
An Introduction to Visualization of Diffusion Tensor Imaging and its Applications

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Summary. Water diffusion is anisotropic in organized tissues such as white matter and muscle. Diffusion tensor imaging (DTI), a non-invasive MR technique, measures water self-diffusion rates and thus gives an indication of the underlying microstructure of tissue. The diffusion rate is often expressed by a second-order tensor. Visualizing DTI in an insightful way is challenging because of the high dimensionality of the diffusion tensor and the complex spatial relationships in a diffusion tensor field. This chapter surveys the different visualization techniques that have been developed for DTI and compares their main characteristics and drawbacks. We also discuss some of the many biomedical applications in which DTI helps extend our understanding or improve clinical procedures. We conclude with an overview of open problems and research directions.

1 Introduction

Diffusion tensor imaging (DTI) is a medical imaging modality that can reveal directional information in vivo in fibrous structures such as white matter or muscles. Although barely a decade old, DTI has become an important tool in studying white matter anatomy and pathology. Many hospitals, universities, and research centers have MRI scanners and diffusion imaging capability, allowing widespread DTI applications.

However, DTI data require interpretation before they can be useful. Visualization methods are needed to bridge the gap between the DTI datasets and understanding of the underlying tissue microstructure. A diffusion tensor measures a 3D diffusion process and has six interrelated tensor components. A volumetric DTI dataset consists of a 3D grid of these diffusion tensors that

form complicated patterns. The multivariate nature of the diffusion tensor and the 3D spatial characteristics of the diffusion tensor field combine to make DTI visualization a challenging task. This chapter compares current visualization techniques and analyzes their strengths and weaknesses.

DTI research is broadly interdisciplinary. Figure 1 gives a simplified illustration of the research domains surrounding DTI. It is worth noting that all of the components in the diagram are interrelated in a loop: new discoveries in one specific area often lead to improvements in the whole DTI field. For example, Pierpaoli *et al.* found incorrect connections in the neural pathways generated from a DTI dataset [1]. Issues like this stimulate research in diffusion imaging, and lead to new methods, in this case high angular resolution imaging [2, 3].

In section 2, we review techniques for DTI data acquisition. In section 3, we survey the computation and visualization techniques. We review some applications of DTI in section 4, discuss some open issues and problems in section 5, and conclude in section 6.

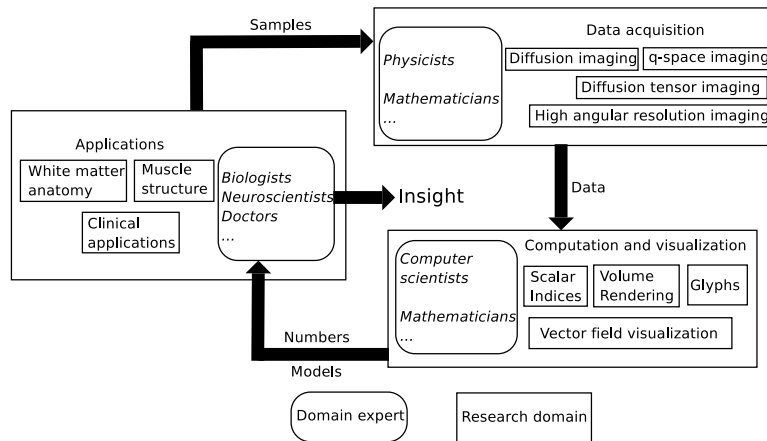


Fig. 1. The research context of DTI. Note that all the research domains are inter-related: progress in one domain can easily propagate into the rest of the field.

2 Diffusion Tensor Imaging

As for any visualization method, the merits of DTI visualization methods depend on the quality of the data. Understanding where the data come from, what they measure, and what their limitations are is an important first step in designing and implementing a visualization scheme.

Water molecules in human tissues constantly collide randomly with one another and with other molecules, a phenomenon called Brownian motion. In pure water, this seemingly random movement results in a dynamically expanding Gaussian distribution of water molecules released from one point [4]. In human tissues, however, cell membranes and large protein molecules limit the motion of water molecules. The geometrical and physical properties of the tissue determine the rate and direction of diffusion. We can thus infer the microstructure of human tissue by measuring the diffusion of the water molecules.

The discovery of the nuclear magnetic resonance (NMR) effect [5, 6] in 1946 was the beginning of work that has led to the current form of diffusion magnetic resonance imaging (MRI). Two important landmarks were the discovery of the spin echo [7], whose signal is perturbed by the water molecule diffusion, and MR imaging [8], which determines exactly where the NMR signal originates within the sample. Diffusion imaging was the first imaging modality that can measure the diffusion of water in human tissues in vivo. Although the exact mechanism of the generation of diffusion MRI signals in biological tissues is not fully understood, it is generally believed that the quantity measured by diffusion MRI is a mixture of intracellular diffusion, intercellular diffusion, and the exchange between the two sides of the the cell membrane [9].

Inferring tissue structure from the diffusion process requires exploring the orientation dependence of the diffusion. This dependence can be described by the diffusion propagator $P(r, r', \tau)$, which is the probability of a water molecule traveling from position r' to r in diffusion time τ [10]. In practice, the number of diffusion directions we can measure in a clinical scan is limited by scanning time, making it impossible to reconstruct the diffusion propagator completely. A diffusion tensor [11] describes the orientation dependence of diffusion assuming free diffusion in a uniform anisotropic medium (Gaussian diffusion). For example, a diffusion tensor is a good model for diffusion in uniformly oriented white matter structures such as the corpus callosum, but is insufficient in areas where different tracts cross or merge. The coefficients of the diffusion tensor, \mathbf{D} , are related to the diffusion-weighted MRI (DWI) signals by [12]: $\tilde{\mathbf{I}} = \mathbf{I}_0 \exp(\mathbf{b} : \mathbf{D})$, where \mathbf{I}_0 is the 0-weighted diffusion image, the tensor \mathbf{b} characterizes the diffusion-encoding gradient pulses used in the MRI sequence, and $\mathbf{b} : \mathbf{D} = \sum_{i=1}^3 \sum_{j=i}^3 \mathbf{b}_{ij} \mathbf{D}_{ij}$ is the tensor dot product.

A 3D diffusion tensor is a 3×3 positive symmetric matrix:

$$\mathbf{D} = \begin{bmatrix} \mathbf{D}_{xx} & \mathbf{D}_{xy} & \mathbf{D}_{xz} \\ \mathbf{D}_{xy} & \mathbf{D}_{yy} & \mathbf{D}_{yz} \\ \mathbf{D}_{xz} & \mathbf{D}_{yz} & \mathbf{D}_{zz} \end{bmatrix}$$

Diagonalizing \mathbf{D} , we get three positive eigenvalues λ_1, λ_2 and λ_3 (in decreasing order) and their corresponding eigenvectors $\mathbf{e}_1, \mathbf{e}_2$ and \mathbf{e}_3 . Many scalar indices and visualization methods are based on the eigenvalues and eigenvectors of DTI measurements, as discussed in section 3.

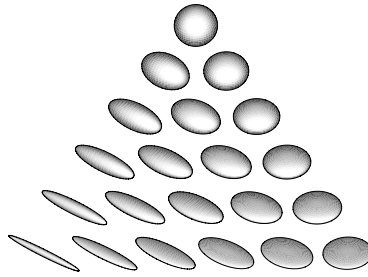


Fig. 2. Barycentric space of diffusion tensor ellipsoids.

One geometric representation of Gaussian diffusion is a diffusion ellipsoid. These ellipsoids represent the surface of constant mean-squared displacement of diffusing water molecules at some time τ after they are released from one point. The shape of a diffusion ellipsoid is inherently related to the eigenvalues and eigenvectors of the diffusion tensor: the three principal radii are proportional to the eigenvalues and the axes of the ellipsoid aligned with the three orthogonal eigenvectors of the diffusion tensor. Figure 2 shows ellipsoids representing different kinds of diffusion; the difference among the shapes of the ellipsoids are discussed in section 3.1. DTI measurements have been validated within acceptable error on the fibrous muscle tissue of the heart [13, 14]. However, in a voxel containing nonuniformly oriented neural fibers (see Figure 12), DTI measures an average signal from all the fibers within the voxel, which usually results in an apparent reduction of anisotropy and increase in uncertainty [15]. To resolve the uncertainty in these areas, q -space spectral imaging [16] and other high angular resolution diffusion imaging methods [17, 18] have been explored.

Image acquisition for DTI is a very active research area. Progress is frequently reported on resolution improvement and reductions in imaging time, noise, and distortion.

3 DTI Visualization

Meaningful visualization of high-dimensional data is challenging because of the high dimensionality of the diffusion tensor and the complex interrelationships in diffusion tensor fields. The last decade has seen several approaches to visualizing diffusion tensor data, most of them based on reducing the dimensionality of the data by extracting relevant information from the tensor. One possible classification of the different visualization techniques is by the dimensionality to which the tensor is reduced. Another important characteristic is the ability of these algorithms to show local or global information. Our discussion here groups the visualization methods on the basis of these two criteria. Anisotropy indices reduce the 6D information to a scalar value (1D). *Volume*

rendering for DTI uses anisotropy indices to define transfer functions that show the anisotropy and shape of the tensor. *Tensor glyphs* do not reduce the dimensionality of the tensor, instead using primitives that show the 6D tensor as such; however, these techniques cannot show global information. *Vector field visualization* reduces the tensor field to a vector field, and therefore to 3D. Several techniques can be used for vector-field visualization that show local as well as global information. In section 3.5, algorithms are described in which the vector field information is extended to the whole tensor. Finally in section 3.6, several interaction schemes in DTI visualization are discussed.

3.1 Scalar Indices

The complexity of a DTI dataset requires a complicated visualization scheme; however, medical researchers and practitioners alike are trained to read scalar fields on gray-level images slice by slice. Scalar datasets, although limited in the amount of information they can convey, can be visualized with simplicity and clarity and thus interpreted quickly and easily. It can thus be useful to reduce DTI to scalar datasets. Since the advent of diffusion MRI, scalar indices of diffusion MRI data have been designed and visualized successfully alongside multivariate visualization schemes: rather than competing, the two methods complement one another.

The challenges of reducing a tensor-valued diffusion MRI measurement to a scalar index include mapping to a meaningful physical quantity, maintaining invariance with respect to rotation and translation, and reducing the effect of noise. Some scalar indices for DTI data are listed in Table 1.

Mean diffusivity (MD), which measures the overall diffusion rate, is the average of the diffusion tensor eigenvalues and is rotationally invariant. van Gelderen *et al.* [22] demonstrated that, after a stroke, the trace of the diffusion tensor delineates the affected area much more accurately than the diffusion image in one direction.

Before the diffusion tensor model was made explicit in 1994 by Basser *et al.* [11], several different anisotropy indices derived from DWIs had been used, such as anisotropic diffusion ratio [23]. Unfortunately, these anisotropy indices depend on the choice of laboratory coordinate system and are rotationally variant: their interpretation varies according to the relative positions of the MR gradient and the biological tissues, usually resulting in an underestimation of the degree of anisotropy [19]. Therefore it is important to use rotationally invariant anisotropy indices such as Volume ratio (VR), rational anisotropy (RA) or fractional anisotropy (FA), which are based on the rotationally invariant eigenvalues. Note that both RA and FA can be derived from tensor norms and traces without calculating the eigenvalues.

However, rotationally invariant indices such as RA and FA are still susceptible to noise contamination. Pierpaoli *et al.* [19] calculated an intervoxel anisotropy index, the *lattice index* (LI), which locally averages inner products between diffusion tensors in neighboring voxels. LI decreases the sensitivity to

Scalar Index	Equations
Mean diffusivity, $\langle \mathbf{D} \rangle$	$\frac{\mathbf{D}_{xx} + \mathbf{D}_{yy} + \mathbf{D}_{zz}}{3}, \frac{\lambda_1 + \lambda_2 + \lambda_3}{3}, \frac{\text{Trace}(\mathbf{D})}{3}$
[19] Volume ratio, VR	$\frac{\lambda_1 \lambda_2 \lambda_3}{\left(\frac{\lambda_1 + \lambda_2 + \lambda_3}{3}\right)^3}, 27 \frac{\text{Determinant}(\mathbf{D})}{\text{Trace}(\mathbf{D})^3}$
[20] Fractional anisotropy, FA	$\sqrt{\frac{3}{2}} \frac{\ \mathbf{D} - \langle \mathbf{D} \rangle \mathbf{I}\ }{\ \mathbf{D}\ }$
[20] Rational anisotropy, RA	$\frac{\ \mathbf{D} - \langle \mathbf{D} \rangle \mathbf{I}\ }{\ \langle \mathbf{D} \rangle \mathbf{I}\ }, \frac{\sqrt{\text{Var}(\lambda)}}{E(\lambda)}$
[19] Lattice index, LI	$\sum_{n=1}^N a_n \left(\frac{\sqrt{3}}{\sqrt{8}} \frac{\sqrt{\mathbf{A} : \mathbf{A}_n}}{\sqrt{\mathbf{D} : \mathbf{D}_n}} + \frac{3}{4} \frac{\mathbf{A} : \mathbf{A}_n}{\sqrt{\mathbf{D} : \mathbf{D}} \sqrt{\mathbf{D}_n : \mathbf{D}_n}} \right)$
[21] Linear anisotropy, c_l	$\frac{\lambda_1 - \lambda_2}{\lambda_1 + \lambda_2 + \lambda_3}$
Planar anisotropy, c_p	$\frac{2(\lambda_2 - \lambda_3)}{\lambda_1 + \lambda_2 + \lambda_3}$
Isotropy, c_s	$\frac{3\lambda_3}{\lambda_1 + \lambda_2 + \lambda_3}$

Table 1: Some scalar indices for DTI data. $\|\mathbf{D}\| = \sqrt{\mathbf{D} : \mathbf{D}}$ is the tensor norm, $\text{Var}(\lambda)$ and $E(\lambda)$ are the variance and expectation of the three eigenvalues, a_n is a normalized weighting factor, $\mathbf{A} = \mathbf{D} - \langle \mathbf{D} \rangle \mathbf{I}$.

noise and avoids underestimation of the anisotropy when the neighbor voxels have different fiber orientations.

Because they contract the tensor to one scalar value, FA, RA and LI do not indicate the directional variation of the diffusion anisotropy well. For example, a cigar-shaped and a pancake-shaped ellipsoid can have equal FA while their shapes differ greatly. Geometrical diffusion measures [21] have been developed: linear anisotropy, c_l , planar anisotropy, c_p and spherical anisotropy or isotropy, c_s . By construction, $c_l + c_p + c_s = 1$. Thus, these three metrics parameterize a barycentric space in which the three shape extremes (linear, planar, and spherical) are at the corners of a triangle, as shown in Figure 2. It is worth noting that, unlike FA or RA, geometrical diffusion metrics depend on the order of the eigenvalues and are thus prone to bias in the presence of noise [19].

Figure 3 shows one way to compare qualitatively some of the metrics described above by sampling their values on a slice of a DTI dataset of a brain. Notice that the mean diffusivity (MD) is effective at distinguishing between cerebrospinal fluid (where MD is high) and brain tissue (lower MD), but fails to differentiate between different kinds of brain tissue. High fractional anisotropy, FA, on the other hand, indicates white matter, because the

directionality of the axon bundles permits faster diffusion along the neuron fiber direction than across it. FA is highest inside thick regions of uniformly anisotropic diffusion, such as inside the corpus callosum. Finally, while both c_l and c_p indicate high anisotropy, their relative values indicate the shape of the diffusion ellipsoid.

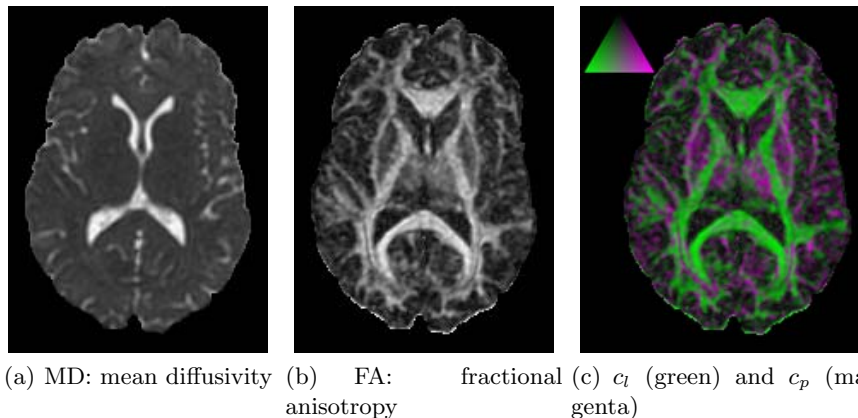


Fig. 3. Different shape metrics applied to one slice of a brain DTI scan.

3.2 Volume Rendering

Volume rendering is a means of visualizing large-scale structure in a tensor field, based on locally measured properties of the tensor data [24]. Volume rendering has the defining property of mapping from the tensor field attributes to a rendered image, without introducing additional geometry. However, volume rendering is inherently flexible in the sense that the volume scene can easily be supplemented with other visualizations (such as glyphs or fiber tracts, described in the following sections) to create a more informative image. Compositing all the scene components together creates an integrated visualization in which local and global aspects of the field may be seen in context. The volume of tensor field attributes can either be pre-computed and stored as a scalar field, or computed implicitly as part of rendering. In either case, an anisotropy index plays the important role of determining the opacity (thus visibility) of each sample. Each sample is then colored and shaded to indicate local shape characteristics, then samples composited as the integral of colors and opacities sampled along each ray.

An essential element of volume rendering is the *transfer function*, which assigns colors and opacities according to locally measured field properties. Traditionally, volume rendering has been applied to visualization of scalar fields, in which the domain of the transfer function is either the scalar value

defining the dataset or additionally includes derived quantities such as the gradient magnitude [25, 26]. The transfer function is usually implemented as a one-dimensional or two-dimensional lookup table. The transfer function domain variables are quantized to generate indices of table entries that contain the colors and opacity of the transfer function range.

The extension of volume rendering to diffusion tensor fields is thus essentially a matter of determining which quantities should serve as transfer function domain variables. To define opacity, the anisotropy indices in Table 1 are used. Fractional anisotropy (FA) is attractive in this respect because it can be expressed in terms of differentiable tensor invariants, so the chain rule can be used to calculate the gradient of FA as a normal for surface shading. Figure 4 shows depiction of basic 3-D structure with volume-rendered isosurfaces of fractional anisotropy. Rather than using a polygonal model of the anisotropy isosurface (as with Marching Cubes [27]), these images are computed with an opacity *step function*: opacity is 0.0 or 1.0 depending on whether FA is below or above the indicated threshold.

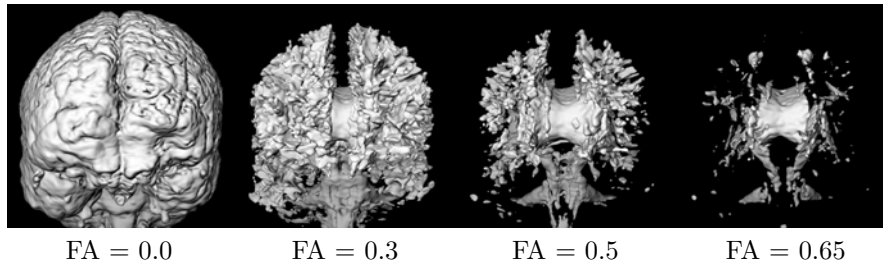


Fig. 4. Volume-rendered isosurfaces at a range of FA values show basic 3D structure of white matter in a DTI brain scan.

Color can be assigned in diffusion tensor volume rendering to indicate either the orientation or the shape of the underlying tensor samples. Applying the standard RGB coloring of the principal eigenvector (Sect. 3.4) allows basic neuroanatomic features to be recognized by their over-all color, as in Figure 5(a). Color can also be used to clarify differences in the shape of anisotropy apart from the anisotropy index used to define opacity. In particular, the difference between linear and planar anisotropy as measured by the c_l and c_p indices (Table 1) can be mapped onto the anisotropy isosurface, as in Figure 5(b) (where the variation from green to magenta for linear to planar anisotropy is the same as in Figure 3(c)). The rendering indicates how features with orthogonal orientations lead to planar anisotropy at their adjacencies. Locations in the brain characterized by this configuration of white matter fibers include the right-left trans-pontine tracts ventral to the inferior-superior corticospinal tracts in the brainstem, and the right-left tracts of the corpus callosum inferior to the anterior-posterior cingulum bundles.

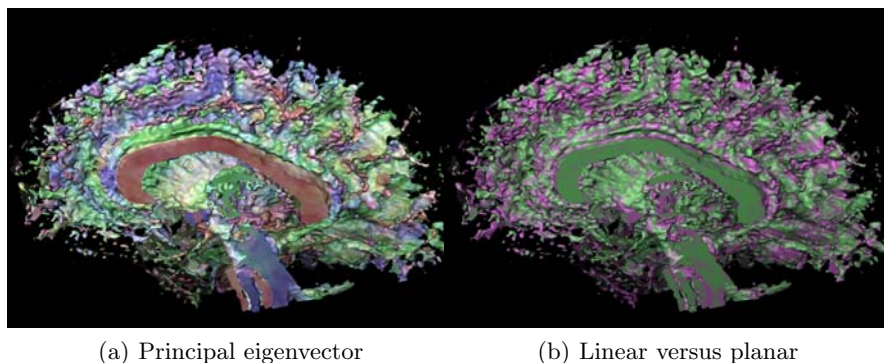


Fig. 5. Volume renderings of half a brain scan, (a) colored according to orientation of principal eigenvector, and (b) the distribution of linear (green) and planar (magenta) anisotropy. Surface is defined by $FA = 0.4$.

A recent application of volume rendering to diffusion tensor visualization is based on converting the tensor field to scalar fields, as described by Wenger *et al.* [28]. The approach here is to precompute multiple scalar volumes, that can be layered and interactively rendered with 3D texture-mapping graphics hardware [29]. The renderings in Figure 6 demonstrate visualizations which combine a volume rendering of the ventricles, together with a collection of fiber tracts rasterized into a color-coded scalar volume, to illustrate the relationship between the distribution and direction of the fiber tracts and the large-scale patterns of anisotropy. The flexible combination of the different scalar volumes into the final rendering permits interactive exploration and generation of visualizations.

There are currently no implementations that can volume render directly from a diffusion tensor volume to an image at interactive rates. The computational speed and flexibility of modern graphics hardware is increasing at such a rate, however, that this should soon be feasible. For example, two-dimensional transfer functions took minutes to render (in software) when introduced in 1988 [26], but can now be rendered at multiple frames per second with commodity graphics hardware [30]. Whether applied to scalar or tensor data, the intrinsically data-parallel nature of volume rendering means it is well suited to streaming-based processors found on modern graphics hardware [31]. We anticipate that volume-rendering graphics hardware will play an increasing role in the interactive visualization of diffusion tensor data.

3.3 Tensor Glyphs

Another avenue of DTI visualization has focused on using tensor glyphs to visualize the complete tensor information at one point. A tensor glyph is a parameterized graphical object that describes a single diffusion tensor with its size, shape, color, texture, location, etc. Most tensor glyphs have six or more

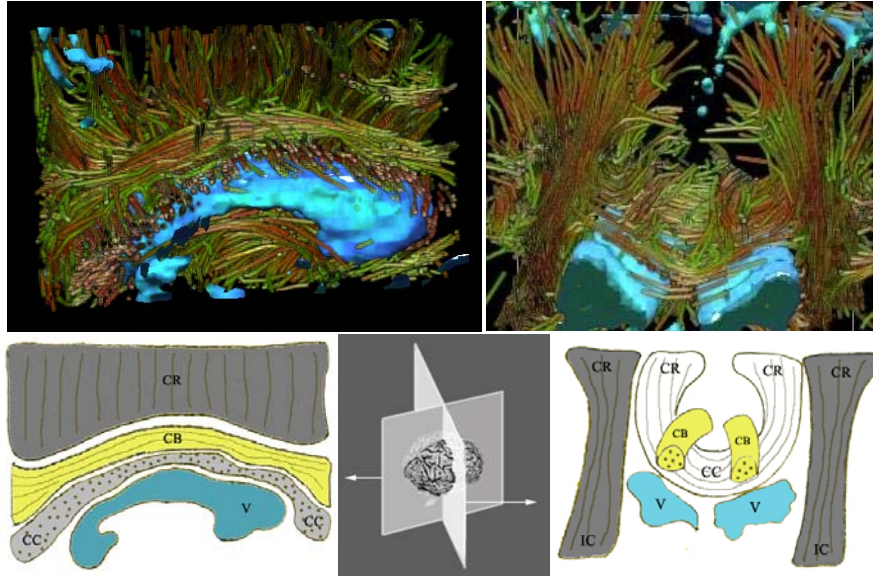


Fig. 6. Interactive volume renderings of a human brain dataset. The volume renderings (top) show collections of threads consistent with major white-matter structures: IC=internal capsule, CR=corona radiata, CB=cingulum bundle, CC=corpus callosum, diagrammed on the bottom. Components of the tensor-valued data control thread direction, color, and density. Direct volume rendering simultaneously shows the ventricles (labeled V) in blue for anatomical context.

degrees of freedom and can represent a diffusion tensor completely. However, tensor glyphs do not expose relationships and features across a diffusion tensor field, rather, they imply these relationships from the visual correlation and features of the individual glyphs. While exploiting many different types of tensor glyphs, from boxes to ellipsoids to superquadrics, tensor glyph designers aim to make the mapping between glyphs and diffusion tensors faithful, meaningful and explicit.

The diffusion ellipsoid described in section 2 above is the most commonly used representation of a diffusion tensor. Pierpaoli *et al.* [19], in the first use of ellipsoids as tensor glyphs, associated ellipsoid size with the mean diffusivity, indicated the preferred diffusion direction by the orientation of the diffusion ellipsoid. Arrays of ellipsoids were arranged together in the same order as the data points to show a 2D slice of DTI data.

Laidlaw *et al.* normalized the size of the ellipsoids to fit more of them in a single image [32] (see Figure 7(a)). While this method forgoes the ability to show mean diffusivity, it creates more uniform glyphs that better show anatomy and pathology over regions.

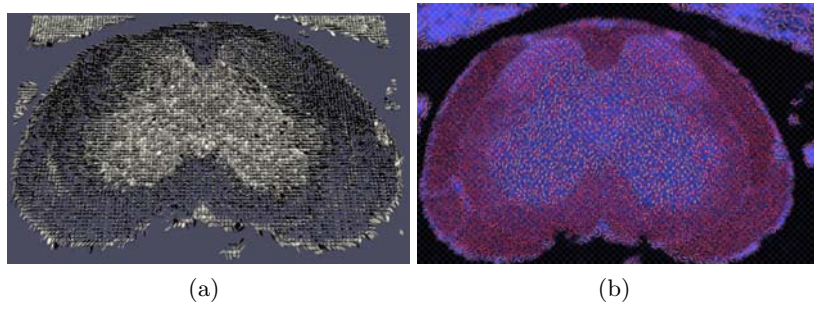


Fig. 7. (a) Arrays of normalized ellipsoids visualize the diffusion tensors in a single slice. (b) Brush strokes illustrate the direction and magnitude of the diffusion: background color and texturemap show additional information.

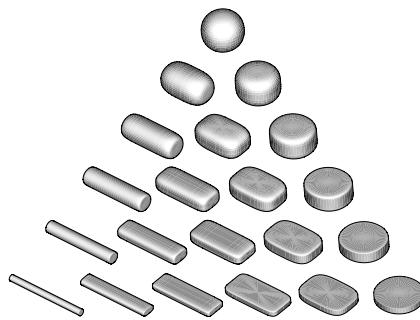


Fig. 8. Superquadrics as tensor glyphs, sampling the same barycentric space as in Figure 2.

Laidlaw *et al.* [32] also developed a method that uses the concepts of brush strokes and layering from oil painting to emphasize the diffusion patterns. They used 2D brush strokes both individually, to encode specific values, and collectively, to show spatial connections and to generate texture and a sense of speed corresponding to the speed of diffusion. They also used layering and contrast to create depth. This method was applied to sections of spinal cords of mice with experimental allergic encephalomyelitis (EAE) and clearly showed anatomy and pathology (see Figure 7(b)).

Boxes and cylinders have also been used to show the directions and relative lengths of all three eigenvectors. Boxes clearly indicate the orientation of the eigenvectors. They also have fewer polygons and are thus faster to render. But their flat faces usually make it hard to infer the 3D shapes from a 2D image (see Figure 9(a) below).

Kindlmann adapted superquadrics, a traditional surface modeling technique, to generate tensor glyphs [33]. The class of shapes he created includes spheres in the isotropic case, while emphasizing the differences among the

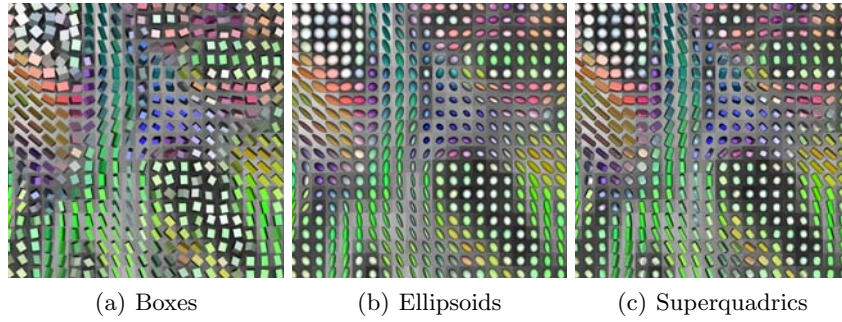


Fig. 9. A portion of a brain DTI scan as visualized by three different glyph methods (overall glyph sizes have been normalized).

eigenvalues in the anisotropic cases. As shown in Figure 8, cylinders are used for linear and planar anisotropy and intermediate forms of anisotropy are represented by approximations to boxes. As with ellipsoid glyphs, a circular cross-section accompanies equal eigenvalues, for which distinct eigenvectors are not defined.

The differences among some of the glyph methods can be appreciated by comparing their results on a portion of a slice of a DTI brain scan, as shown in Figure 9. The individual glyphs have been colored with the principal eigenvector colormap. The directional cue given by the edges of box glyphs 9(a) is effective in linearly anisotropic regions, but can be misleading in regions of planar anisotropy and isotropy, since in these cases the corresponding eigenvectors are not well defined numerically. The rotational symmetry of ellipsoid glyphs 9(b) avoids misleading depictions of orientation, with the drawback that different shapes can be difficult to distinguish. The superquadric glyphs 9(c) aim to combine the best of the box and ellipsoid methods.

3.4 Vector Field Visualization

The tensor field can also be simplified to a vector field defined by the main eigenvector, \mathbf{e}_1 . This simplification is based on the assumption that in the areas of linear anisotropy, \mathbf{e}_1 defines the direction of linear structures. The sign of \mathbf{e}_1 has no meaning.

One commonly used method to visualize DTI data is to map \mathbf{e}_1 to color, e.g., directly using the absolute value of the \mathbf{e}_1 components for the RGB channel: $R = |\mathbf{e}_1 \cdot \mathbf{x}|$, $G = |\mathbf{e}_1 \cdot \mathbf{y}|$, $B = |\mathbf{e}_1 \cdot \mathbf{z}|$

The saturation of this color is weighted by an anisotropy index to de-emphasize isotropic areas (see figure 10).

Other methods have been proposed to visualize the global information of 2D as well as 3D vector fields [34], and there are well established 2D vector-field visualization methods [35]. Although 2D techniques have been extended

to 3D, the visualization of 3D vector fields is still a challenging problem due to visual cluttering and computational cost.

We concentrate here on 3D DTI data. The most commonly used technique to visualize DTI data is streamline tracing; in DTI-specific literature this is also called fiber tracking [36] or tractography [37]. There is a direct analogy between the streamlines and the linear structures to be visualized (e.g., fibers). Furthermore, streamlines in 3D can easily be visualized by regions in order to avoid cluttering. Streamline tracing is based on solving equation:

$$p(t) = \int_0^t \mathbf{v}(p(s)) ds \quad (1)$$

where $p(t)$ is the generated streamline and \mathbf{v} corresponds to the vector field generated from \mathbf{e}_1 . $p(0)$ is set to the initial point of the integral curve.

The streamline technique has three main steps: definition of initial tracking points (i.e., seed points), integration, and the definition of stopping criteria. Seed points are usually user defined: the user specifies one or more regions of interest (ROI). Interior of the ROIs are sampled and the samples are used as seed points. Equation (1) is solved by numerical integration via such schemes as: Euler forward and second- or fourth-order Runge-Kutta.

Stopping criteria avoids calculation of the streamline where the vector field is not robustly defined. In areas of isotropic or planar diffusion, the value of \mathbf{e}_1 can be considered random, and thus has no meaning for the underlying structure. The user can usually set a threshold based on the anisotropy indices (e.g., FA, RA or C_l) to describe the areas where the vector field is defined; the value of this threshold depends on the data-acquisition protocol and the

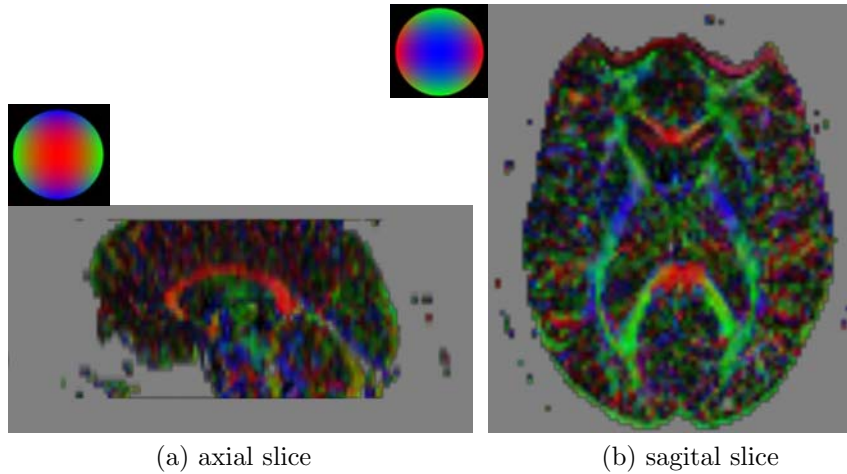


Fig. 10. Mapping of \mathbf{e}_1 to the RGB channel shown in 2D slices of a healthy volunteer brain.

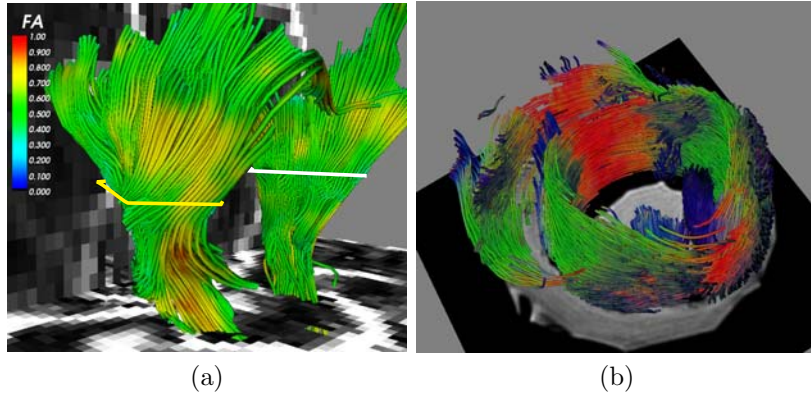


Fig. 11. (a) Streamline tracing using two ROIs to trace the corona radiata in a data set of a healthy volunteer brain. (b) Streamlines in a data set of a goat heart using the tracing seeding technique by Vilanova *et al.* [38]

nature of the object that is being scanned. Other criteria can also be used, such as the curvature or length of the streamline.

Hyperstreamlines are an extension to streamlines for second-order tensor fields [39], first used by Zhang *et al.* for DTI data [40]. Hyperstreamlines employ all eigenvalues and eigenvectors. A streamline defines the axis of a generalized cylinder whose cross-section perpendicular to the axis is an ellipse defined by \mathbf{e}_2 and \mathbf{e}_3 and λ_2 and λ_3 , respectively.

Streamline-tracing techniques for DTI have several disadvantages that are constantly being addressed. In areas of non-linear diffusion the main eigenvector is not robustly defined [15]. However, linear structures can be present in areas with nonlinear diffusion, appearing where the linear structure direction is not coherent within a voxel (see figure 12) or arising from noise. Most DTI tracing algorithms consider only the areas where the vector field is defined robustly. Several authors have proposed methods to trace within areas of isotropic or planar diffusion following the most probable diffusion direction based on some heuristics (e.g., [41, 42]). Some of these methods are based on regularization techniques that are commonly used in image processing for noise removal.

Another difficulty in streamlines is seeding. The seed points can be defined by the user. In a healthy person with known anatomy, users can estimate where the interesting bundles are and where to seed. However, in some cases, there are no real clues to the possible underlying structure and user seeding can miss important structures. Defining the seed points to cover the whole volume can be computationally expensive, however and furthermore, too many seed points, clutter the image and it becomes difficult to extract useful information.

Zhang *et al.* [40] employed uniform seeding throughout the entire volume and developed a culling algorithm as a postprocessing step to control

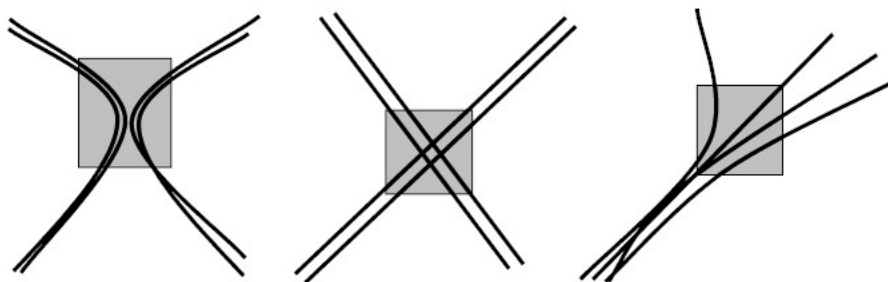


Fig. 12. Regions on which fibers are present but the diffusion tensor is planar: (left) kissing fibers, (middle) two fiber bundles crossing and (right) diverging fibers. Gray regions have a tensor with planar diffusion.

the streamlines density. This allows inside structures to be visible and outside structures still to be adequately represented. The metrics for the culling process include the length of a trajectory, the average linear anisotropy along a trajectory, and the similarity between a trajectory and the group of trajectories already selected.

Vilanova *et al.* [38] extended of Jobard *et al.*'s seeding algorithm [43] for 3D DTI data (see Figure 11(b)). Here seeding and generation of streamlines depend on a parameter that defines the density of the streamlines (i.e., minimal distance between streamlines). This method allows control of cluttering and a less computationally expensive generation of streamlines than seeding the whole volume regularly. However, if the density is set to a low value this method does not guarantee that the important structures are visible, since only the distance between streamline seed points is taken into account. Generally, the fiber bundles are more interesting than an individual, and here several authors have proposed ways to cluster the streamlines to obtain bundles (e.g., [44, 45, 46, 47]). These algorithms differ primarily in the metrics used to define the similarity between streamlines and clusters, which are mainly based on the shape and distance between fiber pairs. It is not clear which metric gives the best clustering results. Bundles are a compact representation of the data, that alleviates cluttering; however, these algorithms have the disadvantage of relying solely on the results of the streamline-tracing algorithm, and therefore are very sensitive to its errors.

3.5 Beyond Vector Field Visualization

The previous section presented several visualization methods on which the diffusion tensor data are simplified to the main diffusion direction to reconstruct the underlying linear structure. In doing this of course information is lost. In this section, we present several approaches that try to rectify this loss and use more information than the main eigenvector.

In the streamline tracing algorithm, the main eigenvector is assumed to represent the tangent vector of an underlying linear structure. In a similar way, it can be assumed that planar anisotropy indicates planar structure. Therefore, the two main eigenvectors define the tangent plane of an underlying planar structure, i.e., streamsurface. Zhang *et al.* [40] presented an algorithm to generate the streamsurface based in the planar anisotropy. Figure 13(a) shows the results of using their algorithm to trace streamlines and streamsurfaces in the whole volume. Vilanova *et al.* [38] used a similar algorithm in combination with streamline tracing to show the areas where linear structures cross, kiss, converge or diverge (see Figure 12). Figure 13b shows streamlines generated by a few seed points (in the yellow circle). Instead of stopping, a streamsurface is traced when a streamline reaches an area of planar anisotropy. In addition, the possible continuations of the initial streamline going through the streamsurface are traced further.

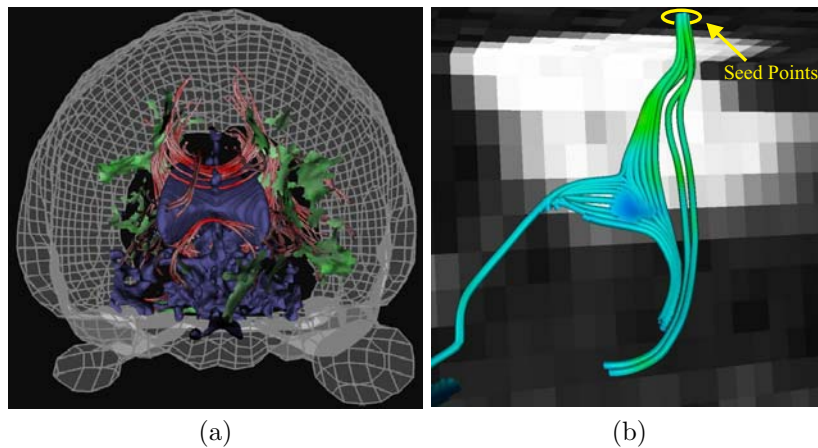


Fig. 13. (a) Red streamlines (represented as cylinders) and green streamsurfaces generated using the method of Zhang *et al.* [40] show linear and planar anisotropy, respectively, together with anatomical landmarks for context; (b) Streamlines using seed points (yellow region), trace streamsurfaces and show the possible prolongation of the fiber bundle, generated using the algorithm Vilanova *et al.* algorithm [38]

Streamsurfaces are extensions of streamlines, but the tensor information is still simplified and not treated as a whole. Parker *et al.* [48] and Brun *et al.* [49] modelled all possible paths from a given starting point. Parker *et al.* used a front-propagation method with a speed function based on the underlying tensor field. The path between the starting point and any point in the volume is defined, by using the time of arrival of the front to each point and a gradient descent algorithm. A connectivity metric describes the likelihood of connection of each path. Brun *et al.* [49] modelled the paths as a probability distribution, that is discretely represented by weighted samples from it. For

each path, a connectivity is also assigned according to diffusion tensor and the path's shape. Batchelor *et al.* [50] propose a method based on simulating the diffusion defined by the diffusion tensor, and use a probabilistic interpretation of the time of arrival of the diffusion front to quantify the connectivity of two points. O'Donnell *et al.* [51] describe a similar idea: a flux vector field based on solving the steady-state concentration is created. Paths generated in this vector field have a measure of connectivity based on the flow along the paths; the maximum flow indicates the most probable connection. They also present a method based on warping the space locally using a metric defined by the inverse of the diffusion tensor. Finding the minimum-distance path (i.e., geodesic) in this warped space provides a reconstruction of a possible underlying linear structure and a numerical measure of connectivity between two points (i.e., distance).

The advantage of these methods is that they are well defined in the complete space, even in areas with planar or isotropic diffusion. Furthermore, they give a quantitative measure of connectivity. Their drawbacks are that they are computationally expensive and any pair of points in the space is connected. Therefore, it is necessary to define not just a starting point but also end points, or to establish criteria for which points are considered to be connected (e.g., a percentile of the most probable connections).

There have been several efforts to visualize the global information of the second-order tensor field in general [52, 53]. Recently, Zheng and Pang [54] presented an extended the vector-field visualization method LIC (line integral convolution) to tensor data. As in the 3D extension of the LIC, cluttering is a problem, when this method is applied to DTI data, not much more than the outer shell of the anisotropic areas is visible.

Hesselink *et al.* [55] presented a method to extract topology skeletons of second-order 3D tensor fields. These skeletons are mainly defined by points, lines and surfaces that represent the complex structure of a tensor field in a compact and abstract way. The main component of the topology is the calculation of degenerated points whose eigenvalues are equal to each other. The main drawback of this method is the lack of intuitive interpretation of the topology skeletons for tensor fields. It is also very sensitive to noise, so that the resulting skeletons can be very complex and difficult to analyze.

3.6 Interaction

Human-computer interaction (HCI) arises in multiple aspects of DTI visualization: transfer function manipulation, seeding point selection, streamline culling, streamline query, and graphical model exploration, to name a few. We briefly review some of the interaction techniques here.

In volume rendering, transfer functions determine the mapping from the data to color and opacity (see section 3.2). The selection of transfer functions often requires expertise; in addition, it is often done by trial and error, so that it is important that the user be able to select the transfer functions intuitively

and quickly. Kniss *et al.* [30] describes a set of widgets that let the user specify multi-dimensional transfer functions interactively. Wenger *et al.* [28] applied this idea to DTI volume rendering, employing a set of widgets including a barycentric widget for manipulating the geometrical diffusion measures (see Figure 14).

Interaction permeates the whole process of vector field visualization: both seeding points selection and connectivity query involve specifying ROIs. Streamline culling requires selecting certain criteria and setting the corresponding thresholds. And displaying the 3D streamline models often relies on user input to show the models at different scales and perspectives. Akers *et al.* [56] developed a pathway-query prototype to expedite the first two operations, precomputing the pathways and their statistical properties to achieve real-time interaction.

The complexity of the DTI datasets often yields complicated graphical models that are hard to discern in a still picture. Continuing developments in computer graphics constantly change how user interact with these models. Desktop 3D graphics used mouse click and drag to move the models; fish-tank virtual reality display systems added stereo and head tracking [57]. the CAVE provided an immersive virtual environment that engaged the user in whole-body interaction [58] (see Figure 14(b)). However, none of these systems stand alone; each has its strengths and weaknesses depending on certain applications [57].

The interaction schemes can also be combined in hybrid visualization methods. For example, the streamtube-culling widget can be incorporated into the control panel with various other transfer function widgets (see Figure 14(a)). A traditional light-box display of a structural image slice provides context in a complex 3D scene (see Figure 14(b)).

Currently, computational power limits our ability to achieve real-time interaction and precomputed models must often be used for the sake of the speed. In the future, we expect a closer tie between computation and human input for more efficient and effective data exploration.

4 Applications

DTI is especially useful in studying fibrous structures such as white matter and muscle: the anisotropy information it provides reveals the fiber orientation in the tissue and can be used to map the white-matter anatomy and muscle structure in vivo [37]. The diffusion coefficient measures a physical property of the tissue and the measurements can be compared across different times, locations, and subjects. Therefore, DTI has frequently been used to identify differences in white matter due to a variety of conditions. Normal conditions such as age and gender have been reported to affect anisotropy and diffusivity; neural developments such as myelination, physical trauma such as brain injury, and neurodegenerative diseases such as multiple sclerosis and HIV have all

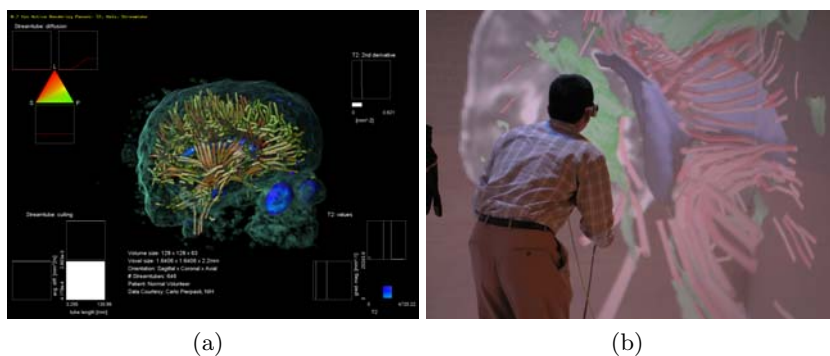


Fig. 14. (a) An interactive exploration tool for DTI volume rendering. Clockwise from upper left are a 2D barycentric widget, a 1D widget, a 2D Cartesian widget, and a 2D Cartesian culling widget. (b) A user explores a complex 3D model in virtual reality.

been indicated by DTI studies to affect white-matter composition, location, or integrity.

The variety of DTI applications provides a valuable testbed for visualization methods. Indeed, without applications to guide the development of computational and visualization tools, these tools are far less likely to be applicable. We introduce some of the applications in this section.

4.1 White matter normal conditions

Some normal conditions can affect the microstructure of white matter. Significant differences were found in diffusivity and anisotropy of the human corpus callosum with gender and handedness [59]. Age also has significant effect on white matter, usually resulting in reduced FA and increased diffusivity [60, 61]. These factors should be considered when selecting control groups for white-matter pathology studies.

The vector field visualization methods introduced in section 3.4 have been employed to reveal connectivity in a normal brain. A common application is to use neuroanatomy knowledge to select the ROIs and then reconstruct neural pathways running through them. Evidence of occipito-temporal connections within the living human brain was found by tracing neural pathways between two ROIs [62]. Expert-defined ROIs for brainstem fibers and associate fibers have been used to generate corresponding tracts [63]. An exciting trend is to combine functional MRI (fMRI), which measures the changes in blood flow and oxygenation in a brain area, with DTI fiber tracking, so that both activated brain areas and the tract connecting them to other brain areas can be visualized at the same time. For example, foci of fMRI activation have been used as ROIs to reveal axonal connectivity in a cat's visual cortex [64].

4.2 White Matter Development

Almost all the neurons that the brain will ever have are present at birth. However, the brain continues to develop for a few years after birth. A significant aspect of brain development is myelination, the continued growth of myelin around the axons. Myelin acts as an isolating membrane and allows a conduction of nerve impulses from ten to one hundred times faster than along a non-myelinated system and, at birth, few fibers are myelinated. The development of myelin is a measure of increasing maturity of the neural system. Previous studies have explored when particular fibers are myelinated, e.g., areas related with primary sensory (vision, touch, hearing, etc.) and motor areas are the first to myelinate [65].

Diffusion tensor imaging has the potential to evaluate brain maturity in newborns. Myelinated fibers have higher anisotropy than non-myelinated ones, i.e., the anisotropy depends on the development phase. The study of newborn brain presents new challenges:

- The anisotropy in the neonatal brain is lower than in the adult brain. Therefore it is more difficult to reconstruct fibers reliably.
- Motion artifacts can play a larger role, since neonates often move more than adults.
- The signal-to-noise ratio is smaller. The neonatal brain is smaller than that of an adult, and hence the voxel size must be smaller, leading to decreased signal. Furthermore, one voxel in a neonate still contains more structures than a voxel in an adults.

The first years of life are a critical time for brain development. Early diagnoses of brain lesions can help diminish the consequences of an injury. For example, neonates who suffer hypoxic ischemic brain damage, have brain injuries caused by lack of oxygen and nutrients arising from blood flow problems. Diffusion weighted imaging has already proved useful in detecting this injury. Diffusion tensor imaging might provide further information about structure and the development of the neonatal brain. Figure 15(a) shows the fibers corresponding to a data set of a premature neonate of 26 weeks and scanned at six weeks old. Several fiber structures are visible (e.g., corona radiata in blue). However, the corpus callosum is not visible: the arrow indicates where the fibers are missing. Further investigation of all MR images of this neonate confirmed that this patient lacks a corpus callosum. Figure 15(b) shows the result of tracing streamlines using ROIs to visualize the corpus callosum and the corona radiata in a full-term neonate scanned after four weeks of birth. The DTI data does not reveal any alteration in the fibers despite the neonate had meningitis.

4.3 White matter injury and disorders

DTI has proven effective in studying a range of white-matter disorders including brain injury, brain tumor, focal epilepsy, multiple sclerosis, tuberous

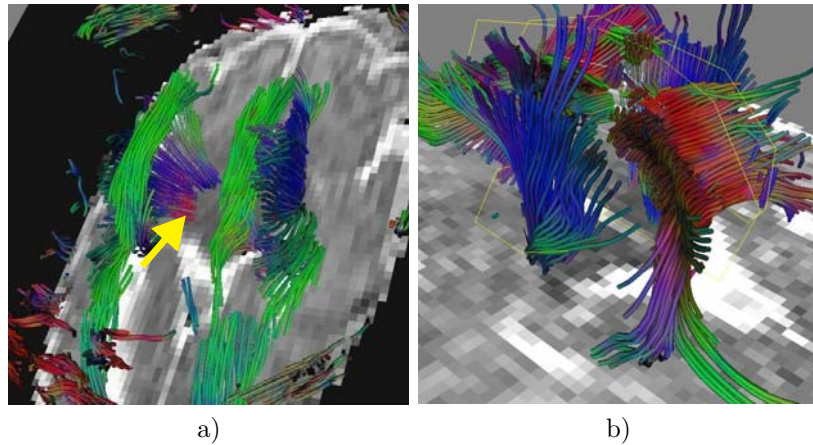


Fig. 15. Studies of fibers in neonatal brains with different data sets. (a) Premature neonate lacking corpus callosum (see arrow), (b) full-term neonate where no fiber abnormalities were found. Corpus callosum and corona radiata are seen.

sclerosis, Parkinson’s disease, Alzheimer’s disease, schizophrenia, HIV infection, Krabbe’s disease, chronic alcohol dependence, ALS, X-linked ALD, and CADASIL. Reviews of these studies can be found in [66, 67, 68, 69]. We select three application areas in which pathological causes differ greatly, resulting in different patterns and subtleties of the changes in white matter. Effective analysis of these cases can be realized only by applying processing and visualization methods accordingly.

Brain tumor

It is estimated that 17,500 people in the U.S. die from primary nervous-system tumors each year [70]. A better understanding of the pathophysiology of brain tumors is essential if we are to find effective treatments. Cortical disconnection syndromes may play a significant role in clinical dysfunction associated with this disorder.

Tractography methods have been applied to study patterns of white-matter tract disruption and displacement adjacent to brain tumors. Wieshmann *et al.* [71] found evidence of displacement of white-matter fibers of the corona radiata in a patient with low-grade glioma when compared with spatially normalized data collected from 20 healthy volunteers. Mori *et al.* [72] found evidence of displacement and destruction of the superior longitudinal fasciculus and corona radiata in two patients with anaplastic astrocytoma. Gossel *et al.* [73] observed distortion of the pyramidal tract in a patient with a high-grade glioma. Witwer *et al.* [74] found evidence of white matter tract edema. Zhang *et al.* [75] observed the pattern of linear and planar diffusion

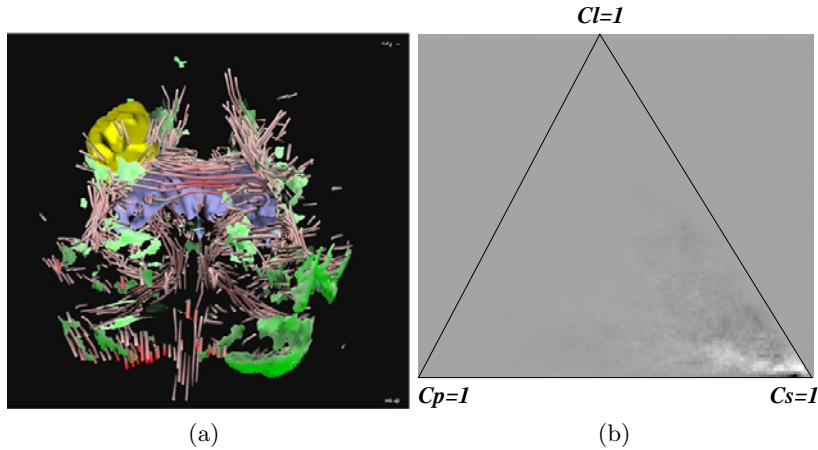


Fig. 16. Visual exploration and quantitative analysis of a tumor brain. (a) A 3D visualization showing streamtubes and streamsurfaces as well as tumor and ventricles. (b) The difference histogram obtained by subtracting normalized barycentric histograms calculated from tumor-bearing and contralateral sections. Here zero maps to medium gray because the difference is signed. Note that the most striking difference occurs near the $c_s = 1$ vertex.

around the tumor and analyzed the asymmetries of white-matter fiber tracts between the tumor and the contralateral hemispheres.

Figure 16 shows visual exploration and quantitative analysis of a tumor brain [75]. The streamtubes and streamsurfaces visualize both linear and planar diffusion. The displacement of fiber tracts around the tumor is accompanied by a cradle of streamsurfaces, indicating a local increase of planar anisotropy. The normalized distribution of anisotropy is calculated on a barycentric space (see section 3.1) for both the tumor side and contralateral side of the brain. The difference in the two distributions (Figure 16(b)) clearly indicates a decrease in linear anisotropy and an increase in planar anisotropy in the tumor side of the brain.

As Figure 17 indicates, the geometrical alteration of fiber structures surrounding the tumors can have different patterns [38]. In Figure 17(a), the fibers are pushed to the left by the presence of the tumor; in Figure 17(b), the fibers seem to be destroyed: the structure around the tumor is not moved, but in the tumor area no fibers are present.

Tumors and their surrounding edema often cause gross changes in the neural fibers around them. DTI can benefit tumor growth study and surgery planning by modeling these changes geometrically. Scalar index analysis complement the geometrical modeling by quantifying these changes.

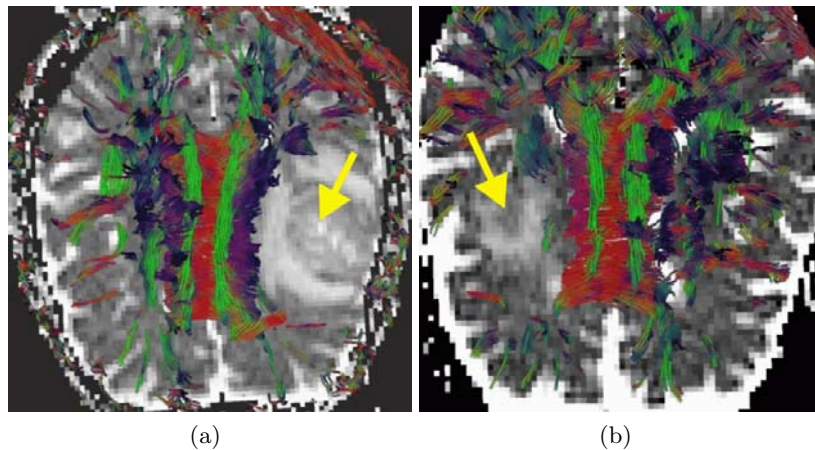


Fig. 17. Two cases of adult tumor brain. (a) shows the fibers are pushed by the tumor. (b) shows no fiber in the tumor area, indicating the destruction of neural structures there.

Multiple sclerosis

Multiple sclerosis (MS) is a chronic disease of the central nervous system that predominantly affects young adults during their most productive years. Pathologically, MS is characterized by the presence of areas of demyelination and T-cell predominant perivascular inflammation in the brain white matter. Recent studies on MS have shown an elevated mean diffusivity and reduced diffusion anisotropy [76] in MS lesion areas. The lesions with more destructive pathology are generally shown to have the highest diffusivity.

Analyzing the interrelationship between the MS lesion and the affected fiber pathways might help in understanding the mechanism of the axonal damage. The visualization of DTI models with coregistered MS lesion masks in Figure 18 can be utilized to determine the relationship between focal lesions and the neuronal tracts that are anatomically related. Figure 18(b) suggests the different effects that the focal lesions might have on the fibers. Note that the streamtubes sometimes continue through the lesions (A) and sometimes break within them (B). Figure 18(c) depicts only the fiber pathways that are confined in the lesion area.

MS lesions are often dispersed and show different levels of severity. Visualizing the affected tracts can clarify the various effects of the lesions. Also, the connection of partially damaged tracts to the gray matter might help explain the disabling effect of MS.

HIV neurodegeneration

Human immunodeficiency virus (HIV) is an aggressive disease that affects multiple organ systems and body compartments, including the central ner-

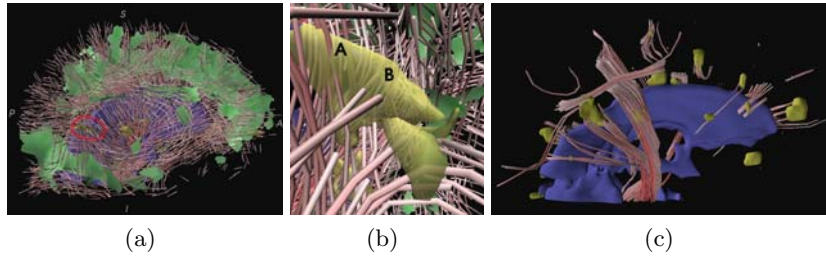


Fig. 18. Visualization of coregistered DTI and MS lesion models. (a) The whole brain with streamtubes, streamsurfaces, lesion masks and ventricles. (b) A closeup view of white matter fibers near the MS lesions. The streamtubes around the lesion area give some clues about white matter structural changes there. (c) The same brain and view as (a) but showing only streamtubes that contact the lesions, thus clarifying the white matter structures involved.

vous system (CNS). Structural imaging studies of HIV patients' brains reveal morphometric changes in the subcortical gray and white matter regions [77]. However, because of the relatively poor sensitivity of structural imaging to white-matter abnormalities in patients with mild HIV [78], the relationship between cognition and white-matter abnormalities in structural MRI has not been fully determined. These limitations can be overcome by DTI. Recent DTI studies have demonstrated abnormalities among patients with HIV, even in the absence of white-matter abnormalities on fluid-attenuated inversion recovery (FLAIR) structural MRI scans [79, 80]. Most recently, Ragin *et al.* [81] reported strong relationships between whole-brain fractional anisotropy and severity of dementia among a small cohort of HIV patients ($n = 6$).

In cases such as HIV infection, where the white-matter structural changes may be too subtle to detect with structural imaging, DTI can be used to quantify the changes.

4.4 Myocardial Structure

Diffusion tensor MRI can also be used to measure directionally constrained diffusion applies to tissues outside the nervous system. Understanding the complex muscular structure of the mammalian heart is another important application. The efficiency of the heart is due in part to its precise arrangement of myofibers (contractile muscle cells), especially the myocardium (the muscular wall) of the left ventricle, which responsible for pumping blood to the rest of the body. The pattern of myofiber orientation in the myocardium is *helical*: between the epicardium and endocardium (outer and inner surface) there is roughly a 140 degree rotation of myofiber orientation, from -70 to $+70$ degrees. Computational simulations of heart dynamics require an accurate model of the myofibril orientation in order to model both the contractile

mechanics of the myocardium and the pattern of electrical wave propagation within it [82]. The principal eigenvector as measured by DT-MRI has been confirmed to align with the myofiber orientation [13, 14]. Recent work (Figure 4.4) has applied superquadric tensor glyphs to visualize the myofiber twisting, and to inspect other anatomical features revealed by DT-MRI [83].

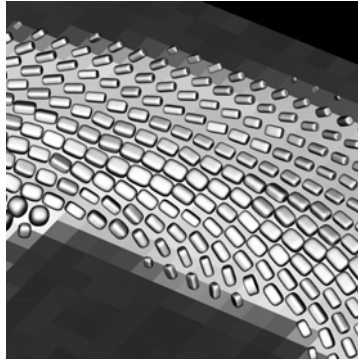


Fig. 19. Visualization of transmural twist of myofibers in canine myocardium, seen in a short axis slice. The edges of the superquadric glyphs help show the flat inclination at midwall and the differences among the eigenvalues at various locations.

As is clear from the descriptions above, the applications of DTI are increasingly diverse. Associated with the breadth of application areas is a need for a wide variety of visualizations techniques. Characterizing a tumor's effect on white matter integrity is based on fiber tracking, while the effect of neurodegenerative diseases may be quantified in terms of anisotropy metrics, and myocardial structure is described by a continuous rotation of the principal eigenvector. Successfully applying DTI to new research areas and problem domains demands that visualization tools be flexible enough to support experimentation with the range of techniques, so as to evaluate the appropriateness of each. This in turn requires that the modes of interaction efficiently support the exploration and parameter setting needed for creating visualizations, ideally in a manner friendly to application-area experts who may not be visualization experts. DTI visualization methods and their application will remain an active research area.

5 Open Problems

We have presented several visualization techniques for DTI data that have been proposed in the last decade. These methods try to show the relevant information to physicians and researchers such that they can get insight on the data. These methods usually simplify the tensor information or are not

able to show its continuity. Further study of methods where the global whole tensor information can be shown is necessary.

In clinical practice, anisotropy indices, such as FA or trace, are commonly used. Although, they show just a few information of the tensor, their visualization is similar to what radiologies are used to, and they are easy to understand and quantify. Other popular visualization techniques are based on tractography or fiber tracking, probably due to its direct analogy from streamlines to fibers. However, most of these techniques require some input from the user (e.g., seed point) and therefore they are user dependent. Important information can be missed if the user fails to give the right input. This might be quite challenging for data sets of patients where there is no real clue about what to expect. Non user dependency is critical for comparison and evaluation of diseases. Some methods have tried to achieve that by reconstructing linear structures in the whole volume so that all data is shown. The main problems in this case are the computational cost and the huge amount of data to inspect. Therefore, there is the need of good navigation tools that allow the user to inspect the data easily. For example, grouping or clustering of data without losing the detail can help the navigation. In order to explore the data, it is critical that the interaction is intuitive and in real-time. Interaction is also important for the setting of parameters, such as, transfer functions or thresholds (e.g., c_l in fiber tracking to define areas with linear structure). This is necessary to explore new applications of DTI data and to robustly analyze the results. Visualization of uncertainty measures can also help in the analysis of data.

At the moment, quantification can be done based on anisotropy indices. However quantification is an open problem in DTI when more DTI information is used. It is possible to evaluate the data qualitatively, however quantitative evaluation is difficult and needs further research. Quantification is important to get clinical acceptance. It should be possible to evaluate the methods and generate statistics and distinguish between diseased and non-diseased data. It should be possible to build models according to the different parameters that influence the results such as age, and sex.

Validation is an important issue for DTI. There have been few validation studies to be able to conclude that what is measured corresponds with the anatomy [1, 13]. At the moment and to our knowledge, there is no gold standard to validate the results of the techniques developed in this field.

One main open problem is the communication between different scientific fields to advance in the use of DTI in clinical practice. It is important that the physicians and technicians are able to communicate in a way the necessary software and tools to advance in the clinical investigations for DTI are developed.

We presented several potential applications for DTI. However due to the open problems presented before there are few applications that are being commonly used in clinical environments. There is research in which applications DTI can be used in daily practice, or brings interesting new insight.

Finally, although not dealt in this chapter, a main research issue is the protocols for DTI data acquisition in order to improve quality and reduce scanning times. Furthermore in image processing a lot of research has been devoted to scalar and less to vector images, but few research has been done in image processing techniques for tensor data. Filters for noise removal, interpolation, feature extraction, etc. are of relevant importance for the development of DTI. Second order diffusion tensor does not contain enough information to disambiguate areas where a voxel contains non-coherent linear structures. New representations for diffusion that show its more complex behavior are being researched. Visualization and image processing techniques might need to adapt to the complexity of this new data.

6 Conclusions

DTI is the only modality that allows the visualization of tissue microstructure (e.g., white matter or muscle) *in vivo*. Meaningful visualizations are crucial to analyze and get insight in high-dimensional data such as DTI. We have presented several visualization techniques that have been developed in recent years. All visualization techniques have their advantages and disadvantages compared to the others. A combination of different visualization techniques might be the best solution to provide most insight in the data. However, there still essential disadvantages that need to be overcome, such as user dependency.

Several potential applications for DTI have also been presented. A lot of research is being done in the study of white matter. The study of muscle such as the heart can also benefit from DTI. The goals of the research can differ from understanding, development and diagnoses. All these applications show the power of DTI to be able to see what some years ago was impossible. The variety and amount of applications of DTI is constantly increasing.

DTI is a relative young and exciting new field of research that brings together several disciplines. Research in each of these disciplines is crucial to achieve fruitful results in the application and use of DTI data.

Acknowledgments

We thank the BioMedical NMR group at the Eindhoven University of Technology and Maxima Medical Center in Veldhoven, Drs. Raimond Winslow and Elliot McVeigh of Johns Hopkins University, and Andrew Alexander of the W. M. Keck Laboratory for Functional Brain Imaging and Behavior at the University of Wisconsin-Madison, for providing some of the datasets and evaluations used in this chapter. We thank Dr. Mark Bastin of the University of Edinburgh, Dr. Jack Simon of the University of Colorado Health Science Center, and Dr. Robert Paul of the Brown Medical School for providing some

of the data sets and for contributing to the section on white matter injury and disorders.

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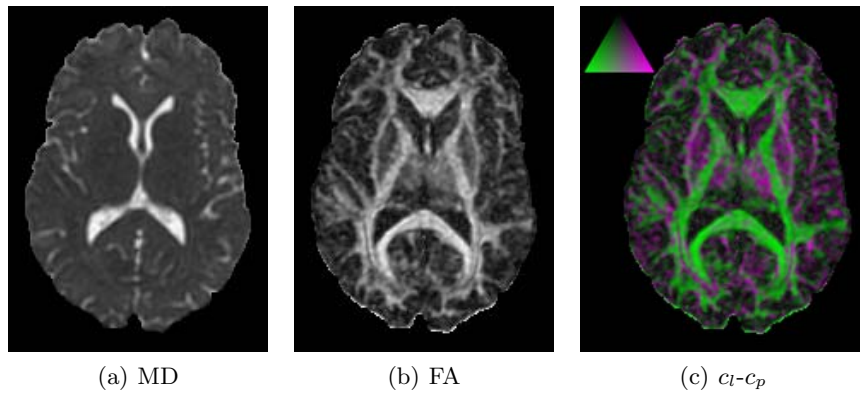


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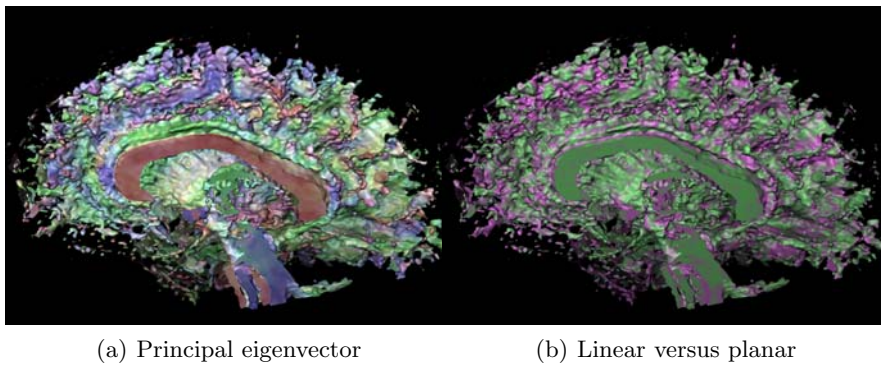


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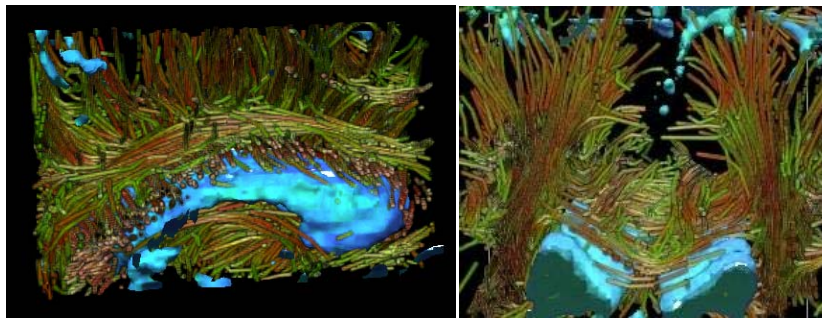


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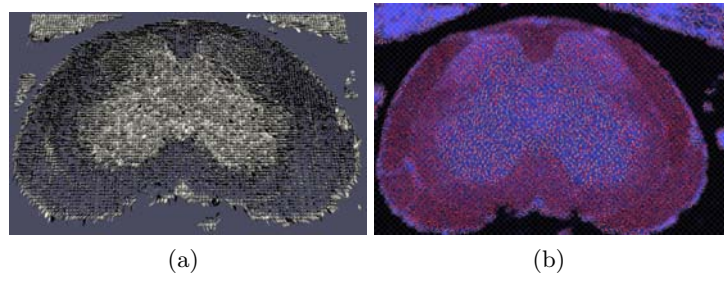


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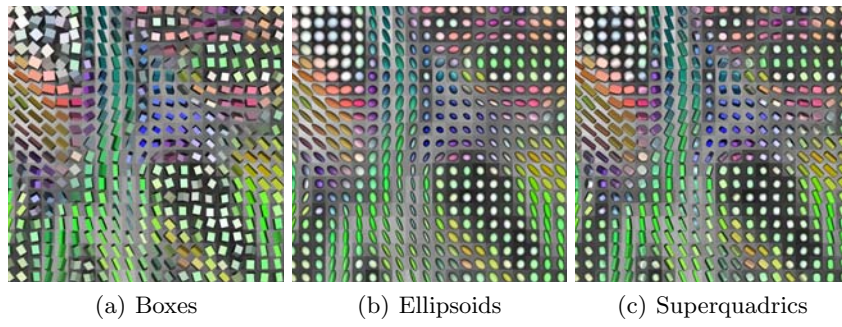


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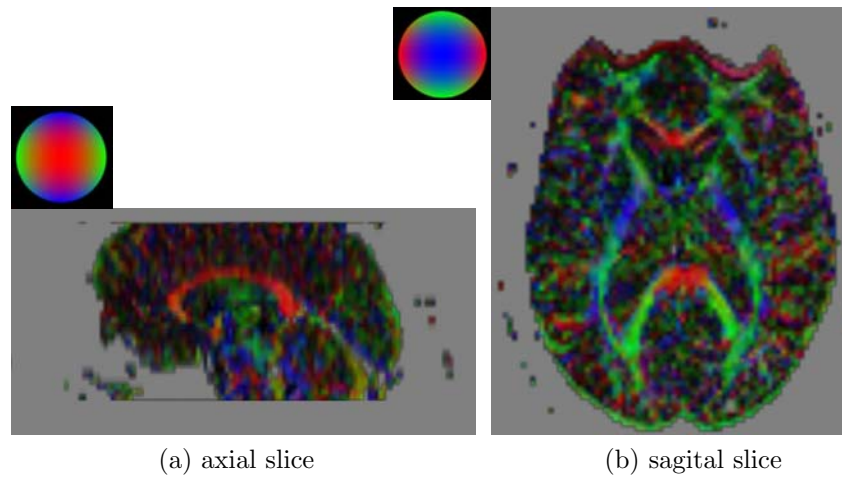


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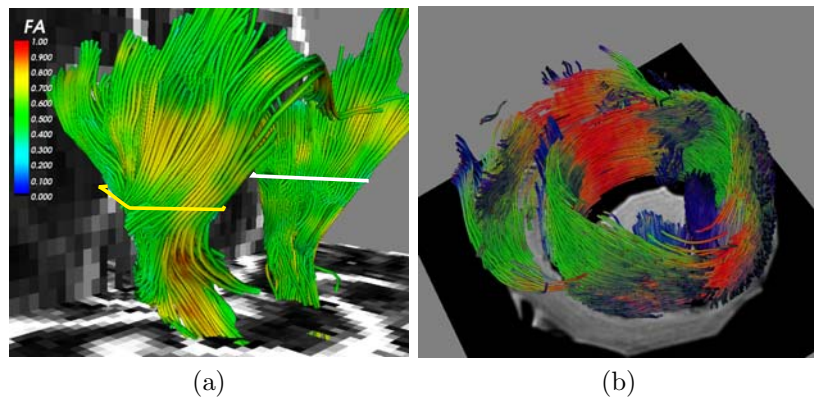


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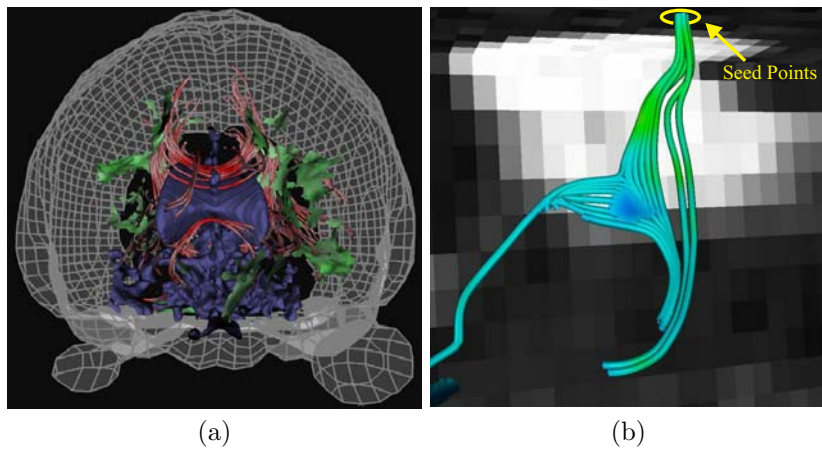


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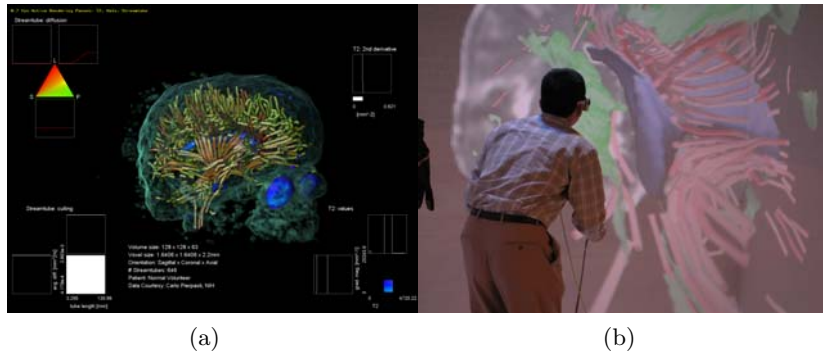


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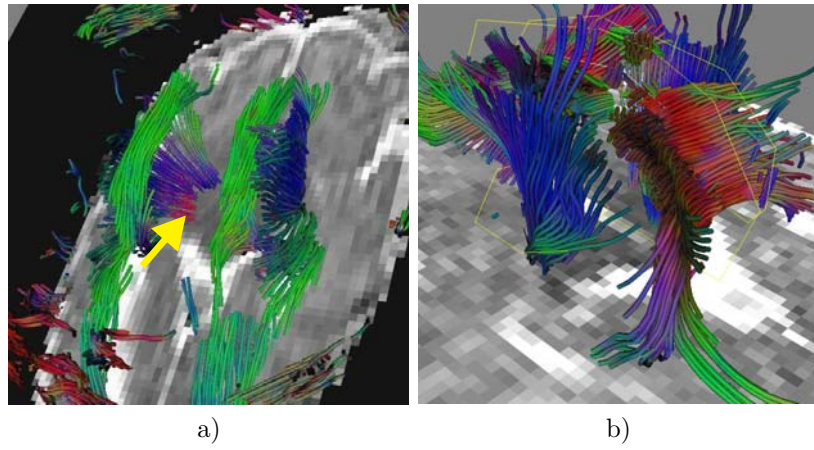


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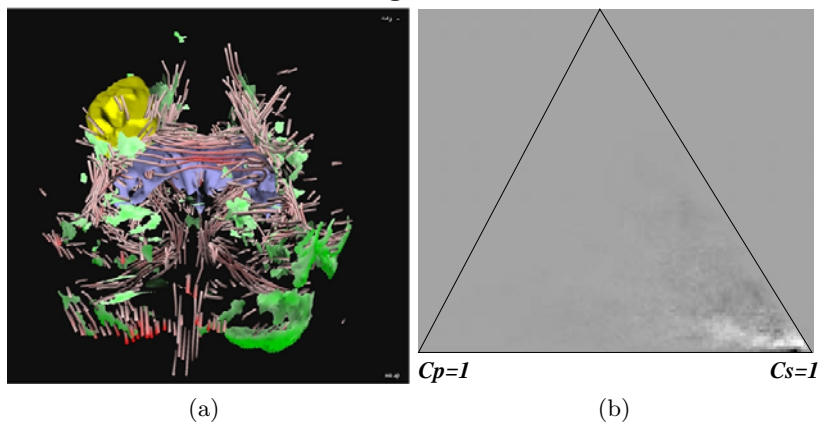


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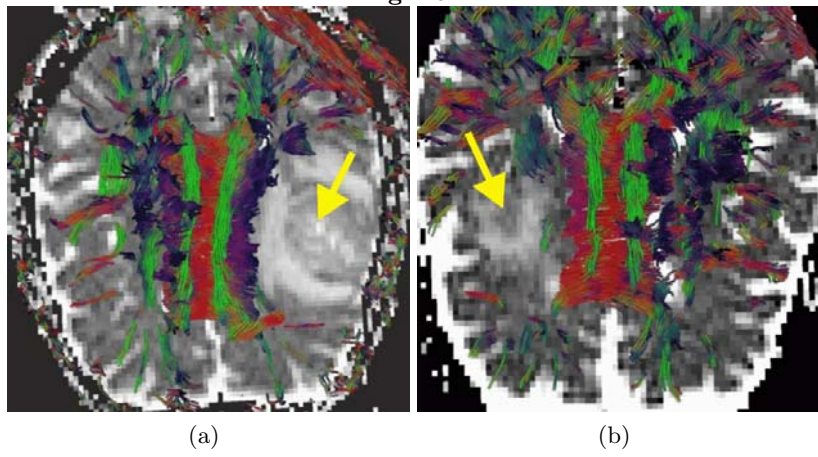


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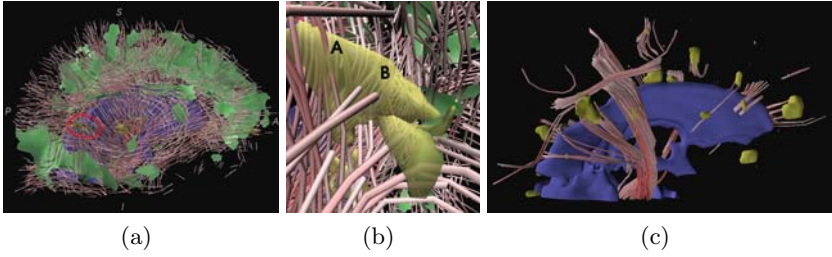


Fig. 18.

