

## **Title: Diffusion Analysis Using MRI Studio**

Susumu Mori, Ph.D, Johns Hopkins University, Department of Radiology

### **Highlights:**

- Brief overview of MriStudio platform
- Introduction of new MriCloud platform for fully automated tensor calculation through an web interface
- Comprehensive quality control report
- Atlas-based quantitative analysis

### **Introduction:**

DtiStudio was introduced in 2001 and evolved into MriStudio by integrating two other programs, DiffeoMap and RoiEditor, for downstream quantitative image analysis such as image normalization and automated white matter segmentation. Historically, these programs have focused on simple tensor-based analysis using the 3x3 tensor model to estimate the anatomical features of the brain. Current MriStudio and new MriCloud remain with the tensor-based analysis and place their emphasis on the following four areas; 1) atlas-based quantitative analysis, 2) fully automated and platform-free analysis using a web-based interface and cloud computation, 3) comprehensive quality control report, and 4) tensor-based probabilistic tracking using dynamic programming. In following sections, details will be provided.

### **Methods:**

All programs are written in C++. MriStudio program family runs in Windows. The programs are available in [www.mristudio.org](http://www.mristudio.org) and can be downloaded after registration. The new MriCloud is web-based and platform-free. Google Chrome is recommended for MriCloud. The service is available at [www.mricloud.org](http://www.mricloud.org). Users need to register in the opening window or can use their Google account for the credential.

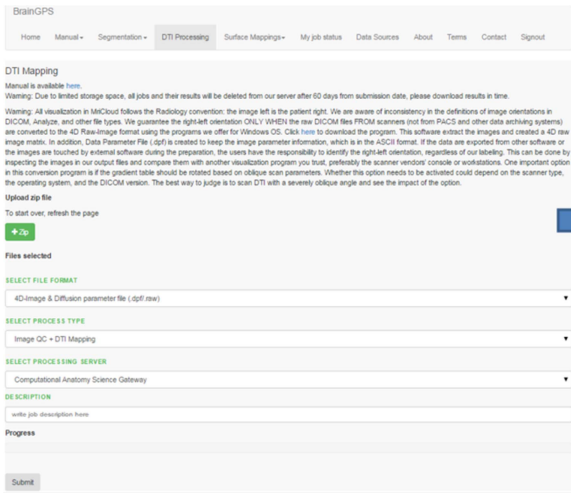
### **Results:**

#### Atlas-based quantitative analysis:

After diffusion tensor is calculated by DtiStudio, the DTI-derived images such as FA, MD, and other images can be normalized to the MNI space using DiffeoMap. The image normalization is based on advanced diffeomorphic non-linear transformation. Because of the computational resources required for this transformation, DiffeoMap employs cloud-computation, in which users' data are sent to a centralized computation facility in Johns Hopkins University in a transparent manner. The normalized images can be used for voxel-based analysis, in which voxel intensities such as FA and MD are analyzed at more than 1 million voxel locations inside the brain. Using RoiEditor, this voxel information can be reduced to approximately 200 pre-defined brain structures in the JHU-MNI atlas allowing structure-by-structure analysis. In this manner, a DTI data set with, for example, FA, MD, RD, and PD images, is reduced to a table consist of 200 structures x [FA, MD, RD, PD]. This table can be directly comparable across subjects or correlated with connectivity-based analysis among the 200 structures.

#### MriCloud: New web-based software using cloud computation:

For better accessibility to advanced DTI data analysis, a beta-version of MriCloud was released in December, 2014, which is fully automated and platform-free. The figure below shows the interface of the data submission through a web browser. Users need to use DICOM data directly from scanners without any modifications by PACS or other third-party software, which will be first converted to the Analyze format locally to remove all fields that would contain personal ID. Then the data will be compressed into a zip file and uploaded to the cloud server. The progression of data processing can be monitored and the results be downloaded from "My Job Status."

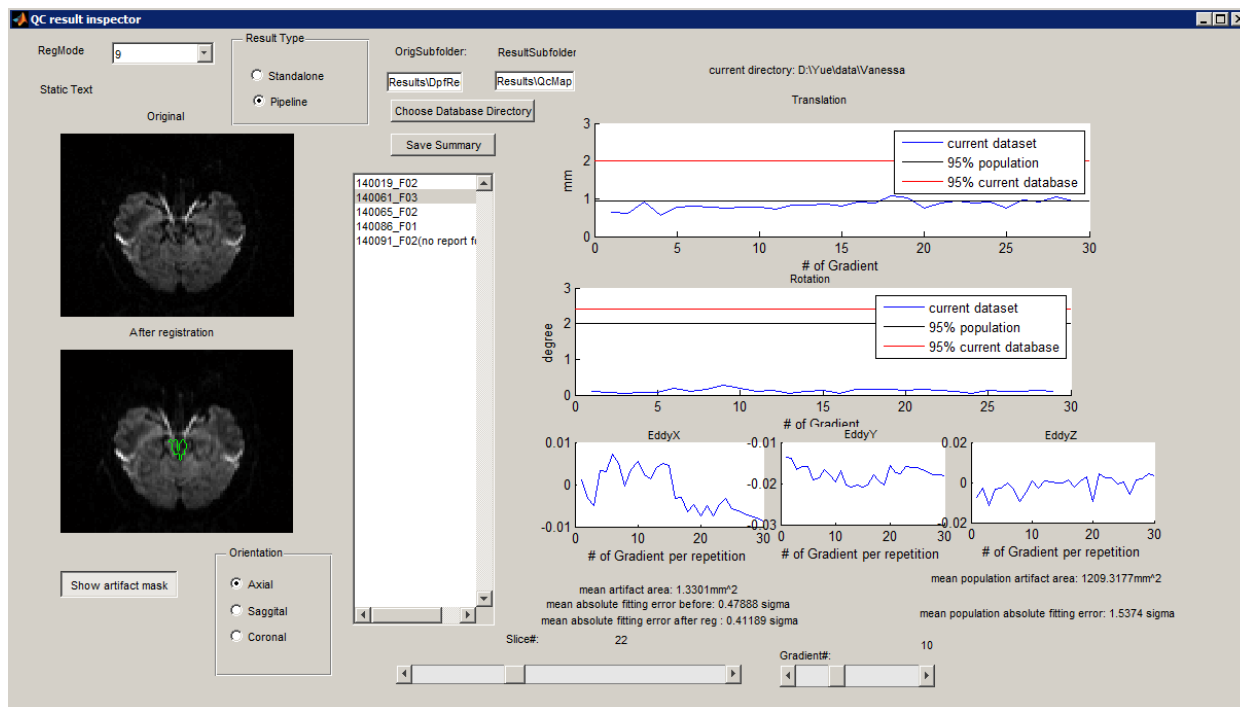


ID	Submission Date	Job Type	Description	Status	Action	Delete
395	2014-10-21 23:34 UTC	T1PreProcessing	E04e1#21	finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
412	2014-10-27 13:33 UTC	T1PreProcessing		finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
473	2014-10-15 19:09 UTC	T1PreProcessing	#16	finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
477	2014-10-16 18:57 UTC	T1PreProcessing		finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
482	2014-10-27 19:43 UTC	T1PreProcessing		finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
495	2014-11-20 19:22 UTC	DTISeg	Test01_701	finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
496	2014-11-21 10:24 UTC	T1PreProcessing		finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>
611	2014-12-18 14:29 UTC	T1PreProcessing		finished	<a href="#">Download Result</a> <a href="#">View result</a>	<a href="#">Delete</a>

Currently, only the tensor calculation and quality control modules are implemented in this platform, but we are extending the capability to automated tractography and atlas-based segmentation based on a multi-atlas approach.

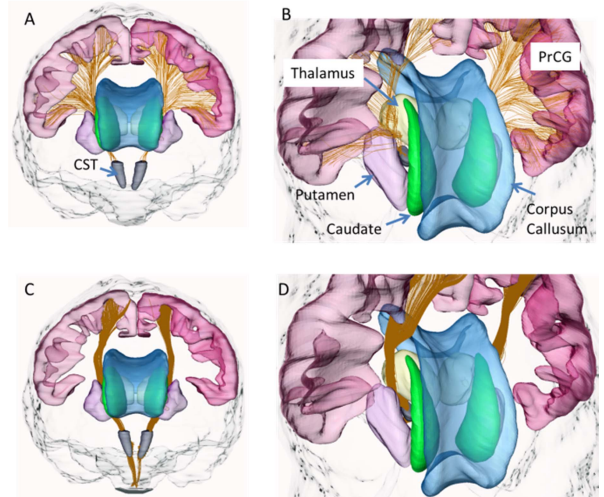
### Comprehensive QC report:

Both MriStudio and MriCloud offer extensive QC reports. This includes the amount of translation and rotation motions obtained after linear image registration. These registration-based reports are reliable only when the registration is accurate, but in reality many types of motion problems are not readily correctable by post-processing registration. These include regional signal drop, ghosting, and mismatch between the even and odd-numbered slices. For more comprehensive analysis, the QC pipeline monitors the fitting quality and rejects outliers. The number of the outliers and the amount of fitting residuals are stored in voxel-by-voxel manner and statistical reports are generated. The meaning of these numbers is, however, difficult to interpret. These collections of information should be compiled for the entire study and quality of individual data should be interpreted with respect to the population data. Our MatLab program, shown below, can read the QC reports of population data and perform the population-based analysis to define the average value of each measure and identify outlier data. The figure below shows the interface of the population analysis.



### Probabilistic tracking using dynamic programming (DP):

The tensor model is known to have limitations in accurately delineating the fiber structures inside each voxel, especially when there are a significant amount of secondary fiber populations with different orientations. Instead of obtaining more information from each voxel using one of the high-angular resolution methods, the DP finds the most probable pathway between two regions with known connections. The figure below shows examples of the corticospinal tract (A and C) and thalamocortical connections (B and D) comparing the DP (A and B) and FACT (C and D) approaches. For example, The DP can reveal connections between the pons and the entire motor cortex for the corticospinal tract. This method however should be used only for well characterized tracts with established connectivity knowledge. The results are useful to study, for example, the FA values of the known tracts, rather than discovering new connections. This module is now available in DtiStudio.



### **Discussion and Conclusion:**

Design of diffusion studies can be divided into three steps. First step is data acquisition. Certain types of diffusion studies require unique data acquisition schemes such as a large number of gradient orientations and high (or multiple) b-values. Second step is to generate images. There are many types of diffusion-derived images proposed in the past including scalar values (e.g. MD, FA, RD, AD, etc), vectors (e.g. eigenvectors), or tensors. Generation of maps to describe complex fiber architectures in each voxel, such as fiber orientation, population, or density maps, also belong to this second step. In the third step, we need to define structures of interest (as small as one voxel or a collection of voxels), reduce the image information into scalar values, and quantify voxel properties to compare the values across subjects.

In the past decade, many methods and tools have been developed for the second step, in order to extract more anatomical information from diffusion-weighted images from each voxel. Our software is based on the conventional tensor model for the first and second step, and its main focus is on the third step. In the standard MNI coordinate, a brain contains more than 1.2 million voxels. Our atlas-based analysis and MriCloud platform are designed to reduce this large voxel information to structural representations, which can be more readily compared across subjects and makes it easier to integrate information from multiple modalities, including anatomical and functional connectivity. Integration of various unique capabilities across different tools through the modern internet-based communication could be an important future direction of the research community.