TRACK-HD Historical DTI Review

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Introduction

Background

The TRACK-HD study is finishing it's 2nd year in December 2009. There is approximately 40 minutes of scan time used for performing the mandatory TRACK-HD protocol. Each of the sites were given approval to do an "add-on" scan with the subjects under with the remaining time on a year-to-year basis. It was agreed that all data would be shared with the TRACK-HD team, that no more that no more than 20 minutes were required, and that TRACK-HD steering committee could discontinue, change, or insert a new protocol into that 20 minute slot as it saw fit.

Motivation

All four sites choose to do an “add-on” imaging study in the 20 minute time slot in one or both of the first years. UBC did a Spectroscopy add on study that will not be discussed in this report. Leiden collected 74 DTI scans in the first year, London collected 66 scans in the second year, and Paris collected 79 Scans in year1, 75 scans in year 2 where 58 of the subjects were scanned in both years with the desired 50 direction scan sequence.

There is a reasonable possibility that TRACK-HD will receive a 2 year extension (that is that there are still 3 years of uncollected data). Under the assumption that DTI data would be a valuable addition to the study, a historical review of the already collected data was requested.

At least two possible paths were proposed for inclusion of DTI in the TRACK-HD study:

OPTION	PRO	CON
Let each site continue with their current protocols.	--Longest possible intra-site longitudinal data could be collected.	--Inter-site data is not compatible. --There was no coordination between sites for what, or how the DTI data should be collected --Analysis of the data for all of TRACK will be much more complicated.
Require each site to conform to a new DTI protocol	--All data will follow a rigorous data collection protocol, this will allow for enhanced QC procedures to be put into place. --All data will be collected consistently so that cross-site analysis can more easily be done.	--Historical data will not be easily or consistently integrated with prospective data collection.

Overall Approach

1. Work with Paris, Leiden, London to identify mechanisms for de-identifying and uploading the TRACK DTI data to Iowa. This involved configuring a secure ftp service for transferring the data, developing proper network access, and coordinating passwords authentication.

2. Organize the DTI data from 3 sites. After the data was received, the dicom files were separated into a directory hierarchy such that each directory contained only those dicom files that belonged to a particular scan sequence.
3. Updated analysis tools to support data DICOM data in formats and/or use of new DICOM fields to store information regarding the diffusion weighted images.
4. Map DTI data to previously processed structural data This mapping was done by pairing the date and time stamps of the DTI and morphometric DICOM data sets.
5. Document in detail what each of the protocols is as reported by the data, and contrast that with what the sites stated the protocols were.
6. Modify processing tools to accommodate the unique data collection methods of each of these 3 data sets See Appedix for details.
7. Run Quality control tools to identify common failure characteristics of the DTI protocols

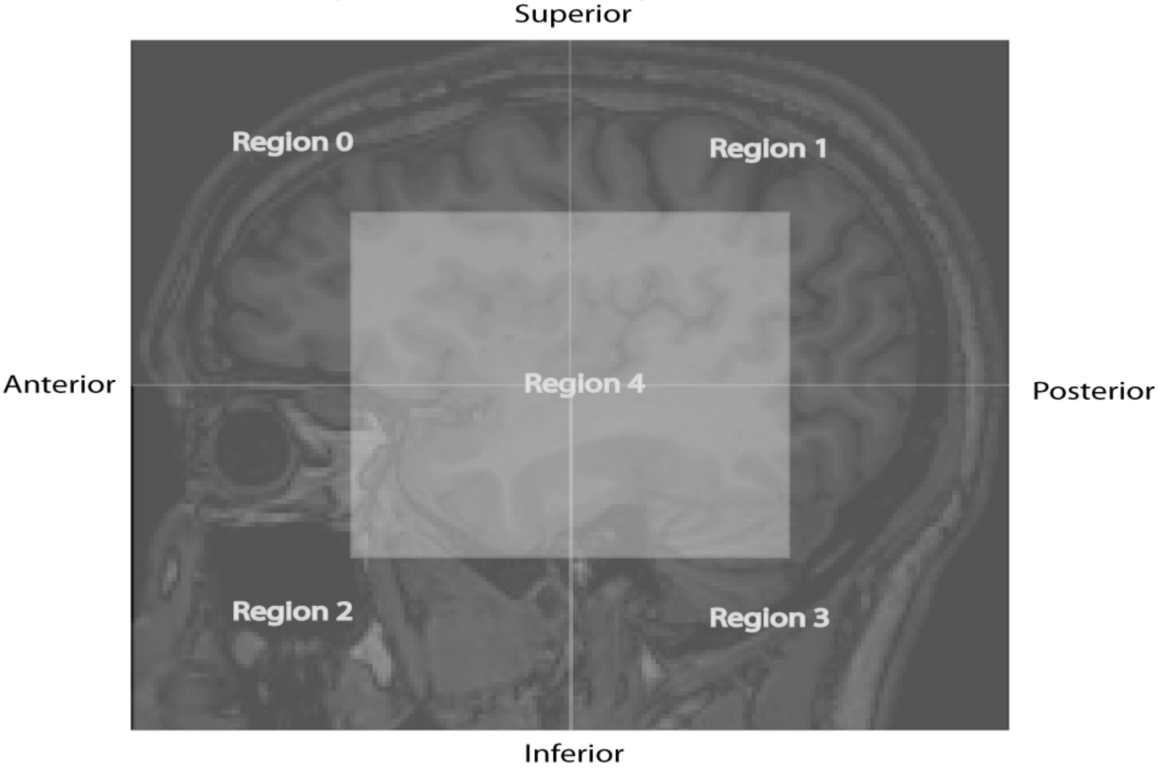
Tools Used For Analysis:

- Dcmtk (http://dicom.offis.de/dcmtk) --DCMTK is a collection of libraries and applications implementing large parts the DICOM standard.
- DicomToNrrd: (http://www.na-mic.org/Wiki/index.php/NAMIC_Wiki:DTI:DICOM_for_DWI_and_DTI && http://www.na-mic.org/Wiki/index.php/NAMIC_Wiki:DTI:Nrrd_format) A tool to convert from Dicom to the Nrrd file format that is consistently interpreted across a wide number of tools developed in collaboration with the "National Alliance for Medical Image Computing".
- GTRACT: (http://www.nitrc.org/projects/vmagnotta/): GTRACT is a Diffusion Tensor fiber tracking suite that includes streamline tracking tools. The fiber tracking includes a guided tracking tool that integrates apriori information into a streamlines algorithm. This suite of programs is built using the NA-MIC toolkit and uses the Slicer3 execution model framework to define the command line arguments. These tools can be fully integrated with Slicer3 using the module discovery capabilities of Slicer3.
- DTIPrep: (http://www.nitrc.org/projects/dtiprep/) DTIPrep performs a "Study-specific Protocol" based automatic pipeline for DWI/DTI quality control and preparation. This is both a GUI and command line tool. The configurable pipeline includes image/diffusion information check, padding/Cropping of data, slice-wise, interlace-wise and gradient-wise intensity and motion check, head motion and Eddy current artifact correction, and DTI computing.
- BRAINS: (http://www.nitrc.org/projects/brains/) The BRAINS (Brain Research: Analysis of Images, Networks, and Systems) image analysis software has been developed to study the brain thus providing a better understand of psychiatric and neurological disorders.

Quality Metrics Investigated

DTIPrep offers automated quality control checking for diffusion-weighted MRI data in eight main steps:

1) Image information checking, --Image information checking involves comparing a given scan's protocol parameters (dimension, sizes, spacing, space directions) with a set of protocol parameters specified by the user.
2) Diffusion information checking, --Diffusion information checking involves comparing a given scan's protocol parameters (diffusion gradient vector coordinates) with a set of protocol parameters specified by the user.
3) Slice-wise checking-- Slice-wise checking calculates correlation values between each slice (subregion and entire slice comparisons) within a single diffusion gradient volume. There are 5 subregions numbered 0 through 4 and are labeled as follows:



The sub-regions are divided based on the voxel indices(i, j, k) and the above figure assumes data collected in the standard dicom LPS coordinate system. This is not necessarily the case when data is collected given different space cosines. So the sub region 0 starts with i=0 and j=0 and sub region 3 starts with i= imax/2 and j=jmax/2. This is to add sensitivity to vibration artifact detection. The correlation values are used to designate slices that do not correlate well with neighboring slices. Gradients containing slices with poor correlation values are removed from the scan.

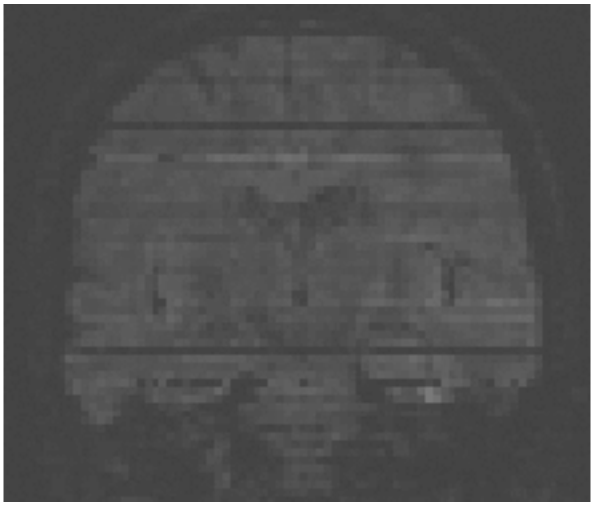
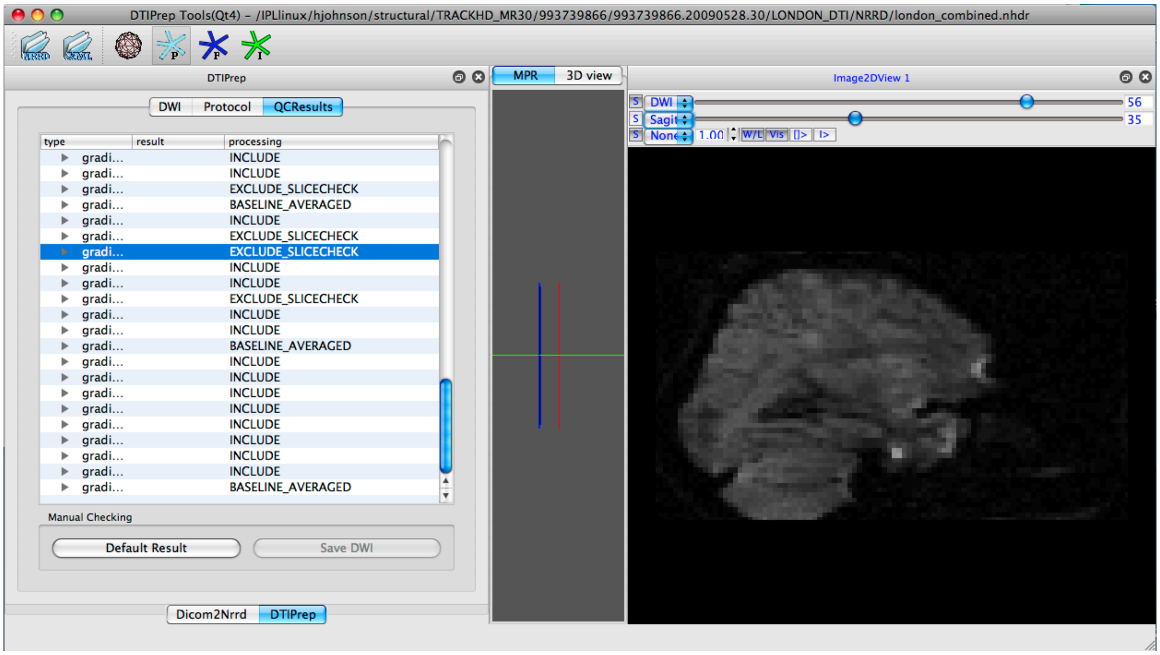


Figure 1 Example Leiden data slice removed as part of the DTI Prep slice checking algorithm. Notice banding related artifacts that may be due to subject motion, table vibrations, or scanner stability.

4) Interlace-wise checking-- Interlace-wise checking compares every other slice and thus removes gradients that were affected by venetian blind artifacts due to motion that occurs during a single volume collection.
5) Baseline averaging, -- co-register and average all the B0 images together
6) Eddy-current and head motion artifacts correction, -- After the images with interlace-wise intra volume motion are removed, the motion is corrected and gradient directions adjusted so that all intensity images are co-registered (i.e. rigidly motion corrected) with gradients adjusted accordingly for the given rotational changes.
7) Gradient-wise checking, --Gradient-wise checking detects residual motion artifacts.
8) Quality Control report production—A text file is created reporting all actions taken during the process. A final report generated containing information on which gradients were removed at each step. The remaining good gradients and the averaged B0 image volumes are written to a corrected NRRD file format.


DTIPrep Tools(Qt4) – /IPLlinux/hjohnson/structural/TRACKHD_MR30/993739866/993739866.20090528.30/LONDON_DTI/NRRD/london_combined.nhdr

type	result	processing
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		EXCLUDE_SLICECHECK
gradi…		BASELINE_AVERAGED
gradi…		INCLUDE
gradi…		EXCLUDE_SLICECHECK
gradi…		EXCLUDE_SLICECHECK
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		EXCLUDE_SLICECHECK
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		BASELINE_AVERAGED
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		INCLUDE
gradi…		BASELINE_AVERAGED

Figure 2 DTIPrep Gui Interface with QC Results Display

Site Data Reports

Leiden data

The Leiden data was delivered in the very new DICOM multi-frame format from a Philips scanner running software version “2.1.3\2.1.3.5\Gyroscan PMS/DICOM 4.0 MR datadefs $Revision: 6.30 $”. The was the first time that this DICOM format was seen, and tool modifications were necessary in order to properly read this data (See Appendix for details). All of the Leiden data was collected with an oblique scan angle. This required the gradients to be interpreted with respect to a measurement frame consistent with the DICOM ImageOrientationPatient (0x0020,0x0037) field. Once this was accomplished, all data were verified to have been consistently collected.

The Leiden data consisted of 74 diffusion-weighted imaging scans, each with dimensions of 112 pixels x 112 pixels x 64 slices per volume x 32 unique diffusion gradient directions with a single B0 volume. All 74 scans were processed with DTIPrep. Gradients were removed by DTIPrep based on three different quality control checking methods: slice-wise, gradient-wise, and interlace-wise. Overall, the three checking methods removed a total of 626 gradients from the original total 2112 gradients (29.6%), with an average of 8.46 gradients removed per scan. Slice-wise checking removed the majority of the gradients (600 gradients, 95.8% of removed), while gradient-wise checking removed 23 (3.67%) and interlace-wise checking removed 3 (0.479%).

Quality control method	No. of gradients removed	% of removed gradients
Slice-wise	600	95.8
Gradient-wise	23	3.67
Interlace-wise	3	0.479

Gradient information

Across all three quality control checking methods, the diffusion gradient removed the most was 4 (Figure 3). Diffusion gradient number 4 was removed in 58.11% of scans. The diffusion gradients removed most often were clustered around number 4 and included gradients number 6 (56.76%), 5 (54.05%), 8 (54.05%), and 3 (50%). The gradient removed the least (aside from number 0, which was never removed since its b value was 0) was number 29 (6.76%).

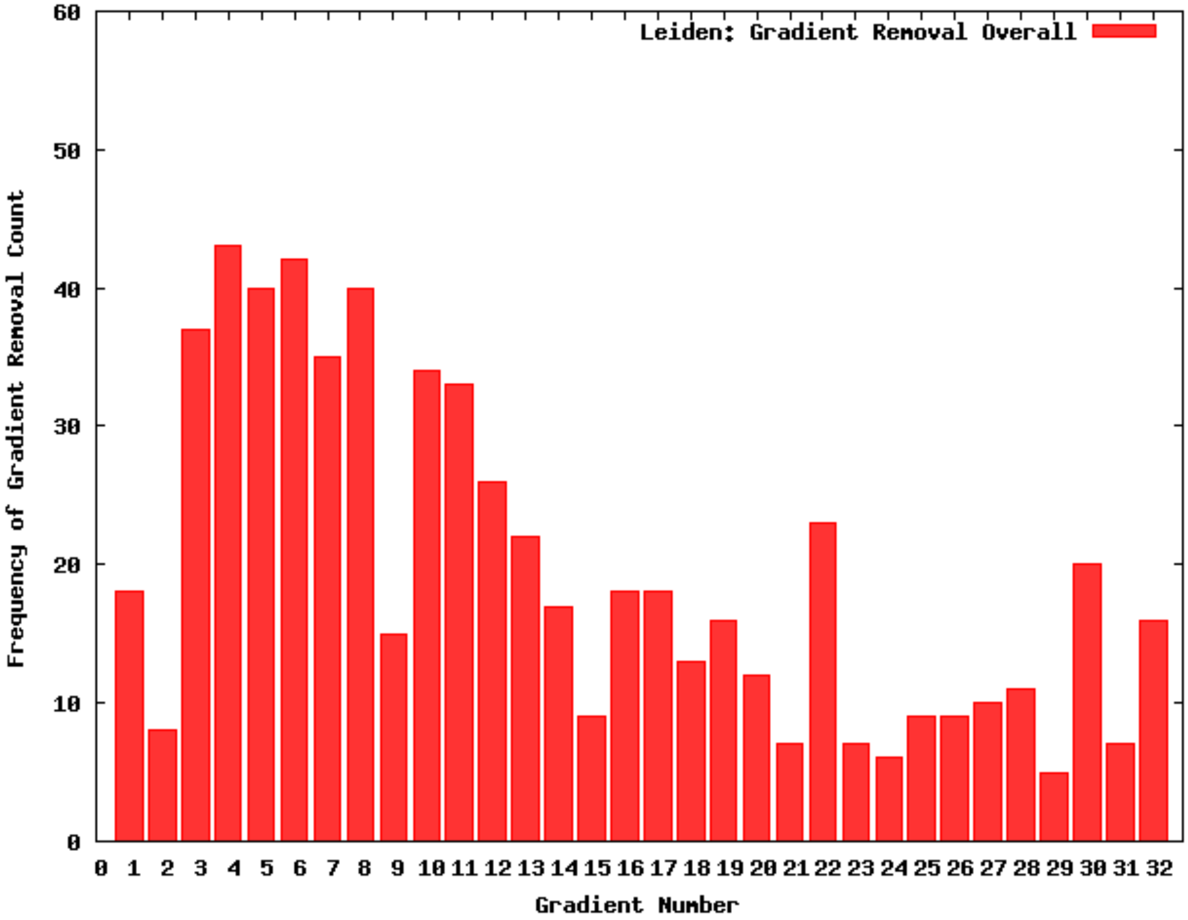


Figure 3: Frequency of gradient removal from all quality control checking methods.

Slice-wise checking: gradient removal by region

The slice-wise check calculated slice-to-slices correlation values in 5 smaller regions (0 through 4) and entire slice-to-slice correlation values (called “whole” in DTIPrep, region 5 in our histogram). Of the smaller regions, region 3 caused the most gradients to be removed by the slice-wise check (100 gradients or 16.67% of all slice-wise check removals). Region 1 caused the least number of gradient removals (15 gradients or 2.50% of all slice-wise check removals). However, whole slice-to-slice comparisons caused the most gradients to be removed overall with 313 gradients or 52.17% of all slice-wise check removals (Figure 4).

Regions	Frequency of removal	% of slice-wise check exclusions
0	67	11.17
1	15	2.50
2	54	9.00
3	100	16.67
4	51	8.50
5 (whole)	313	52.17

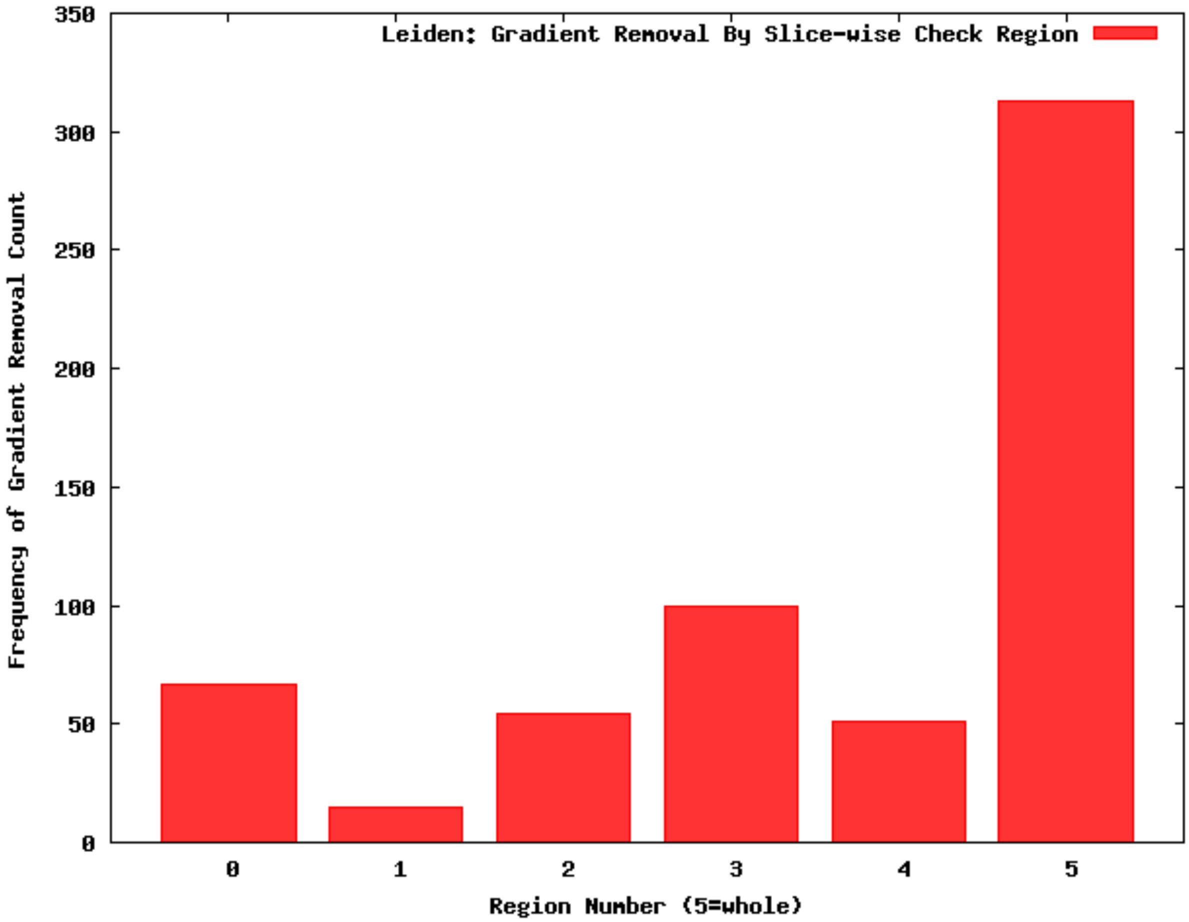


Figure 4: Frequency of gradient removal via the slice-wise checking method, separated by slice region.

Slice-wise checking: slice information

Slice-wise checking identified individual slices that did not correlate well with its neighboring slice. If one or more slices in a given gradient did not correlate well with its neighboring slice, then that slice is designated with a poor correlation value and that entire gradient was removed from its scan. Out of the total 156,288 slices in the Leiden data set (64 slices per gradient x 33 gradients per scan x 74 scans) where each slice was present 2042 times, 1033 slices (0.661%) were designated as not correlating well with its neighboring slice. The most commonly designated slice was slice number 11, being having a poor correlation value 55 times or 2.25% of the time (Figure 5). The highest percentages of poor correlation designation was seen clustered around the most commonly designated slice, which included slices 7 (1.76%), 10 (2.01%), 12 (2.01%), and 13 (2.09%). Slices 1 through 6 and 58 thorugh 64 were never designated with a poor correlation value.

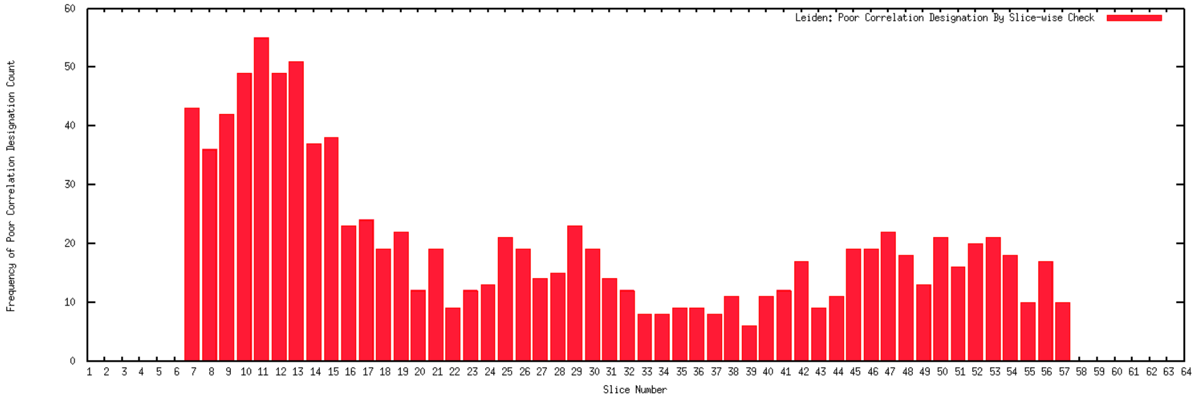


Figure 5: Frequency of slice designation with a poor correlation value.

London data

The London data is from a Siemens scanner with two custom programmed imaging sequences. This data did not conform to either the DICOM standard or the Siemens conformance statements with regards to reporting the gradient directions in the dicom files.

Siemens Dicom private tags:

From: http://wiki.na-mic.org/Wiki/index.php/NAMIC_Wiki:DTI:DICOM_for_DWI_and_DTI

A Siemens DICOM Conformance Statement is available at
http://www.medical.siemens.com/siemens/en_INT/rg_marcom_FBAs/files/brochures/DICOM/mr/dcs_trio.pdf

```
0019;000A;SIEMENS MR HEADER  ;NumberOfImagesInMosaic          ;1;US;1
0019;000B;SIEMENS MR HEADER  ;SliceMeasurementDuration        ;1;DS;1
0019;000C;SIEMENS MR HEADER  ;B_value                         ;1;IS;1
0019;000D;SIEMENS MR HEADER  ;DiffusionDirectionality         ;1;CS;1
0019;000E;SIEMENS MR HEADER  ;DiffusionGradientDirection      ;1;FD;3
0019;000F;SIEMENS MR HEADER  ;GradientMode                    ;1;SH;1
0019;0027;SIEMENS MR HEADER  ;B_matrix                        ;1;FD;6
0019;0028;SIEMENS MR HEADER  ;BandwidthPerPixelPhaseEncode    ;1;FD;1
```

DICOM supplement 49 diffusion tags:

These are defined in Supplement 49. In particular see section C.8.12.5.9 "MR Diffusion Macro" on pages 94 and 95.

ftp://medical.nema.org/medical/dicom/final/sup49_ft.pdf

```
0018 9075 CS 1 Diffusion Directionality
0018 9076 SQ 1 Diffusion Gradient Direction Sequence
0018 9087 FD 1 Diffusion b-value
0018 9089 FD 3 Diffusion Gradient Orientation
0018 9117 SQ 1 MR Diffusion Sequence
0018 9147 CS 1 Diffusion Anisotropy Type
```

This sequence involved a non-standard custom sequence, and that the necessary information to properly interpret this data is not included in the DICOM headers.

Sequence information provided by London DTI Team

```
const double daDiffGrads_36a[36][3]=
{
 {-0.278590, 0.948576, 0.150306},
 { 0.923215,-0.362997, 0.126124},
 {-0.607712, 0.077141, 0.790402},
 { 0.661510, 0.749911, 0.006173},
 {-0.020026,-0.576391, 0.816928},
 { 0.580539, 0.068549, 0.811342},
 {-0.122014, 0.589755, 0.798312},
 { 0.949992, 0.086143,-0.300156},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 { 0.208215,-0.891081, 0.403263},
 { 0.456964, 0.642255, 0.615380},
 {-0.611822,-0.502190, 0.611129},
 { 0.576347,-0.522314, 0.628500},
 {-0.651714, 0.630831, 0.421095},
 { 0.927325, 0.216334, 0.305397},
 {-0.015834, 0.014472, 0.999770},
 {-0.154722,-0.987867,-0.013398},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 {-0.378698,-0.766359, 0.518923},
 { 0.726209,-0.666170, 0.169821},
 { 0.276048, 0.217697, 0.936165},
 {-0.141862, 0.824696, 0.547496},
 {-0.837437,-0.532713, 0.122130},
 {-0.830952, 0.381428, 0.405009},
 { 0.768559,-0.194100, 0.609624},
 {-0.239236,-0.285484, 0.928044},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 { 0.291451, 0.863987, 0.410588},
 {-0.370819, 0.344175, 0.862576},
 { 0.734088, 0.444365, 0.513473},
 { 0.304862,-0.464001, 0.831722},
 {-0.997625, 0.026724,-0.063488},
 {-0.132838,-0.935923, 0.326194},
 {-0.762479,-0.186326, 0.619604},
 { 0.446139,-0.883423, 0.143262},
 { 1.000000, 0.000000, 0.000000}  // b0 image
};
```

```
const double daDiffGrads_36b[36][3]=
{
 { 0.006778, 0.955284, 0.295611},
 { 0.065038,-0.295413, 0.953153},
 {-0.524955, 0.742151,-0.416694},
 {-0.637493, 0.376534, 0.672179},
 { 0.839210, 0.379789,-0.389213},
 { 0.532848, 0.370235, 0.760920},
 { 0.926285,-0.117378, 0.358076},
 {-0.423944,-0.882753, 0.202533},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 {-0.055576, 0.316879, 0.946836},
 { 0.601245,-0.789791,-0.121382},
 {-0.834875,-0.510044,-0.206975},
 {-0.063469,-0.795508, 0.602610},
 {-0.959665, 0.216672, 0.179153},
 {-0.522214,-0.248724, 0.815738},
 { 0.539573,-0.252383, 0.803221},
 { 0.137929, 0.746604, 0.650813},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 {-0.125640, 0.985406,-0.114845},
 {-0.413285, 0.619494, 0.667400},
 { 0.611904, 0.712455, 0.343485},
 {-0.332668,-0.557425, 0.760663},
 { 0.792823,-0.455369, 0.405057},
 {-0.835774, 0.104423, 0.539052},
 { 0.797023, 0.136705, 0.588273},
 {-0.328467, 0.034648, 0.943880},
 { 1.000000, 0.000000, 0.000000}, // b0 image
 { 0.963101, 0.267540,-0.029315},
 { 0.269452,-0.711937, 0.648492},
 {-0.419397,-0.897620,-0.135587},
 { 0.827364,-0.548564,-0.120610},
 { 0.307510,-0.090828, 0.947200},
 {-0.645004,-0.682074, 0.344595},
 {-0.407192, 0.822667, 0.396753},
 { 0.218118, 0.504810, 0.835219},
 { 1.000000, 0.000000, 0.000000}  // b0 image
};
```

Although they are called b0 images the reference images have b = 100 s/mm^2 the rest of the images have b = 1000 s/mm^2

32.1282 mT/m for the diffusion encoding gradients (when b = 1000 s/mm^2).

Make sure that you input 100 s/mm^2 for the reference images (i.e. the actually diffusion weighting is 900 = 1000-100 and NOT 1000 s/mm^2).

pulse onset separation DELTA = 35.1 ms

pulse width delta = 18.1 ms

TE = 90 ms

resolution = 2.3 mm isotripic

There were 60 slices with 96 x 96 matrix
Also, the 1st and 37 images (dir:-0.278590 0.948576 -0.150306, b=1000 and dir: 0.006778 0.955284 -0.295611, b=1000 respectively) have banding in them. You can see the banding in the saggital view. I don't think these artifacts make a significant difference, but if you have any problems it might be worth removing them from your datasets and trying again.

Due to the missing data in the dicom headers, we had to assume that all London data was collected orthogonal to the scanner (i.e. an identity direction cosign matrix), injected the directions provided into the images with the assumption that they were always correct with respect to that scan orientation.

Each pair of 36 volume scans were concatenated into single 72 volume sequence (since the gradients were not redundant in the two scans).

The London data set consisted of 61 diffusion-weighted imaging scans, each with dimensions of 96 pixels x 96 pixels x 55 slices per volume x 64 unique diffusion gradient directions and 8 B0 images. NOTE: Contrary to the reported number of slices and resolution, the DICOM header files reported that there were only 55 slices and that the slice thickness was 2.5mm. 57 scans were processed with DTIPrep (4 scans were incomplete in some way). Gradients were removed by DTIPrep based on three different quality control checking methods: slice-wise, gradient-wise, and interlace-wise. Overall, the three checking methods removed a total of 561 gradients from the original total 4104 gradients (13.7%), with an average of 9.84 gradients removed per scan. Slice-wise checking removed the majority of the gradients (556 gradients, 99.1% of removed), while gradient-wise checking removed none, and interlace-wise checking removed 5 (0.09%).

Quality control method	**No. of gradients removed**	**% of removed gradients**
Slice-wise	556	99.1
Gradient-wise	0	0.00
Interlace-wise	5	0.09

Gradient information

Across all three quality control checking methods, the diffusion gradient removed the most was 4 (Figure 6). Diffusion gradient number 0 was removed in 56.14% of scans. The diffusion gradients removed most often were not clustered around number 0 and included gradients number 2 (29.82%), 63 (29.82%), 25 (28.07%), 5 (26.32), 1 (24.56%), 14 (24.56%), 37 (24.56%), and 70 (24.56%). The gradient removed the least was number 8 (6.76%). Gradients whose b values were equal to 0 (gradients 17, 26, 35, 44, 53, 62, and 71) were never removed.

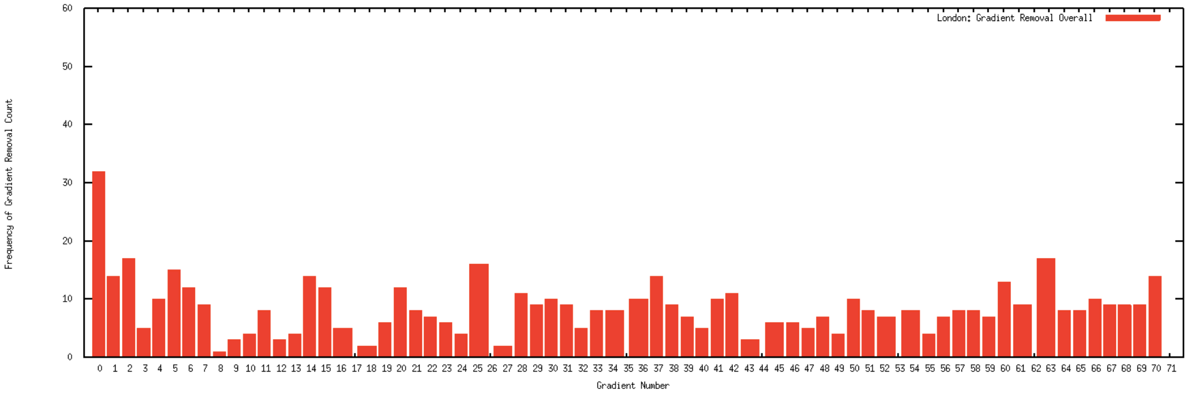


Figure 6: Frequency of gradient removal from all quality control checking methods.

Slice-wise checking: gradient removal by region

The slice-wise check calculated slice-to-slices correlation values in 5 smaller regions (0 through 4) and entire slice-to-slice correlation values (called “whole” in DTIPrep, region 5 in histogram). Of the smaller regions, region 0 caused the most gradients to be removed by the slice-wise check (123 gradients or 22.12% of all slice-wise check removals). Region 2 caused the least number of gradient removals (20 gradients or 3.60% of all slice-wise check removals). However, whole slice-to-slice comparisons caused the most gradients to be removed overall with 230 gradients or 41.37% of all slice-wise check removals (Figure 7).

Regions	**Frequency of removal**	**% of slice-wise check exclusions**
0	123	22.12
1	89	16.01
2	20	3.60
3	40	7.19
4	54	9.71
5 (whole)	230	41.37

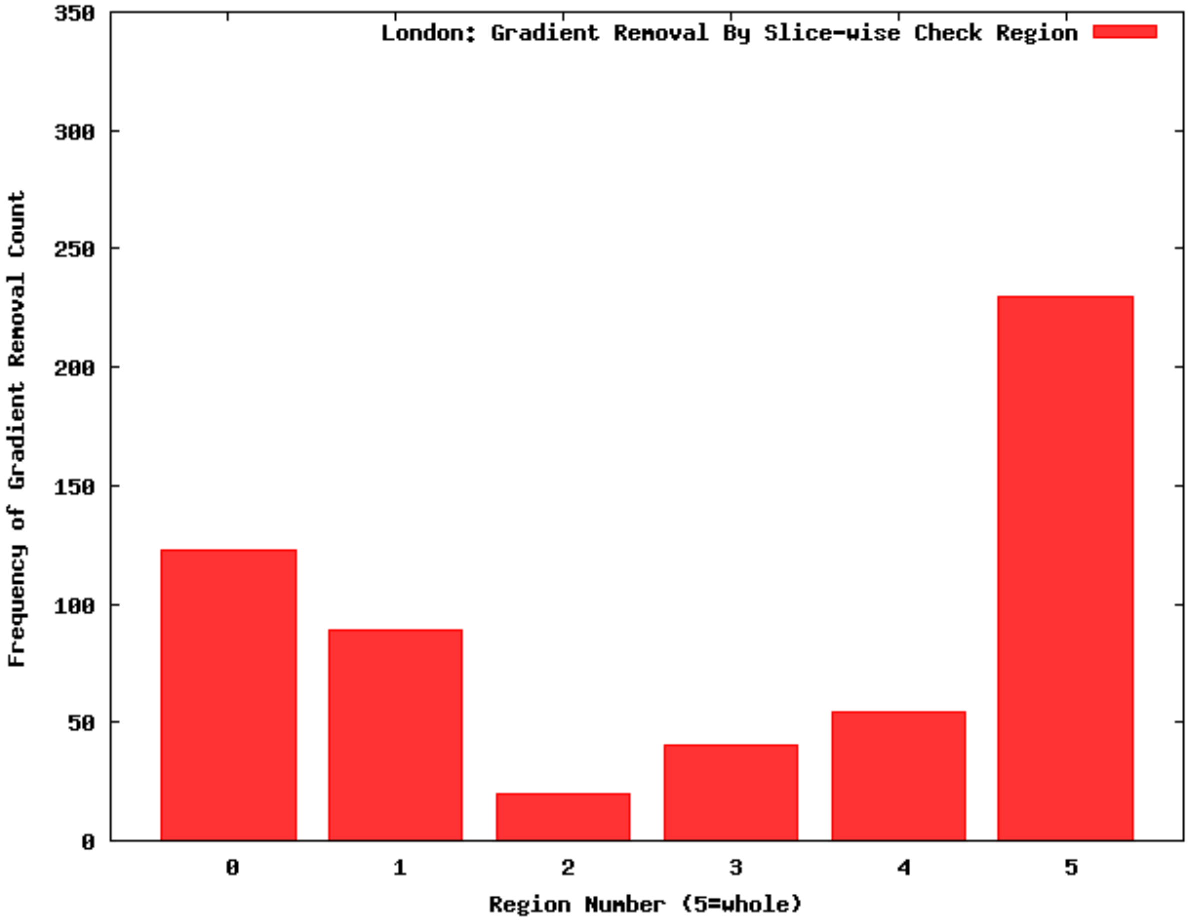


Figure 7: Frequency of gradient removal via the slice-wise checking method, separated by slice region.

Slice-wise checking: slice information

Slice-wise checking identified individual slices that did not correlate well with its neighboring slice. If one or more slices in a given gradient did not correlate well with its neighboring slice, then that slice is designated with a poor correlation value and that entire gradient was removed from its scan. Out of the total 225,720 slices in the London data set (55 slices per gradient x 72 gradients per scan x 57 scans) where each slice was present 4104 times, 755 slices (0.33%) were designated as not correlating well with its neighboring slice. The most commonly designated slice was slice number 22, being having a poor correlation value 39 times or 0.95% of the time (Figure 8). The highest percentages of poor correlation designation was seen clustered around the most commonly designated slice, which included slices 23 (0.83%), slice 24 (0.83%), 19 (0.76%), 21 (0.76%), 25 (0.63%), 16 (0.61%), and 18 (0.61%). Slices 1 through 5 and 50 through 55 were never designated with a poor correlation value.

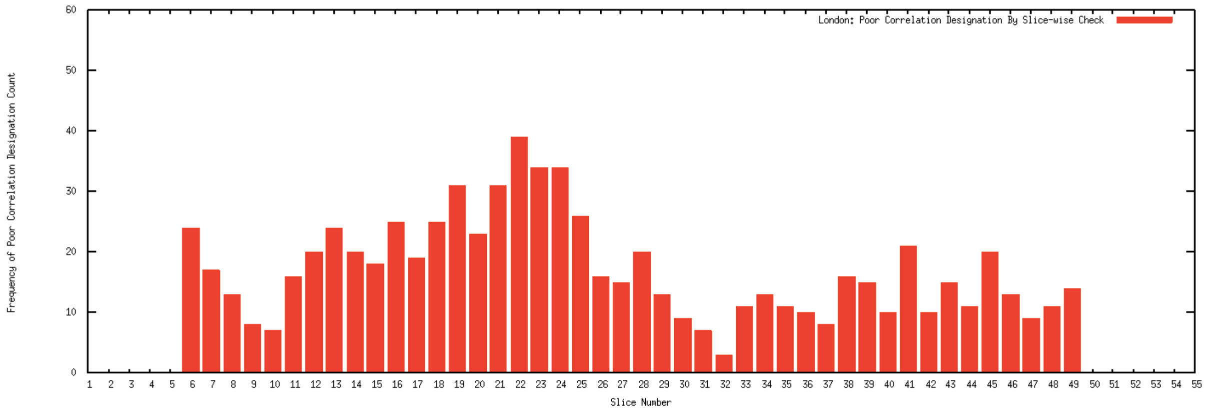


Figure 8: Frequency of slice designation with a poor correlation value.

Paris 2008 data

In year 1 of the paris data collection there were 15 scans done with only 12 directions. These 12 direction scans were not analyzed. There was a scanner software upgrade from VB13 to VB15 between years 1 and 2

One common oddity associated with this data set is that the gradient directions reported in the dicom headers from year 1 and year 2 are not consistent. It is assumed that the differences are due to patient head orientation, but a consistent method to reconcile the different gradient was not found.

All of the 2008 data have exactly the same gradients listed:
20080602 DWMRI_gradient_0001:=0.522326 0.384463 -0.761159

All the 2009 have slightly different gradients listed for each scan:
20090527 DWMRI_gradient_0001:=-0.521538 -0.384017 0.761925
20090617 DWMRI_gradient_0001:=-0.520586 -0.384672 0.762245
20090216 DWMRI_gradient_0001:=-0.521702 -0.383303 0.762172
20090617 DWMRI_gradient_0001:=-0.521276 -0.384026 0.7621

The Paris 2008 data set consisted of 64 50 direction diffusion-weighted imaging scans, each with dimensions of 128 pixels x 128 pixels x 60, 62, 70, or 80 slices per volume x 50 unique diffusion gradient directions and a single B0 image. All 64 50 direction scans were processed with DTIPrep. Gradients were removed by DTIPrep based on three different quality control checking methods: slice-wise, gradient-wise, and interlace-wise. Overall, the three checking methods removed a total of 268 gradients from the original total 3264 gradients (8.21%), with an average of 4.19 gradients removed per scan. Slice-wise checking removed the majority of the gradients (267 gradients, 99.6% of removed), while gradient-wise checking removed none, and interlace-wise checking removed 1 (0.04%).

Quality control method	**No. of gradients removed**	**% of removed gradients**
Slice-wise	267	99.6

Gradient-wise	0	0.00
Interlace-wise	1	0.04

Gradient information

Across all three quality control checking methods, the diffusion gradients removed the most were 8 and 17 (Figure 9). Diffusion gradient numbers 8 and 17 were removed in 17.19% of scans. The diffusion gradients removed most often were not clustered around numbers 8 and 17 and included gradients number 13 (15.63%), 43 (15.63%), 45 (15.63%), 6 (14.06%), 12 (14.06%) 38 (14.06%), 39 (14.06%), 19 (12.50%), 26, (12.50%) 28 (12.50%), 34 (12.50%), 36 (12.50%), 46 (12.50%), 48 (12.50%), 3 (10.94%), and 49 (10.94%). The gradient removed the least were numbers 7, 15, and 50 (1.56%). Gradients 0 and 30 were never removed. Gradient 0 had a b value of 0.

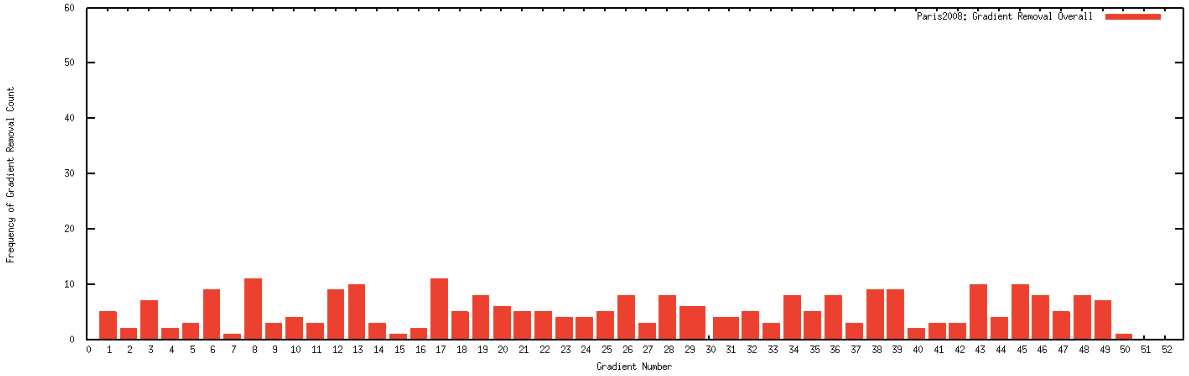


Figure 9: Frequency of gradient removal from all quality control checking methods.

Slice-wise checking: gradient removal by region

The slice-wise check calculated slice-to-slices correlation values in 5 smaller regions (0 through 4) and entire slice-to-slice correlation values (called "whole" in DTIPrep, region 5 in histogram). Of the smaller regions, region 0 caused the most gradients to be removed by the slice-wise check (65 gradients or 24.34% of all slice-wise check removals). Region 2 caused the least number of gradient removals (5 gradients or 1.87% of all slice-wise check removals). However, whole slice-to-slice comparisons caused the most gradients to be removed overall with 133 gradients or 49.81% of all slice-wise check removals (Figure 10).

Regions	Frequency of removal	% of slice-wise check exclusions
0	65	24.34
1	43	16.10
2	5	1.87
3	8	3.00
4	13	4.87
5	133	49.81

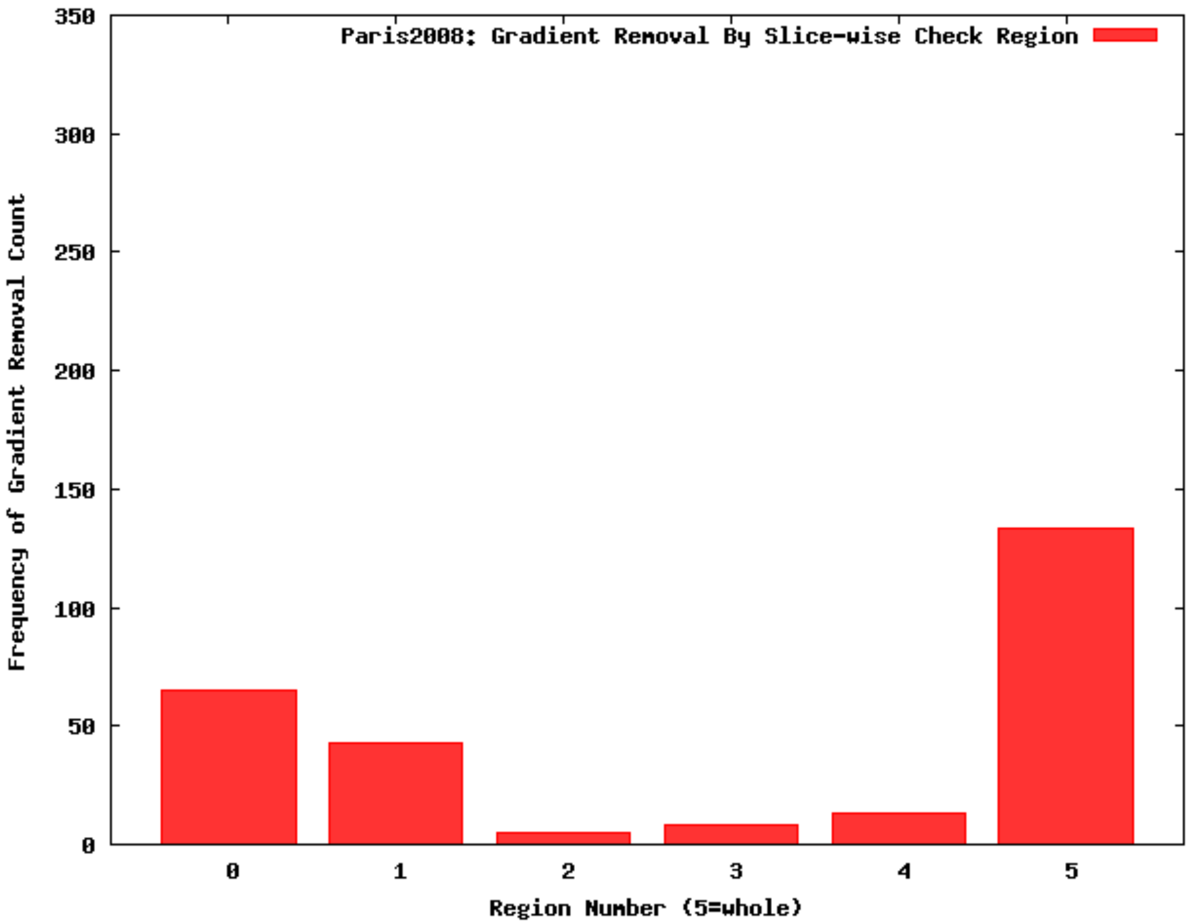


Figure 10: Frequency of gradient removal via the slice-wise checking method, separated by slice region.

Slice-wise checking: slice information

Slice-wise checking identified individual slices that did not correlate well with its neighboring slice. If one or more slices in a given gradient did not correlate well with its neighboring slice, then that slice is designated with a poor correlation value and that entire gradient was removed from its scan. Data sets containing 60 and 80 slices per gradient are presented here.

60 slice per gradient data sets (Figure 11)
Out of the total 113,220 slices in the Paris 2008 60-slice data set (60 slices per gradient x 51 gradients per scan x 37 scans) where each slice was present 2220 times, 215 slices (0.19%) were designated as not correlating well with its neighboring slice. The most commonly designated slice was slice number 23, having a poor correlation value 17 times or 0.77% of the time (Figure 11). The highest percentages of poor correlation designation were seen clustered around the most commonly designated slice, which included slices 21 (0.59%), 10 (0.45%), 11 (0.41%), and 22 (0.41%). Slices 1 through 6, 26, 39, 44, 54 through 56, and 58 through 60 were never designated with a poor correlation value.

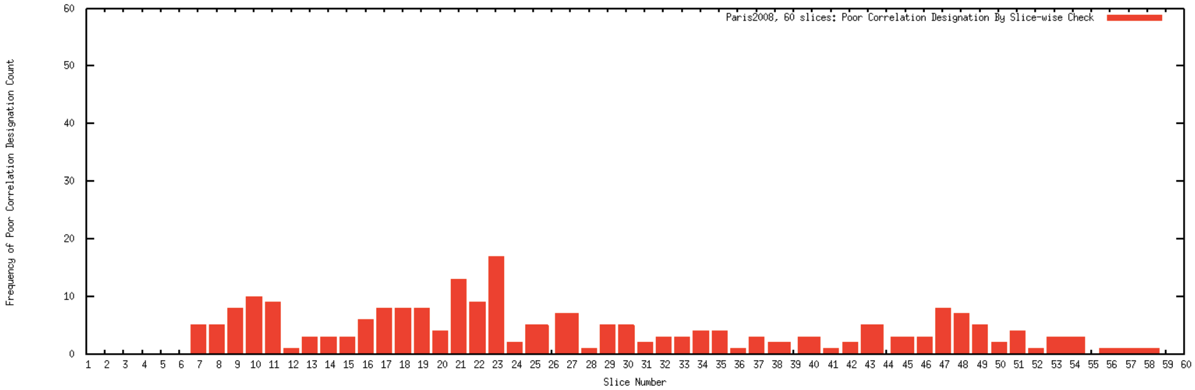


Figure 11: Frequency of slice designation with a poor correlation value.

80 slices per gradient (Figure 12)
Out of the total 81,600 slices in the Paris 2008 80-slice data set (80 slices per gradient x 51 gradients per scan x 20 scans) where each slice was present 1600 times, 159 slices (0.19%) were designated as not correlating well with its neighboring slice. The most commonly designated slice was slice number 17, being having a poor correlation value 11 times or 0.65% of the time (Figure 12). The highest percentages of poor correlation designation were not clustered around the most commonly designated slice, which included slices 37 (0.63%), slice 11 (0.50%), 13 (0.44%), 18 (0.44%), 14 (0.38%), 16 (0.38%), 35 (0.38%), and 57 (0.38%). Slices 1 through 8, 29, 31, 32, 44, 49, 50, 52, 56, 66, 70, and 72 through 80 were never designated with a poor correlation value.

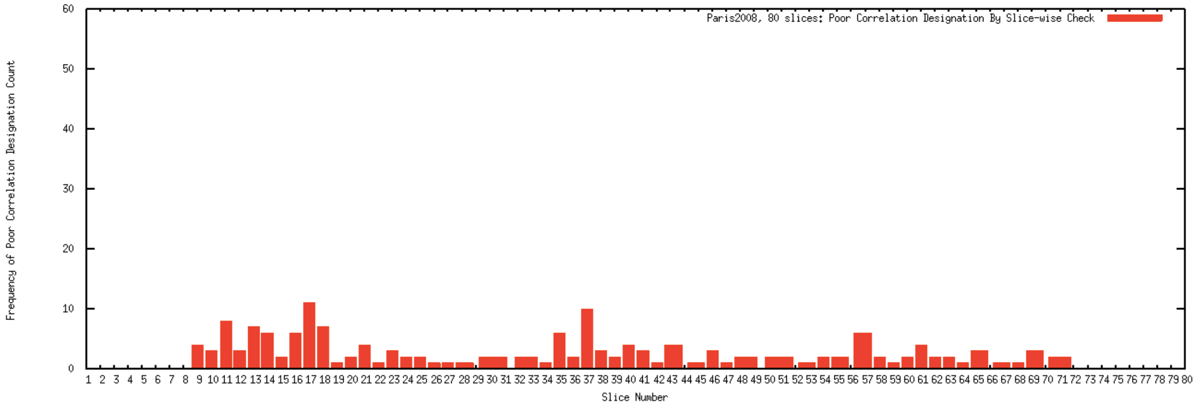


Figure 12: Frequency of slice designation with a poor correlation value.

Paris 2009 data

The Paris 2009 data set consisted of 75 50 direction diffusion-weighted imaging scans, each with dimensions of 128 pixels x 128 pixels x 60 slices per volume x 50 unique diffusion gradient directions and a single B0. All 75 scans were processed with DTIPrep. Gradients were removed by DTIPrep based on three different quality control checking methods: slice-wise, gradient-wise, and interlace-wise. Overall, the three checking methods removed a total of 278 gradients from the original total 3825 gradients (7.27%), with an average of 3.71 gradients removed per scan. Slice-wise checking removed the majority of the gradients (239 gradients, 86.0% of removed), while gradient-wise checking removed 1 (0.36%), and interlace-wise checking removed 38 (13.7%).

Quality control method	No. of gradients removed	% of removed gradients
Slice-wise	239	86.0
Gradient-wise	1	0.36
Interlace-wise	38	13.7

Gradient information

Across all three quality control checking methods, the diffusion gradients removed the most were 8 and 17 (Figure 13). Diffusion gradient number 40 was removed in 21.57% of scans. The diffusion gradients removed most often were not clustered around number 40 and included gradients number 46 (19.61%), 30 (17.65%), 45 (17.65%), 50 (17.65%), 31 (15.69%), 32 (15.69%), 36 (15.69%), 38 (15.69%), 42 (15.69%), and 48 (15.69%). Gradients 0 was never removed since it had a b value of 0.

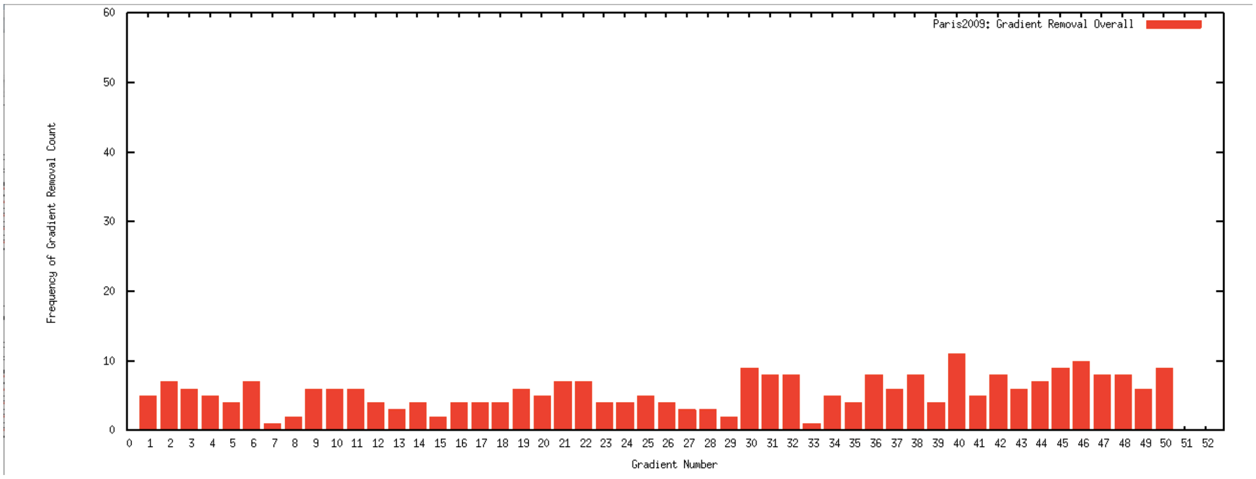


Figure 13: Frequency of gradient removal from all quality control checking methods.

Slice-wise checking: gradient removal by region

The slice-wise check calculated slice-to-slices correlation values in 5 smaller regions (0 through 4) and entire slice-to-slice correlation values (called “whole” in DTIPrep, region 5 in histogram). Of the smaller regions, region 1 caused the most gradients to be removed by the slice-wise check (44 gradients or 18.41 % of all slice-wise check removals). Region 3 caused the least number of gradient removals (9 gradients or 3.77% of all slice-wise check removals). However, whole slice-to-slice comparisons caused the most gradients to be removed overall with 146 gradients or 61.09% of all slice-wise check removals (Figure 14).

Regions	Frequency of removal	% of slice-wise check exclusions
0	24	10.04

1	44	18.41
2	3	1.26
3	9	3.77
4	13	5.44
5	146	61.09

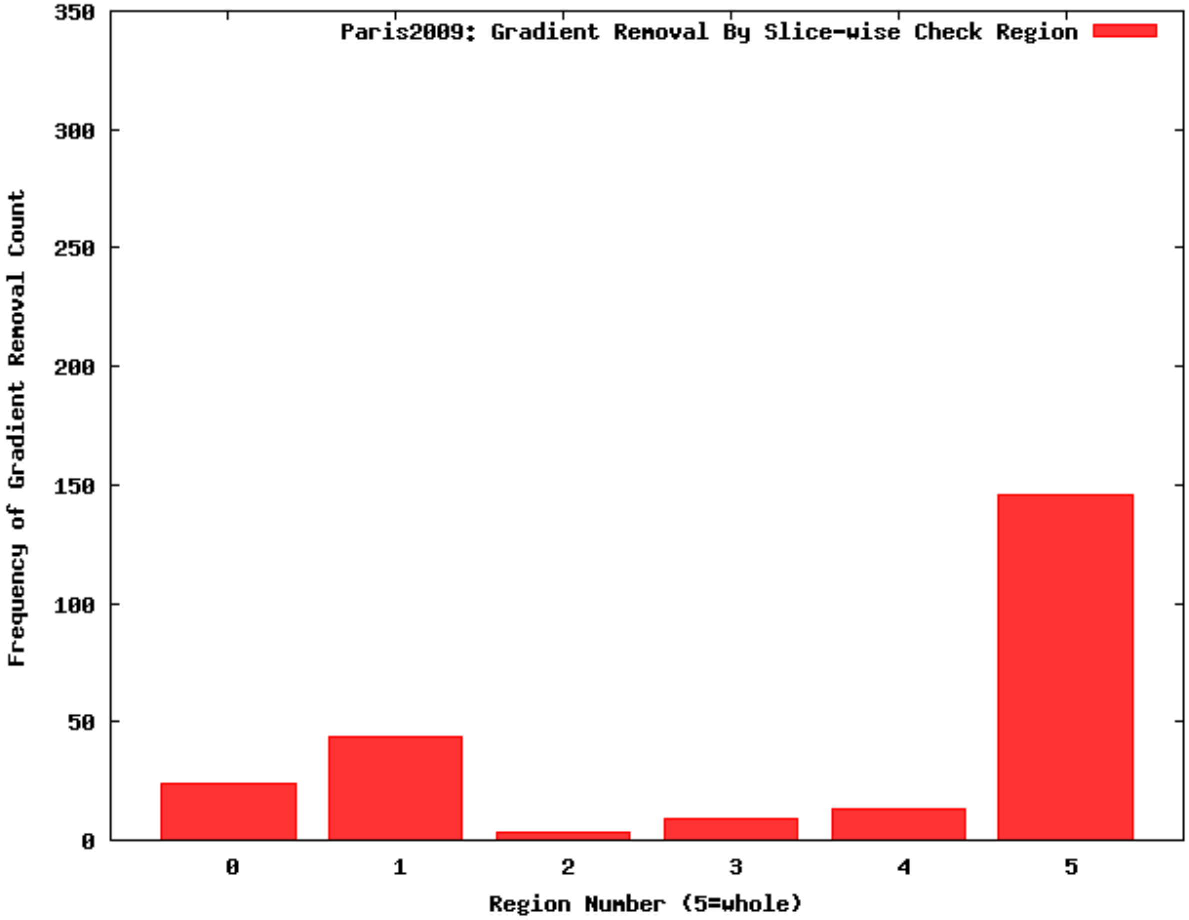


Figure 14: Frequency of gradient removal via the slice-wise checking method, separated by slice region.

Slice-wise checking: slice information

Out of the total 229,500 slices in the Paris 2009 data set (60 slices per gradient x 51 gradients per scan x 75 scans) where each slice was present 4500 times, 380 slices (0.17%) were designated as not correlating well with its neighboring slice. The most commonly designated slices were slice numbers 43 and 47, having a poor correlation value 17 times or 0.38% of the time (Figure 15). The highest percentages of poor correlation designation were not clustered around the most commonly designated slice, which included slices 49 (0.36%), 29 (0.33%), 45 (0.31%), 51 (0.31%), 10 (0.29%), 50 (0.29%), and 52 (0.29%). Slices 1 through 6 and 54 through 60 were never designated with a poor correlation value.

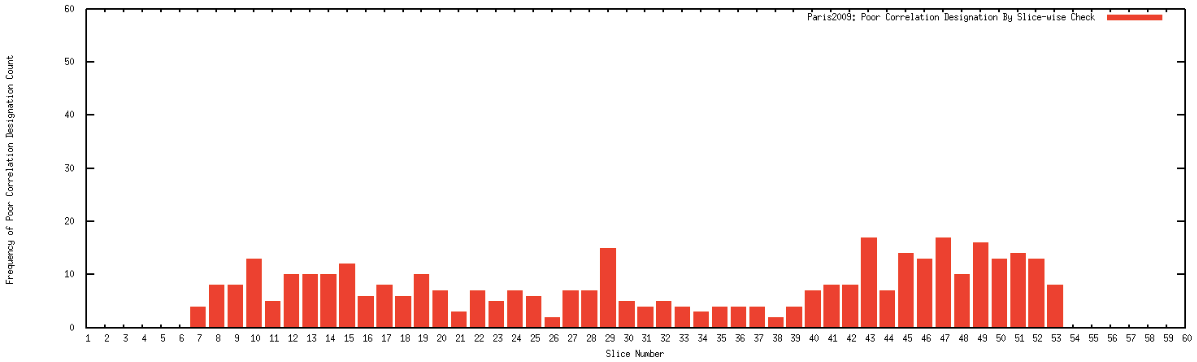


Figure 15: Frequency of slice designation with a poor correlation value.

Summary

Site	Year	Bad Gradients Removed	Average Remining Gradient Directions
Paris	2008	8.21%	45.8
Paris	2009	7.27%	46.4
Leiden	2008	29.6%	22.5
London	2009	13.7%	55.2

The Leiden and London data were very consistent with respect to the defined protocols for data collection. The Paris data protocol seemed to have a lot of variability (number of slices changed dramatically from 60 to 80 slices, 19% of year 1 data only had 12 directions, and year 2 gradient directions were not consistent from scan to scan). Please note that the year 2 gradient direction inconsistency is like resolvable by understanding how they are related to the oblique scan angles.

The Paris and Leiden data were both collected at 2.0mm isotropic voxels, and the London data was collected with 2.5mm isotropic voxels.

From visual inspections, and backed up by the QC mechanisms, the Paris and London data were the cleanest with respect to noise. From a purely qualitative visual perspective, the London seemed to display less noise (that is likely due to the larger voxel sizes).

Many of the Leiden data sets had significant drop out effects that seemed to be most prominent in the inferior part of the scans. The drop-out effects of the Leiden data should be closely examined and carefully considered before applying fiber tracking methods. For scans with more than 16 good gradient directions it is likely that the data is suitable for gross scalar measurements (FA/ADC for large ROI type analysis).

There was no redundancy of gradients collected in any of the sequences. This means that if any gradient direction were bad all estimates from that direction would be absent.

Appendix:

Leiden Gradient and Slice analysis tables

Leiden Gradient Gradient no.	Frequency of removal	% of scans that lost this gradient
0	0	0.00
1	18	24.32
2	8	10.81
3	**37**	**50.00**
4	**43**	**58.11**
5	**40**	**54.05**
6	**42**	**56.76**
7	35	47.30
8	**40**	**54.05**
9	15	20.27
10	34	45.95
11	33	44.59
12	26	35.14
13	22	29.73
14	17	22.97
15	9	12.16
16	18	24.32
17	18	24.32
18	13	17.57
19	16	21.62
20	12	16.22
21	7	9.46
22	23	31.08
23	7	9.46
24	6	8.11
25	9	12.16
26	9	12.16
27	10	13.51
28	11	14.86
29	5	6.76
30	20	27.03
31	7	9.46
32	16	21.62

Leiden Slice no.	Frequency of poor correlation designation	% of slices designated with poor correlation value
1	0	0.00
2	0	0.00
3	0	0.00

4	0	0.00
5	0	0.00
6	0	0.00
7	**43**	**1.76**
8	36	1.47
9	42	1.72
10	**49**	**2.01**
11	**55**	**2.25**
12	**49**	**2.01**
13	**51**	**2.09**
14	37	1.52
15	38	1.56
16	23	0.94
17	24	0.98
18	19	0.78
19	22	0.90
20	12	0.49
21	19	0.78
22	9	0.37
23	12	0.49
24	13	0.53
25	21	0.86
26	19	0.78
27	14	0.57
28	15	0.61
29	23	0.94
30	19	0.78
31	14	0.57
32	12	0.49
33	8	0.33
34	8	0.33
35	9	0.37
36	9	0.37
37	8	0.33
38	11	0.45
39	6	0.25
40	11	0.45
41	12	0.49
42	17	0.70
43	9	0.37
44	11	0.45
45	19	0.78
46	19	0.78
47	22	0.90
48	18	0.74
49	13	0.53
50	21	0.86

51	16	0.66
52	20	0.82
53	21	0.86
54	18	0.74
55	10	0.41
56	17	0.70
57	10	0.41
58	0	0.00
59	0	0.00
60	0	0.00
61	0	0.00
62	0	0.00
63	0	0.00
64	0	0.00

London Gradient and Slice analysis tables

London Gradient no.	**Frequency of removal**	**% of scans that lost this gradient**
0	**32**	**56.14**
1	**14**	**24.56**
2	**17**	**29.82**
3	5	8.77
4	10	17.54
5	**15**	**26.32**
6	12	21.05
7	9	15.79
8	1	1.75
9	3	5.26
10	4	7.02
11	8	14.04
12	3	5.26
13	4	7.02
14	**14**	**24.56**
15	12	21.05
16	5	8.77
17	0	0.00
18	2	3.51
19	6	10.53
20	12	21.05
21	8	14.04
22	7	12.28
23	6	10.53
24	4	7.02
25	**16**	**28.07**
26	0	0.00
27	2	3.51

28	11	19.30
29	9	15.79
30	10	17.54
31	9	15.79
32	5	8.77
33	8	14.04
34	8	14.04
35	0	0.00
36	10	17.54
37	**14**	**24.56**
38	9	15.79
39	7	12.28
40	5	8.77
41	10	17.54
42	11	19.30
43	3	5.26
44	0	0.00
45	6	10.53
46	6	10.53
47	5	8.77
48	7	12.28
49	4	7.02
50	10	17.54
51	8	14.04
52	7	12.28
53	0	0.00
54	8	14.04
55	4	7.02
56	7	12.28
57	8	14.04
58	8	14.04
59	7	12.28
60	13	22.81
61	9	15.79
62	0	0.00
63	**17**	**29.82**
64	8	14.04
65	8	14.04
66	10	17.54
67	9	15.79
68	9	15.79
69	9	15.79
70	**14**	**24.56**
71	0	0.00

London Slice no.	**Frequency of poor correlation designation**	**% of slices designated with poor correlation value**
1	0	0.00

2	0	0.00
3	0	0.00
4	0	0.00
5	0	0.00
6	24	0.58
7	17	0.41
8	13	0.32
9	8	0.19
10	7	0.17
11	16	0.39
12	20	0.49
13	24	0.58
14	20	0.49
15	18	0.44
16	**25**	**0.61**
17	19	0.46
18	**25**	**0.61**
19	**31**	**0.76**
20	23	0.56
21	**31**	**0.76**
22	**39**	**0.95**
23	**34**	**0.83**
24	**34**	**0.83**
25	**26**	**0.63**
26	16	0.39
27	15	0.37
28	20	0.49
29	13	0.32
30	9	0.22
31	7	0.17
32	3	0.07
33	11	0.27
34	13	0.32
35	11	0.27
36	10	0.24
37	8	0.19
38	16	0.39
39	15	0.37
40	10	0.24
41	21	0.51
42	10	0.24
43	15	0.37
44	11	0.27
45	20	0.49
46	13	0.32
47	9	0.22
48	11	0.27

49	14	0.34
50	0	0.00
51	0	0.00
52	0	0.00
53	0	0.00
54	0	0.00
55	0	0.00

Paris 2008 Gradient and Slice analysis tables

Paris 2008 Gradient no.	Frequency of removal	% of scans that lost this gradient
0	0	0.00
1	5	7.81
2	2	3.13
3	**7**	**10.94**
4	2	3.13
5	3	4.69
6	**9**	**14.06**
7	1	1.56
8	**11**	**17.19**
9	3	4.69
10	4	6.25
11	3	4.69
12	**9**	**14.06**
13	**10**	**15.63**
14	3	4.69
15	1	1.56
16	2	3.13
17	**11**	**17.19**
18	5	7.81
19	**8**	**12.50**
20	6	9.38
21	5	7.81
22	5	7.81
23	4	6.25
24	4	6.25
25	5	7.81
26	**8**	**12.50**
27	3	4.69
28	**8**	**12.50**
29	6	9.38
30	0	0.00
31	4	6.25
32	5	7.81
33	3	4.69
34	**8**	**12.50**

35	5	7.81
36	**8**	**12.50**
37	3	4.69
38	**9**	**14.06**
39	**9**	**14.06**
40	2	3.13
41	3	4.69
42	3	4.69
43	**10**	**15.63**
44	4	6.25
45	**10**	**15.63**
46	**8**	**12.50**
47	5	7.81
48	**8**	**12.50**
49	**7**	**10.94**
50	1	1.56

Paris 2008 Slice no.	**Frequency of poor correlation designation**	**% of slices designated with poor correlation value**
1	0	0.00
2	0	0.00
3	0	0.00
4	0	0.00
5	0	0.00
6	0	0.00
7	5	0.23
8	5	0.23
9	8	0.36
10	**10**	**0.45**
11	**9**	**0.41**
12	1	0.05
13	3	0.14
14	3	0.14
15	3	0.14
16	6	0.27
17	8	0.36
18	8	0.36
19	8	0.36
20	4	0.18
21	**13**	**0.59**
22	**9**	**0.41**
23	**17**	**0.77**
24	2	0.09
25	5	0.23
26	0	0.00
27	7	0.32
28	1	0.05
29	5	0.23

30	5	0.23
31	2	0.09
32	3	0.14
33	3	0.14
34	4	0.18
35	4	0.18
36	1	0.05
37	3	0.14
38	2	0.09
39	0	0.00
40	3	0.14
41	1	0.05
42	2	0.09
43	5	0.23
44	0	0.00
45	3	0.14
46	3	0.14
47	8	0.36
48	7	0.32
49	5	0.23
50	2	0.09
51	4	0.18
52	1	0.05
53	3	0.14
54	0	0.00
55	0	0.00
56	0	0.00
57	1	0.05
58	0	0.00
59	0	0.00
60	0	0.00

Paris 2008 Slice no.	**Frequency of poor correlation designation**	**% of slices designated with poor correlation value**
1	0	0.00
2	0	0.00
3	0	0.00
4	0	0.00
5	0	0.00
6	0	0.00
7	0	0.00
8	0	0.00
9	4	0.25
10	3	0.19
11	**8**	**0.50**
12	3	0.19
13	**7**	**0.44**

14	**6**	**0.38**
15	2	0.13
16	**6**	**0.38**
17	**11**	**0.69**
18	**7**	**0.44**
19	1	0.06
20	2	0.13
21	4	0.25
22	1	0.06
23	3	0.19
24	2	0.13
25	2	0.13
26	1	0.06
27	1	0.06
28	1	0.06
29	0	0.00
30	2	0.13
31	0	0.00
32	0	0.00
33	2	0.13
34	1	0.06
35	**6**	**0.38**
36	2	0.13
37	**10**	**0.63**
38	3	0.19
39	2	0.13
40	4	0.25
41	3	0.19
42	1	0.06
43	4	0.25
44	0	0.00
45	1	0.06
46	3	0.19
47	1	0.06
48	2	0.13
49	0	0.00
50	0	0.00
51	2	0.13
52	0	0.00
53	1	0.06
54	2	0.13
55	2	0.13
56	0	0.00
57	**6**	**0.38**
58	2	0.13
59	1	0.06
60	2	0.13

61	4	0.25
62	2	0.13
63	2	0.13
64	1	0.06
65	3	0.19
66	0	0.00
67	1	0.06
68	1	0.06
69	3	0.19
70	0	0.00
71	2	0.13
72	0	0.00
73	0	0.00
74	0	0.00
75	0	0.00
76	0	0.00
77	0	0.00
78	0	0.00
79	0	0.00
80	0	0.00

Paris 2009 Gradient and Slice analysis tables

Paris 2009 Gradient no.	**Frequency of removal**	**% of scans that lost this gradient**
0	0	0.00
1	5	9.80
2	7	13.73
3	6	11.76
4	5	9.80
5	4	7.84
6	7	13.73
7	1	1.96
8	2	3.92
9	6	11.76
10	6	11.76
11	6	11.76
12	4	7.84
13	3	5.88
14	4	7.84
15	2	3.92
16	4	7.84
17	4	7.84
18	4	7.84
19	6	11.76
20	5	9.80

21	7	13.73
22	7	13.73
23	4	7.84
24	4	7.84
25	5	9.80
26	4	7.84
27	3	5.88
28	3	5.88
29	2	3.92
30	**9**	**17.65**
31	**8**	**15.69**
32	**8**	**15.69**
33	1	1.96
34	5	9.80
35	4	7.84
36	**8**	**15.69**
37	6	11.76
38	**8**	**15.69**
39	4	7.84
40	**11**	**21.57**
41	5	9.80
42	**8**	**15.69**
43	6	11.76
44	7	13.73
45	**9**	**17.65**
46	**10**	**19.61**
47	**8**	**15.69**
48	**8**	**15.69**
49	6	11.76
50	**9**	**17.65**

Paris 2009 Slice no.	**Frequency of poor correlation designation**	**% of slices designated with poor correlation value**
1	0	0.00
2	0	0.00
3	0	0.00
4	0	0.00
5	0	0.00
6	0	0.00
7	4	0.09
8	8	0.18
9	8	0.18
10	**13**	**0.29**
11	5	0.11
12	10	0.22
13	10	0.22
14	10	0.22

15	12	0.27
16	6	0.13
17	8	0.18
18	6	0.13
19	10	0.22
20	7	0.16
21	3	0.07
22	7	0.16
23	5	0.11
24	7	0.16
25	6	0.13
26	2	0.04
27	7	0.16
28	7	0.16
29	**15**	**0.33**
30	5	0.11
31	4	0.09
32	5	0.11
33	4	0.09
34	3	0.07
35	4	0.09
36	4	0.09
37	4	0.09
38	2	0.04
39	4	0.09
40	7	0.16
41	8	0.18
42	8	0.18
43	**17**	**0.38**
44	7	0.16
45	**14**	**0.31**
46	13	0.29
47	**17**	**0.38**
48	10	0.22
49	**16**	**0.36**
50	**13**	**0.29**
51	**14**	**0.31**
52	**13**	**0.29**
53	8	0.18
54	0	0.00
55	0	0.00
56	0	0.00
57	0	0.00
58	0	0.00
59	0	0.00
60	0	0.00

Data tool modifications necessary:

DicomToNrrd Converter

Consulted with Xiaodong Tao of GE Research to coordinate re-writing a major portion of DicomToNrrd to properly deal with the new Philips scanner and oblique collected DTI data. This required the gradients to be interpreted with respect to a measurement frame consistent with the DICOM ImageOrientationPatient (0x0020,0x0037) field. Once this was accomplished, all data were verified to have been consistently collected. In the first pass, David Clunie's dicom3tools were used to un-concatenate the multi-frame files into separate files for each slice of the image.

```
###### David Clunies dicom3tools can convert a multi-frame file into a series
#of single frame file
#  WARNING:  This takes about 2 hours per scan!
#
time
/raid0/homes/hjohnson/Downloads/dicom3tools_1.00.snapshot.20090716/appsrc/dcfile/dcuncat
-unenhance -if $i -of ${UNCATDIR}/uncat_dti_
####_
#
# After conversion it is necessary to zero pad the resulting images
# so they are listed in the proper ordering for some tools to process them. `
for i in uncat_dti_####_[0-9][0-9][0-9][0-9]; do
     newname=$(echo $i|sed "s/uncat_dti_####_\([0-9][0-9][0-9][0-
9]\)/uncat_dti_\1.dcm/g");
     mv $i $newname;
done
for i in uncat_dti_####_[0-9][0-9][0-9];      do
     newname=$(echo $i|sed "s/uncat_dti_####_\([0-9][0-9][0-9]\)/uncat_dti_0\1.dcm/g");
     mv $i $newname;
done
for i in uncat_dti_####_[0-9][0-9];           do
     newname=$(echo $i|sed "s/uncat_dti_####_\([0-9][0-9]\)/uncat_dti_00\1.dcm/g");
     mv $i $newname;
done
for i in uncat_dti_####_[0-9];                do
     newname=$(echo $i|sed "s/uncat_dti_####_\([0-9]\)/uncat_dti_000\1.dcm/g");
     mv $i $newname;
done
```

The measurement frame was converted from DICOM to NRRD properly.

In phase II, Xiodong Tao re-wrote DicomToNrrdConverter to work directly on the multi-frame data. The results were verified to be the same as working with the single slice data. The multi-frame compliant version converts the data more than 20 times faster than the single slice version.

DTIPrep

DTIPrep developers had never seen oblique collected DTI data before this project. Efforts were coordinated to incorporate proper oblique scan measurement frame into the quality control checking tools by verifying that gradient directions were collinear to within 1 degree after correcting for the measurement frame. Additional improvements were made to allow more flexible QC of the Paris data that had varying image sizes. We were unable to determine how to validate the oblique gradient directions from the Paris data (the Philips oblique scan rules did not seem to apply properly) so this QC step was made optional.