Magnetic Resonance Imaging Diffusion Tensor Tractography: Evaluation of Anatomic Accuracy of Different Fiber Tracking Software Packages

Guenther C. Feigl[1], Wolfgang Hiergeist[1], Claudia Fellner[2], Karl-Michael M. Schebesch[1], Christian Doenitz[1], Thomas Finkenzeller[2], Alexander Brawanski[1], Juergen Schlaier[1]

Key words
- Anatomic accuracy
- Brain mapping
- DTI
- Navigation
- Surgery

Abbreviations and Acronyms
DTI: Diffusion tensor imaging
FA: Fractional anisotropy
FACT: Fiber Assignment Continuous Tracking
GTRACT: Guided Tensor Restore Anatomical Connectivity Tractography
MRI: Magnetic resonance imaging
SD: Standard deviation
TE: Echo time
TEND: Tensor deflection
TR: Repetition time

From the [1]Department of Neurosurgery and [2]Institute of Radiology, University Hospital Regensburg, Regensburg, Germany

To whom correspondence should be addressed: Guenther C. Feigl, M.D., Ph.D. [E-mail: guenther.feigl@web.de]

Citation: World Neurosurg. (2014) 81, 1:144-150. http://dx.doi.org/10.1016/j.wneu.2013.01.004

Journal homepage: www.WORLDNEUROSURGERY.org

Available online: www.sciencedirect.com

BACKGROUND: **Diffusion tensor imaging (DTI)—based tractography has become an integral part of preoperative diagnostic imaging in many neurosurgical centers, and other nonsurgical specialties depend increasingly on DTI tractography as a diagnostic tool. The aim of this study was to analyze the anatomic accuracy of visualized white matter fiber pathways using different, readily available DTI tractography software programs.**

METHODS: **Magnetic resonance imaging scans of the head of 20 healthy volunteers were acquired using a Siemens Symphony TIM 1.5T scanner and a 12-channel head array coil. The standard settings of the scans in this study were 12 diffusion directions and 5-mm slices. The fornices were chosen as an anatomic structure for the comparative fiber tracking. Identical data sets were loaded into nine different fiber tracking packages that used different algorithms. The nine software packages and algorithms used were NeuroQLab (modified tensor deflection [TEND] algorithm), Sörensen DTI task card (modified streamline tracking technique algorithm), Siemens DTI module (modified fourth-order Runge-Kutta algorithm), six different software packages from Trackvis (interpolated streamline algorithm, modified FACT algorithm, second-order Runge-Kutta algorithm, Q-ball [FACT algorithm], tensorline algorithm, Q-ball [second-order Runge-Kutta algorithm]), DTI Query (modified streamline tracking technique algorithm), Medinria (modified TEND algorithm), Brainvoyager (modified TEND algorithm), DTI Studio modified FACT algorithm, and the BrainLab DTI module based on the modified Runge-Kutta algorithm. Three examiners (a neuroradiologist, a magnetic resonance imaging physicist, and a neurosurgeon) served as examiners. They were double-blinded with respect to the test subject and the fiber tracking software used in the presented images. Each examiner evaluated 301 images. The examiners were instructed to evaluate screenshots from the different programs based on two main criteria: (i) anatomic accuracy of the course of the displayed fibers and (ii) number of fibers displayed outside the anatomic boundaries.**

RESULTS: **The mean overall grade for anatomic accuracy was 2.2 (range, 1.1—3.6) with a standard deviation (SD) of 0.9. The mean overall grade for incorrectly displayed fibers was 2.5 (range, 1.6—3.5) with a SD of 0.6. The mean grade of the overall program ranking was 2.3 with a SD of 0.6. The overall mean grade of the program ranked number one (NeuroQLab) was 1.7 (range, 1.5—2.8). The mean overall grade of the program ranked last (BrainLab iPlan Cranial 2.6 DTI Module) was 3.3 (range, 1.7—4). The difference between the mean grades of these two programs was statistically highly significant ($P < 0.0001$). There was no statistically significant difference between the programs ranked 1—3: NeuroQLab, Sörensen DTI Task Card, and Siemens DTI module.**

CONCLUSIONS: **The results of this study show that there is a statistically significant difference in the anatomic accuracy of the tested DTI fiber tracking programs. Although incorrectly displayed fibers could lead to wrong conclusions in the neurosciences field, which relies heavily on this noninvasive imaging technique, incorrectly displayed fibers in neurosurgery could lead to surgical decisions potentially harmful for the patient if used without intraoperative cortical stimulation. DTI fiber tracking presents a valuable noninvasive preoperative imaging tool, which requires further validation after important standardization of the acquisition and processing techniques currently available.**

INTRODUCTION

Microsurgical resections of tumors in or near functional areas, including white matter fiber tracts of the brain, represent a great challenge to neurosurgeons. To know what to expect intraoperatively, it is essential for neurosurgeons to have reliable diagnostic imaging available. Visualizing how anatomic structures and functional areas have been displaced by a lesion is essential for planning a surgical approach. A noninvasive imaging technique has been developed in the past 15 years capable of visualizing white matter fiber tracts. This method is diffusion tensor imaging (DTI)—based tractography, which has been used for clinical applications since about 1994 (2)

mainly to avoid neurologic deficits by damaging fibers during the surgical approach. Because DTI tractography is the only noninvasive method available to visualize pathways of white matter fiber tracts, an increasing number of centers have implemented this method in routine imaging of tumor patients. A few studies have been published on implementing DTI tractography for preoperative planning and intraoperative localization of major fiber pathways of the brain (17-19). However, when using DTI tractography, virtual three-dimensional projections of fiber pathways are superimposed on an anatomic image, which in some cases might be misleading. DTI tractography is based on measuring the diffusion of water molecules rather than visualizing the actual anatomic structures of axons. Considering the resolution of diffusion-weighted images, it becomes obvious that this is an attempt to visualize a microscopic entity using a macroscopic resolution. Even though it is generally known that the visualized fiber tracts are based on statistical calculations and probability calculations rather than anatomic facts, the temptation to view DTI tractography images as anatomic facts remains great. Nevertheless, it has been shown that major fiber tracts of the brain can be visualized using DTI tractography (3, 4, 8, 14). Based on this anatomic knowledge, the neurosurgeon has to decide whether or not to rely on the DTI tractography images. Reconstructed fiber tracts can differ depending on the software package, algorithms, and parameter settings being used. Very few data are available on the reliability, reproducibility, and anatomic accuracy of different fiber tracking software packages.

The hypothesis behind this study was that different software packages could potentially show different fibers because various settings are used during data acquisition, and several algorithms are used to perform the fiber tracking. The aim of this study was to compare the results by analyzing the anatomic accuracy of visualized white matter fiber pathways using identical parameter settings in different, readily available DTI tractography software packages.

METHODS

Test Subjects and Scanning Protocol

Approval from the institutional ethics committee was obtained, and each subject gave his or her written consent agreeing to participate in the study. Magnetic resonance imaging (MRI) scans of the head of 20 healthy volunteers (11 men and 9 women; mean age, 34 years; range, 19–56 years) were acquired using a Siemens Symphony TIM 1.5T scanner (Siemens, Erlangen, Germany) and a 12-channel head array coil. None of the volunteers had a neurologic disease, psychiatric disease, or brain injury in his or her previous medical history. Volunteers were scanned in a supine position with their heads embedded in cushioning to minimize motion artifacts.

In several tests preceding this study, the parameter settings for the MRI scans were tested, which included 12 and 64 diffusion directions. However, because no significant differences were observed between the results of these settings and not all the programs included in this study supported >12 directions, 12 directions and 5-mm slices were selected for the standard settings of the scans in this study. DTI sequences were obtained from the average value of three scans, each scan in 12 directions. The following parameter settings were used: repetition time (TR) = 3400 ms; echo time (TE) = 98 ms; bo, 1000 second/mm^2. A total of 23 slices (5-mm) were acquired. The field of view was 230 mm with a matrix of 128 × 128, and the scanning time was 2.24 minutes for each scan.

A T1-weighted three-dimensional magnetization-prepared rapid gradient echo sequence was obtained for anatomic reference using the following settings: TR = 1640 ms; TE = 3.1 ms; inversion time = 900 ms. A total of 160 slices (1-mm) were acquired. The field of view was 230 mm with a matrix of 256 × 256. The scanning time was 7.01 minutes.

Data Processing

All MRI data of all patients were loaded into nine different readily available software packages. The names of the programs and the algorithms they are based on are listed in Table 1. All software packages except for the BrainLab DTI-Software module (iPlan Cranial 2.6 [BrainLab, Feldkirchen, Germany]) and the Siemens DTI Module (Siemens, Erlangen, Germany) were available as free downloads. However, the BrainLab DTI-Software module and the Siemens DTI Module were the only two programs with approvals from the U.S. Food and Drug Administration and Conformité Européenne.

In several tests preceding this study, different fractional anisotropy (FA) values ranging from 0.5–0.25 and different maximal angles (40–70 degrees) were tested. The following identical parameter settings from the best results of these tests were chosen as the standard setting in all programs in this study: FA, 0.15; maximal angle, 60 degrees, bo threshold at 20%, and minimal length of fibers, 25 mm. All smoothing or eddy current corrections were deactivated during data import and during the fiber reconstruction process. However, even though some thresholds had been selected for the purposes of this investigation, none of these FA, angle thresholds, and b values are validated.

To determine the anatomic accuracy of the different fiber tracking packages, the fornices were chosen as an anatomic structure for the comparative fiber tracking (Figure 1). Its high density of fibers, sharp borders to surrounding brain tissue, and 180-degree bend of the fibers in its course between corpora mammillaria and the hypothalamus made it an ideal target for the comparative fiber tracking tests. After transferring the data to the different software modules, in each case the identical coronal slice was selected, and the region of interest was marked as the starting point for the fiber tracking. The region of interest for the fornices was selected in the middle of its course in the coronal slice (axial, coronal, and sagittal) where the third and lateral ventricles are visible as a t-shaped structure, the diameter of the fornices reach a maximum, and the fornices are next to each other (Figure 2). After performing the fiber tracking with the aforementioned settings, screenshots were made of the identical slices in the three planes (axial, coronal, and sagittal) and from an oblique direction for a better impression of the three-dimensional result. Each image was acquired with and without the anatomic T1 image in the background. Because each program uses different views to superimpose the fibers on the anatomic images,