QC results manually within the GUI. With the command line mode, DTIPrep can be readily used in a script for batch processing a large amount of data sets.

4. EXPERIMENTS

In this section, we show some experiment results of DTIPrep. Figure 2, Figure 3, and Figure 4 plot the metrics calculated for slice-wise, interlace-wise and gradient-wise artifacts checking respectively. The DWI data set contains 25 sensitizing directional gradient volumes and 1 baseline volume acquired using a multiple b-valued protocol, with the b-values differing from gradient to gradient. Figure 2 shows the plot of the slice-wise normalized correlations. The X axial is the slice number. We assume that the NCs of all the gradient volumes at each slice number are normally distributed. The outliers then can be discriminated by setting a threshold to $\mathrm{NC}_{\mathrm{mean}} - \alpha \cdot \sigma$. Here we used $\alpha = 3.5$. We can clearly see gradient 18 contains many outlier points in the left part and several in the right middle part. Each outlier point corresponds to a slice with intensity artifact in gradient 18. Thus we excluded gradient 18 from both the gradient direction list and the 3D volume list in the output.

Figure 3 plots the NCs between the interleaved parts of each of the gradient volumes and the rigid transformation parameters found by rigidly registering them. All the NCs are assumed normally distributed, the translation threshold was set to 2mm (1voxel size) and the rotation threshold was set to 0.5 degree. It is clearly shown that there exists a interleaved motion artifact in gradient 18. This also resulted in a lower NC between the interleaved parts. This is consistent with the slice-wise checking. Note that the translation in the Z direction shifted to 1mm other than the translations in X and Y directions centered around 0mm. This is because of the intrinsic half voxel size shift in the Z direction between the interleaved parts of each of the gradient volumes.

Figure 4 plots the rigid registration parameters between each of the gradients and the baseline volume. The translation threshold was set to 2mm (1voxel size) and the rotation threshold was set to 0.8 degree. Obvious motions can be found before gradient 18.It is clearly shown that there exists an interleaved motion artifact in gradient 18. This also resulted in a lower NC between the interleaved parts. This is consistent with the slice-wise checking.

Figure 5 shows some intensity artifacts detected by DTIPrep in some of our projects. In Figure 5, image a shows some electromagnetic interference-like artifact. Image b shows severe signal loss in the middle and anterior part of the brain. Image c shows small checker board-like in a small area of the occipital part of the brain. Image d shows a Venetian blind artifact due to the motion between the interleaved parts of the gradient volume.

Figure 6 shows color coded FA maps of the DTIs estimated from the DWIs before (a) and after (b) QC with DTIPrep. In image a, a wide range of red color exists in several slices due to the “black” artifact in the corresponding slices of the DWI gradient in a direction mainly pointing to X direction. Bright anterior and posterior borders can be seen in image a, which is arise from the eddy current artifacts in the DWIs before QC process. After excluding the gradient volumes containing intensity related artifacts and correcting the eddy current and motion artifacts in the DWI, image b shows a clear color FA map.

5. CONCLUSION

Artifacts are common in DT-MRI acquisitions. They come from both the acquisition system (such as eddy-current artifact and vibration artifact) and the subject being scanned (such as cardiac pulsation artifact and head motion artifact especially for the uncooperative or pediatric subjects). Signal changes produced by these artifacts can be severe and finally result in erroneous diffusion tensor values.

We developed both a DWI QC framework as a DTI preprocessing step and a tool called DTIPrep which implements the QC pipeline, and oversees graphical user interface handling, protocoling and reporting facilities. The tool allows a "study-specific protocol" based execution via an xml-formatted parameter file. Parameter files can be created and edited within the GUI. For each study, a protocol file is created, containing all the data collecting parameters and artifacts detection and correction settings. The tool provides the user with the ability to do the QC both in an automatic and manual mode. With the command line mode, DTIPrep can be readily used in a script for batch processing a large amount of data sets.

Our pipeline has been successfully applied to large scale DTI studies with several hundred DWI datasets in our lab as well as collaborating labs in Utah and Iowa. In our studies, the tool provides a crucial piece for robust DTI analysis. As far as we know, this is the first comprehensive preprocessing tool for DWI/DTI quality control with protocoling, reporting and data correction facilities. DTIPrep is available as open source within the UNC NeuroLib (www.niral.unc.edu) and a page (www.nitrc.org/projects/dtiprep/) in NITRC has also been set up for this tool for collaborative improvement.

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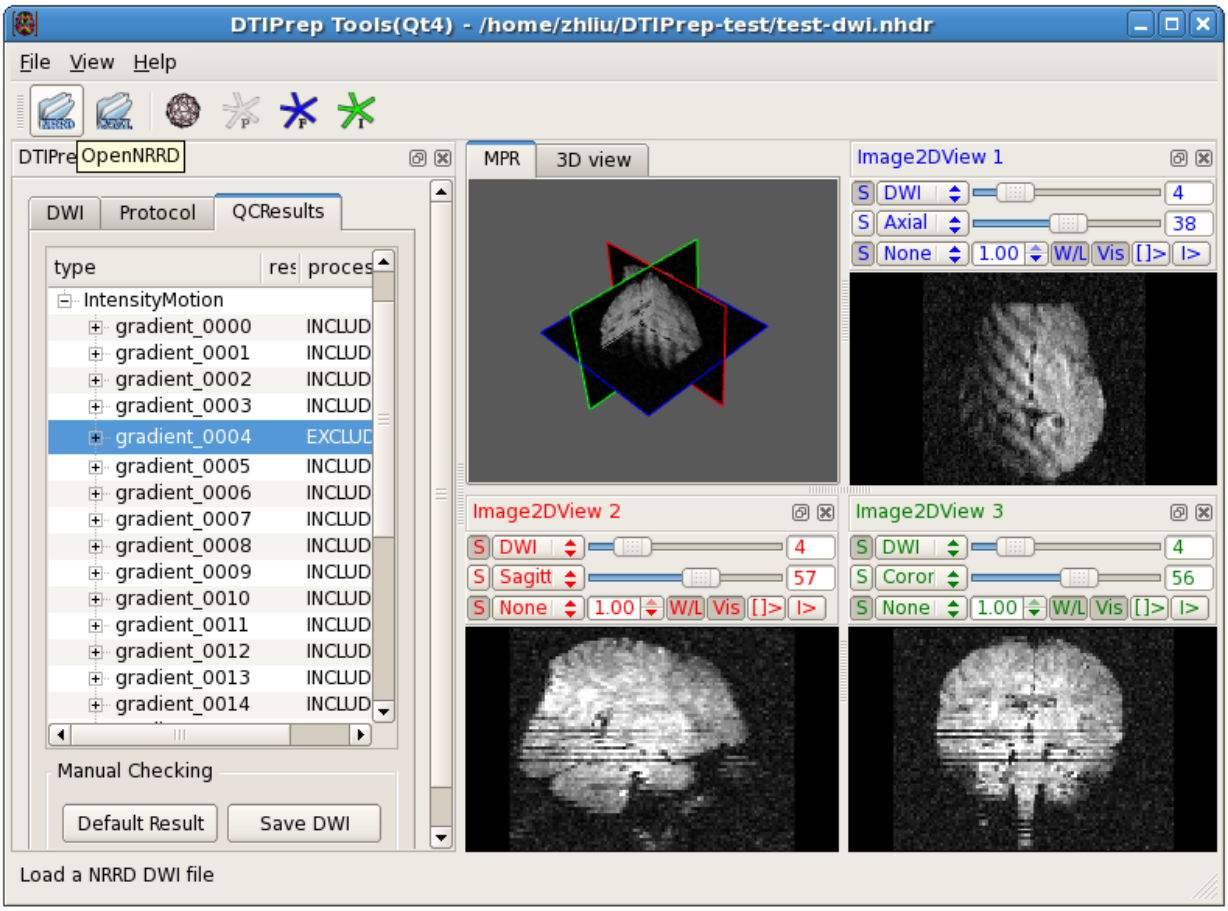


Figure 1. DTIPrep is running in GUI mode. In this picture, the #4 gradient shows intensity artifacts in several slices and it is marked as *EXCLUDE* in the QC result table, indicating that it will be excluded when the *Save DWI* button is clicked.

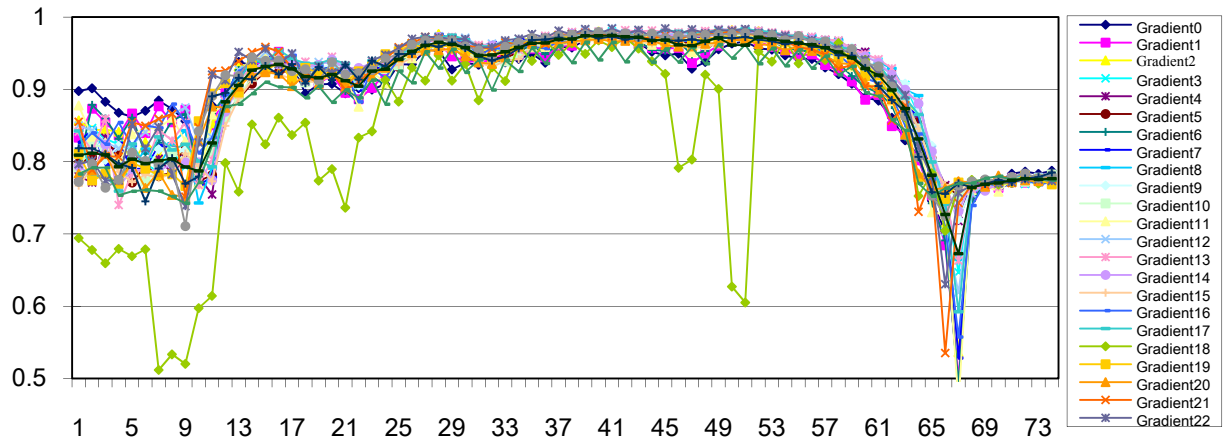


Figure 2. Correlation (in vertical) vs. slice number (in horizon) plot for slice-wise checking shows that gradient-18 is abnormal at several slice locations indicating intensity artifacts in these slices.

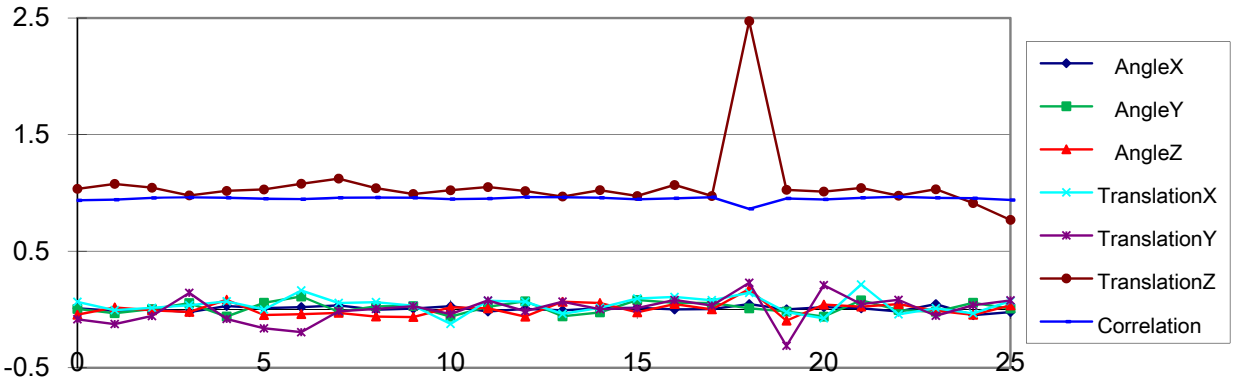


Figure 3. Motion parameters (in vertical) vs. gradient number (in horizon) plot for interlace-wise checking shows a large translation in Z in gradient-18. Correlation (in vertical) vs. gradient number (in horizon) plot also shows a drop for gradient-18. This implies that those slice intensity artifacts are very likely originating from motions between the interleaved acquisitions.

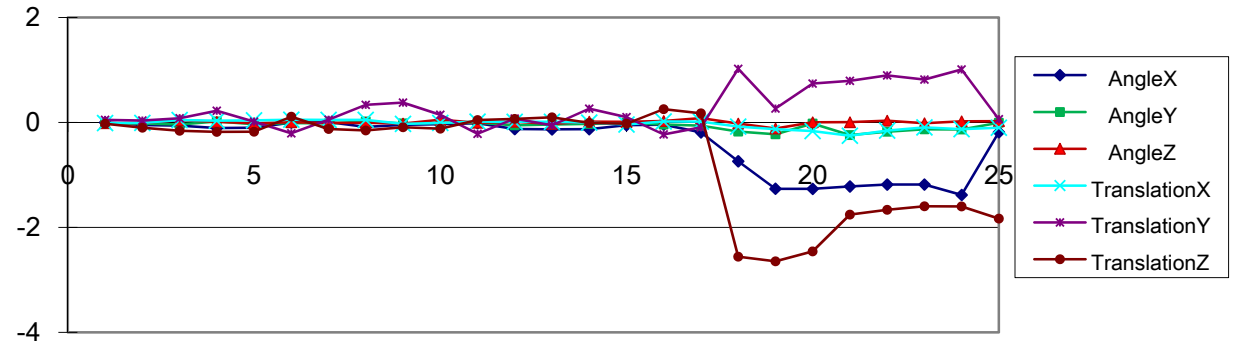
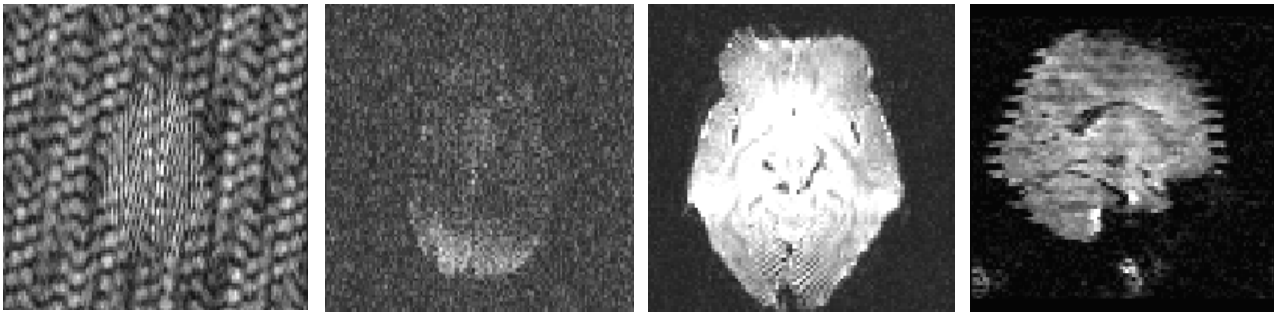
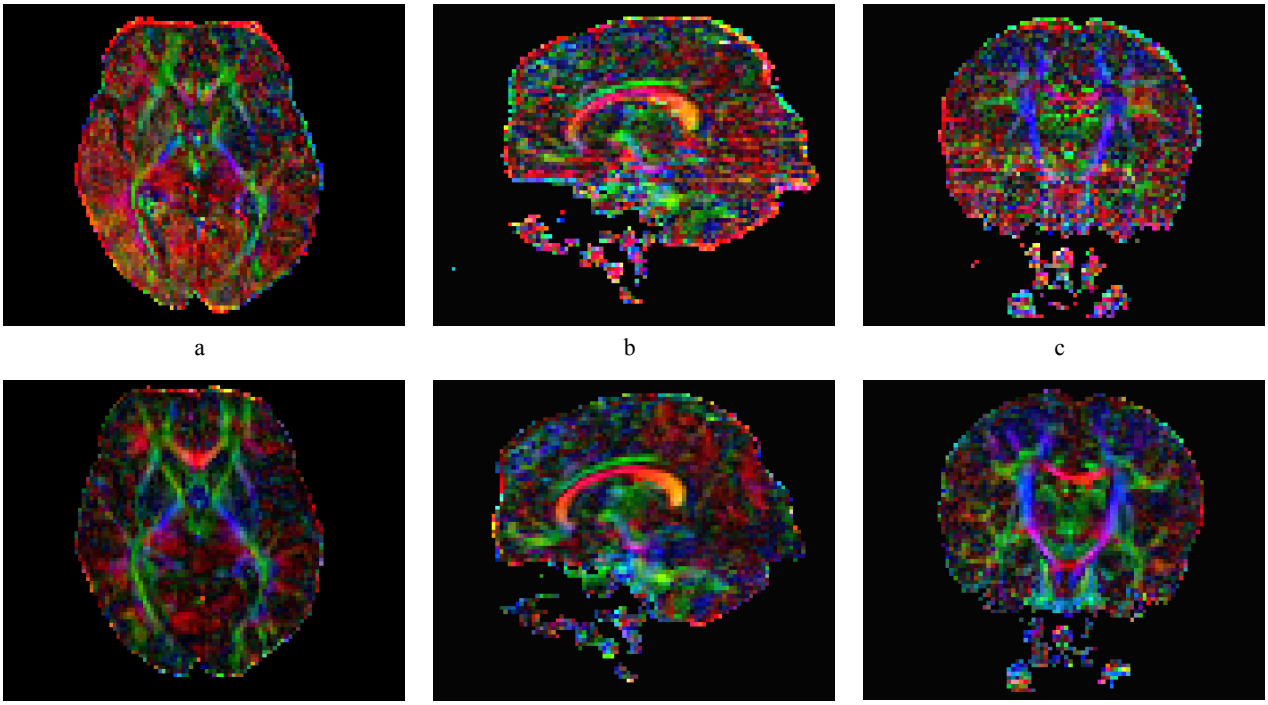


Figure 4. Motion parameters (in vertical) vs. gradient number (in horizon) plot for gradient-wise checking shows large motion occurred after gradient-17. This kind of artifacts can be corrected by registering those gradient volumes to the baseline (usually the first volume if no baseline acquired in a multiple b-valued acquisition).



a b c d

Figure 5. Examples of intensity artifacts detected with DTIPrep. a shows a electromagnetic interference-like artifact; b shows severe signal loss in the middle and anterior part; c shows checker board-like artifact in a small area in the occipital part; d shows Venetian blind artifact due to the motion between the acquisition of the interleaved parts.



a b c

d e f

Figure 6. Orthogonal views of the color coded FA map calculated from a test DWI data set before (a: axial, b: sagittal, c: coronal) and after (d: axial, e: sagittal, f: coronal) QC using DTIPrep.