Towards interactive exploration of DTI data

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Abstract:

Fiber tracking is a powerful technique to analyze Diffusion Tensor Imaging (DTI) data of the brain. It allows tracing paths through the dataset that relate to the primary pathways of white matter axonal structures. The typical approach to do this is to place a region-of-interest (ROI) inside the dataset, and subsequently visualize all paths running through the ROI. Consequently, the resulting fiber structure is highly sensitive to the location and shape of the chosen ROI. Small variations of the ROI can sometimes lead to drastic changes in the resulting fiber tract.
To address this problem, we present a novel approach to interact with DTI data, which allows for an explorative analysis of this highly complex data. It is based on a combination of real-time fiber tracking with an interactive method to generate anatomically meaningful ROIs. ROIs are created and modified interactively in both shape and size, while the effects of these modifications to the resulting fiber tracts are visualized on-the-fly.

Keywords: Interaction, DTI, Fiber Tracking

1 Purpose

Analysis of DTI data is a challenging task. On the one hand, DTI allows insight into tissue properties of the white matter of the brain, with the possibility to reconstruct pathways of axonal fiber structures non-invasively. On the other hand, these reconstructions are based on a cascade of model assumptions, beginning with the measurement of Brownian motion as a surrogate for axonal pathways, continuing on to the noisy process of MR image acquisition, continuing on to the fitting of a tensor model as an attempt to explain the measured diffusion properties, and finally on to the reconstruction of individual fiber bundles by tracing pathways through the tensor field, which are then interpreted as white matter fiber tracts. Unsurprisingly, the notion of uncertainty is inextricably linked to the field of DTI analysis.
Nevertheless, DTI has become a popular tool in various clinical contexts, including neurosurgery and neurology. Especially in neurosurgery, fiber tracking has become a widely used tool to visualize structures in proximity to a target structure during pre-operative planning, or, where available, during intraoperative resection control. In such settings, uncertainty is typically masked away from the user, or handled by simplistic means such as static security-margins around the reconstructed fibers. While a reduction of complexity in both interaction requirements and interpretability of results is an obvious necessity for clinical use, the desire for a manageable presentation and possibility to evaluate and explore DTI uncertainty even in such settings is well-founded [1,2].
One approach to do so is to estimate uncertainty analytically and search for suitable means to visualize it [3]. Another, with respect to clinical integration possibly more feasible approach is to let the user explore the dataset interactively [4]. During the last years, different approaches to real-time fiber tracking have been proposed [5, 6], which appear to be promising tools for this purpose. However, the question of intuitive interaction with such techniques has been rarely addressed. Typically, simple geometric objects like spheres or boxes are defined, which can be moved freely through 3D-space. These, however, cannot produce anatomically plausible tracking results.
To overcome this problem, we propose a novel interaction scheme for DTI fiber tracking that allows for interactive exploration of the dependency between the shape and size of the ROI used for tracking and the resulting fiber bundle. We do this, by combining real-time fiber selection with a method for interactive generation of anatomically meaningful ROIs. ROIs are created and modified interactively in both shape and size, based on the diffusion properties of the underlying region. Like this, contours can be generated, that resemble those that a radiologist would create when drawing manually. These contours are used to interactively update and visualize fibers from a pre-computed whole-brain fiber tracking. As a result, the relationship between the shape of the ROI and the resulting fiber bundle becomes immediately apparent, allowing the user to interactively explore the variations of a given fiber bundle. In contrast to precise definition of accurate ROIs, the user can explore a low-dimensional parameter space interactively and observe the impact to the resulting fiber bundle in real-time.

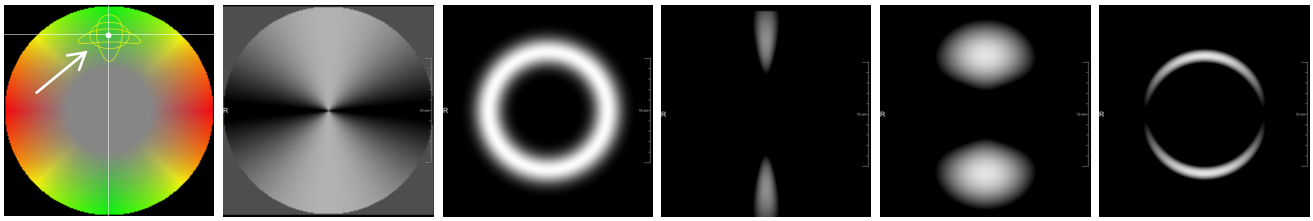

Fig. 1: Illustration of the similarity maps used for the ROI tool. The white arrow indicates the reference position. Some resulting contours are indicated in yellow (a). The angular similarity map (b). The magnitude similarity map (c). Differently weighted combinations of both similarity maps (d-f) allow for varying shapes of the generated contours.

2 Methods

Our method combines an algorithm for interactive generation and modification of anatomically meaningful ROIs for DTI, with a technique for real-time whole-brain fiber selection. Here, we will give a brief overview of both techniques and how they are combined to an interactive exploration tool. A more detailed description of the ROI tool can be found in [7]. Our whole-brain fiber selection method is based on the approach described in [8].

2.1 The ROI wizard

The algorithm for generating anatomically meaningful ROIs is based on the observation that individual white matter fiber bundles can be identified easiest in areas where a large amount of axons runs mostly parallel through the dataset. In the standard color-coded 2d-visualization, which maps the primary diffusion direction and level of anisotropy as a 3d vector into RGB space, such areas appear as blobs of the same color, which helps a radiologist to identify these bundles. Consequently, a useful ROI for fiber tracking should be placed around a group of neighboring voxels with similar diffusion properties. We have implemented a method that allows calculating such contours using a single mouse-click. With this, the user defines a point of reference, for which voxels with similar diffusion properties shall be grouped. Based on this point of reference, two similarity maps are calculated, and combined using a weighting function. First, the angular similarity map φ, measuring the similarity in diffusion direction, and second the magnitude similarity map m, measuring the similarity in fractional anisotropy.

$$\boldsymbol{\varphi}(\boldsymbol{x};\boldsymbol{v_{ref}},\boldsymbol{\sigma_{\varphi}}) = \boldsymbol{e}^{-\frac{\arccos(v(x)^{\mathrm{T}}v_{ref})^2}{\sigma_{\varphi}^2}} \qquad \boldsymbol{m}(\boldsymbol{x};\ \boldsymbol{\lambda_{ref}},\boldsymbol{\sigma_m}) = \boldsymbol{e}^{-\frac{|\lambda(x)-\lambda_{ref}|^2}{\sigma_m^2}}$$

For each voxel x of the DTI dataset, $\lambda(x)$gives the largest eigenvalue and $v(x)$gives the associated normalized eigenvector of the underlying diffusion tensor. λ_{ref} and v_{ref} denote the largest eigenvalue and eigenvector of the user defined point of reference. Both φ and m calculate the similarity between each voxel and the voxel of reference. The similarity is used as an argument for a Gaussian shaped function, which maps all values into the range [0,1]. $\sigma_{\varphi}$and $\sigma_m$individually control the width of the Gaussian envelope. Figs. 1(b) and 1(c) demonstrate this.
Next, a weighted similarity map w is calculated by multiplying m and φ, while interpolating the sigma value in such a way that it is either small for the angular and large for the magnitude similarity, vice-versa, or something in-between. This allows to continuously adjust the weighting between angular and magnitude similarity, thereby allowing to control the shape of the generated contour. Consequently, the blending parameter σ can be more intuitively described as a shape-parameter. F_{φ} and F_m are constant factors the correct for the individual domains of φ and m.

$$w(x;v_{ref},\lambda_{ref},\sigma) = \varphi(\ x;v_{ref},\sigma F_{\varphi}) \times m(\ x;\ \lambda_{ref},(1-\sigma)F_m)$$

Finally, the desired contour is calculated using a marching-squares algorithm on the weighted similarity map. The required threshold responds to the level of similarity. A higher value results in higher similarity of the clustered voxels, while a lower value will also include voxels with less similar diffusion properties. As a result, the threshold parameter for the marching-squares algorithm can be interpreted as a size-parameter for our contour.
To allow for interactive modification of these two parameters, they are mapped to the x- and y- axis of the mouse. The user can modify them after definition of the point-of-reference, by keeping the mouse button pressed. This gives him interactive control of the shape and size of the generated ROI. Upon releasing the mouse button, the contour is finalized. As all computations only need to be carried out on a single visible slice, interactive updates of the calculated contours can be achieved in real-time. Figure 1 illustrates the algorithm on a simple spherical DTI phantom.

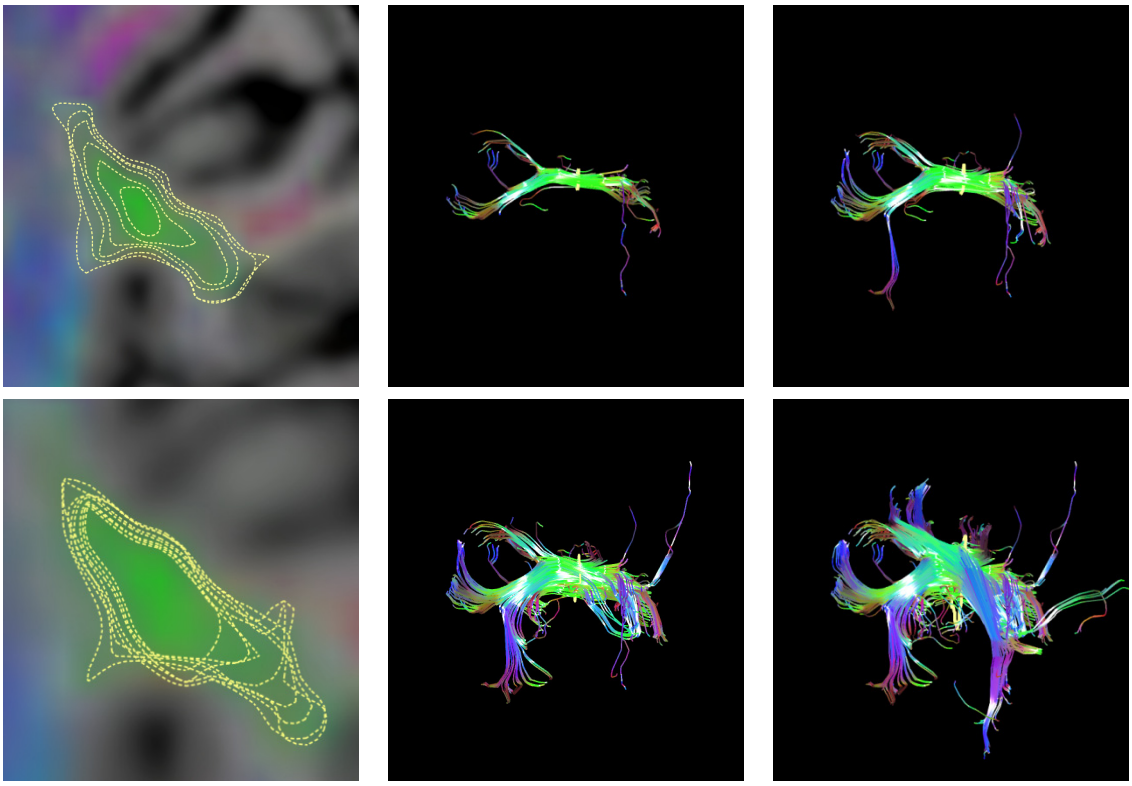

Fig. 2: Relation between contours and resulting fiber bundles, demonstrated for the superior longitudinal fasciculus (SLF). The first column shows multiple contours, all generated for the same point-of-reference. Note how both size and shape of the contours vary. Second and third columns show some corresponding tracking results.

2.2 Real-time fiber selection

In order to allow for interactive visualization of the fibers passing through the generated ROI, the contour is used to query a pre-computed fiber-set stored in a *fibertree*. The fibertree is based on a kD-tree, a space-partitioning data-structure commonly used for efficient range-queries in 3d-space. In addition to a conventional kD-tree, the fibertree optimizes this data-structure with respect to the known geometry of fibers. This is achieved by enclosing segments of fibers inside oriented bounding boxes, which are then sorted into the kD-tree. As a result, the required number of intersection checks for a given input query could be reduced in comparison to a kD-tree.

The fibertree is calculated in a pre-processing step. First, a whole-brain fiber tracking is performed, using all voxels with an FA-value above a definable threshold ($t_{FA} > 0.2$ for our implementation) as seed points. Depending on the density of the seed-point grid, approximately 20.000 to 100.000 fibers are calculated, and sorted into the fibertree. Afterwards, filter queries can be performed in two steps. First, the tree is queried for the bounding rectangle of the contour. The resulting sub-set of fibers is then again filtered with the exact area covered by the contour.

3 Results

We have implemented our method using the freely available rapid-prototyping platform MeVisLab. Interactive update rates were achieved on a mid-level current generation PC (*Intel Core2 Duo T9500, 2.6GHz*), using a seed-point grid of 3*mm*. For the datasets used during our tests, this corresponded to approximately 18.000 to 22.500 fibers in total. The time required for performing the whole brain fiber tracking and setting up the fibertree is ~18 seconds on the same machine. For a finer grid size, the preprocessing time may increase up to one minute. This, however, is not considered critical, as it only needs to be performed once per dataset.

So far, we have not evaluated our method extensively, but rather have used it to qualitatively assess the impact of minor modifications of the ROI to the resulting fiber bundle. We compared the stability of tracking results for the pyramidal tract as well as the superior longitudinal fasciculus (SLF). For the pyramidal tract, we chose a reference point inside the internal capsule using an axial view on the data. The ROI for the SLF was defined on a coronal slice, lateral to the pyramidal tract. Figure 2 shows a selection of ROIs that could be used for tracing the SLF, in combination with some of the resulting fiber bundles. In general, the direct feedback received during the definition of the ROI appeared very helpful. Even a relatively short exploration time of several seconds for the parameter space of the ROI algorithm proved

beneficial to create a mental model of the relationship between the borders of the ROI and the resulting fiber bundle. Especially for structures less clear to delineate, the possibility to explore the dataset in an interactive way was helpful with respect to creating a tracking result corresponding to the expected shape of the fiber bundle.

4 Discussion

In this paper, we presented a novel approach for interactive exploration of fiber tracking based analysis of DTI data. The central idea is to combine real-time fiber tracking with a method to generate and modify ROIs in an anatomically meaningful manner. This allows for interactive exploration of the influence of variations of the defining ROI to the resulting white matter fiber bundle. The generation of ROIs is based on the assumption that a meaningful ROI should cluster voxels with similar diffusion properties. In the color coded 2d representation of DTI data, such areas correspond to blobs of similar color and intensity. When manually delineating a ROI, a radiologist would typically use these blobs as an orientation aid to draw the contour. One should note that although our current implementation is based on real-time fiber-selection, the underlying idea would work equally well when used in combination with real-time fiber-tracking, which would open further options for manipulating parameters of the fiber-tracking algorithm itself.
Our approach allows for creating ROIs based on similarities with respect to a user chosen reference position. The shape and size of the contour can be manipulated interactively by mapping these two parameters to the x- and y-axis of the mouse. This yields an intuitive interaction scheme that not only allows for interactive optimization of the desired ROI, but also reduces interaction time, if compared to the manual process of drawing accurate contours.
The explorative character of our approach is grounded in the interactive update of tracking results based on dynamically changing input parameters. This idea is not necessarily linked to the input ROI alone. Depending on the chosen approach for real-time fiber tracking, one could also consider to interactively manipulate parameters of the tracking algorithm.
An extensive evaluation of the clinical value of our method remains to be done. As such, we are careful with positioning our approach against alternative, currently established approaches to fiber tracking interaction. Our preliminary evaluation has however caused positive expectations. Especially for situations where interaction time is a limiting constraint, such as e.g. during intraoperative resection control, we expect that our method can contribute to make utilization of DTI fiber tracking more reliable and help to establish it as an indispensable tool in clinical environments.

5 References

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