# Tensor Dissimilarity Based Adaptive Seeding Algorithm for DT-MRI Visualization with Streamtubes

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## ABSTRACT

In this paper, we propose an adaptive seeding strategy for visualization of diffusion tensor magnetic resonance imaging (DT-MRI) data using streamtubes. DT-MRI is a medical imaging modality that captures unique water diffusion properties and fiber orientation information of the imaged tissues. Visualizing DT-MRI data using streamtubes has the advantage that not only the anisotropic nature of the diffusion is visualized but also the underlying anatomy of biological structures is revealed. This makes streamtubes significant for the analysis of fibrous tissues in medical images. In order to avoid rendering multiple similar streamtubes, an adaptive seeding strategy is employed which takes into account similarity of tensors in a given region. The goal is to automate the process of generating seed points such that regions with dissimilar tensors are assigned more seed points compared to regions with similar tensors. The algorithm is based on tensor dissimilarity metrics that take into account both diffusion magnitudes and directions to optimize the seeding positions and density of streamtubes in order to reduce the visual clutter. Two recent advances in tensor calculus and tensor dissimilarity metrics are utilized: the Log-Euclidean and the J-divergence. Results show that adaptive seeding not only helps to cull unnecessary streamtubes that would obscure visualization but also do so without having to compute the culled streamtubes, which makes the visualization process faster.

**Keywords:** Visualization, diffusion tensor magnetic resonance imaging, streamtubes, seeding, tensor distance, Log-Euclidean, J-divergence

## 1. INTRODUCTION

Since Basser et al.<sup>1</sup> presented their seminal work on diffusion tensor magnetic resonance imaging (DT-MRI), the processing, analysis, and visualization of this modality has become a primary focus in medical imaging research. As of today, it is the only non-invasive method that allows distinguishing the anatomical structures of the cerebral white matter by measuring local water diffusion through biological tissues. The result from DT-MRI is an image where at each voxel, the direction of water diffusion is locally modeled by a Gaussian probability density function whose covariance matrix is a  $3 \times 3$  symmetric positive definite diffusion tensor.

Given the data structure of diffusion tensors, it is apparent that the standard visualization techniques based on scalar fields cannot be directly applied.<sup>2,3</sup> Some of the methods proposed to overcome this difficulty include computing scalar values from diffusion tensors, such as fractional anisotropy (FA), relative anisotropy (RA), and volume ratio (VR),<sup>4</sup> and then applying the standard scalar field based visualization algorithms such as volume rendering and iso-surface rendering. Though simple, these methods are not recommended as most of the information in the tensors will be lost. Specifically the fact that only diffusion magnitude is employed for the derivation of scalar fields, the information contained in the directions of diffusion will not be utilized. Thus researchers have been proposing several methods that incorporate both the diffusion magnitudes and directions in order to overcome the shortcomings of scalar field visualization of DT-MR images.

In order to visualize both the directions and magnitudes, glyph based techniques were introduced. A common approach is to visualize each tensor as a 3D ellipsoid whose orientation is given by the eigenvectors and whose

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semi-axes lengths are given by the eigenvalues.<sup>5</sup> Using this technique, linear diffusion is visualized by a prolate with a high linear geometric shape, isotropic diffusion is depicted by spherical glyphs, while planar diffusion is visualized by pancake shaped glyphs. Similarly, rectangular prisms (cuboids) whose geometry is determined by the eigenvalues and eigenvectors have been proposed.<sup>6</sup>

Kindlmann et al.<sup>7</sup> proposed tensor field visualization using superquadrics, a traditional surface modeling technique, to generate tensor glyphs. The class of shapes they created includes spheres in the isotropic case, while emphasizing the differences among the eigenvalues in the anisotropic cases. 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 rotational symmetry of ellipsoid glyphs avoids misleading depictions of orientation, with the drawback that different shapes can be difficult to distinguish. The superquadric glyphs aim to combine the best of the box and ellipsoid methods.

While these techniques are generally insightful, they fail to illustrate certain structures in biological tissue such as the fibrous structures in white matter of the brain. Therefore advanced tractography visualization tools such as streamtubes were developed.<sup>3</sup> Such visualization is a natural choice for representing linear anisotropy by showing the underlying linear structures. A streamtube is computed starting from a given seed point following the direction of the major eigenvector. The cross-section of the streamtube is represented by the ratio of the eigenvalues corresponding to the other two eigenvectors.

The challenge with visualization of DT-MR images using streamtubes is two folds: firstly the fine tuning of parameters for selecting candidate seed points, and secondly the choice of appropriate seed points from the candidates so that to avoid visual clutter while having enough streamtubes that reflect the structure of the underlying object. The linear diffusion coefficient is a widely used quantity for selecting candidate seed points<sup>3,8,9</sup> while adaptive seeding strategy remains a challenge.

Directional tracking through vector fields has been a widely used technique in visualization and computer graphics.<sup>10,11</sup> The standard streamline technique advects particles through the vector field and traces their location as a function of time. As such several seeding algorithms have been proposed. Examples include interactive, user-specified seeding,<sup>12</sup> evenly spaced streamlines,<sup>10,13</sup> and topology guided seeding.<sup>14</sup>

Extending the idea of streamline tracing, Delmarcelle and Hesselink<sup>8,9</sup> proposed a hyper-streamlines approach to trace changes through tensor fields, following the dominant eigenvector direction. These methods have been employed for datasets derived from simulation results and have recently been extended for DT-MRI data visualization. These methods generally work by starting from given seed points within the image and following the preferred direction of diffusion along the major eigenvectors. The challenge in using these methods generally lies in the selection of seed points. A simple approach is to select seed points (tensors) with high linear diffusion coefficients, drawn from a uniform random distribution. However this method fails to discriminate seed points density where there are high linear diffusion coefficients oriented in different directions.

Zhang et al.<sup>3</sup> proposed visualizing DT-MR images using streamtubes and streamsurfaces. They compute the streamtubes evenly in the whole volume and then use culling algorithms, based on geometric distance between pairs of streamtubes, in order to discard some of the streamtubes for better visualization. The fact that streamtubes are discarded after they are computed makes such visualization expensive and slow.

In this paper, we extend the technique of DT-MRI visualization using streamtubes by incorporating an adaptive seeding strategy to selectively choose seed points and avoid unnecessary computation of streamtubes. The result is a speed-up in the rendering process and an improvement in the final visualization. Another goal of this paper is to use a seeding strategy that is not only based on geometric distance between streamlines but also reflects the directions of diffusion in the tensor field. Specifically, we use tensor dissimilarity measures based on the Log-Euclidean framework<sup>15</sup> and J-divergence metric<sup>16</sup> for adaptive seeding strategy. Regions with dissimilar tensors are populated with more seed points compared to regions of similar tensors. This results in faster rendering, less occlusion, and more insightful visualizations.

The rest of this paper is organized as follows. In section 2.1, we briefly review diffusion tensor field basics and describe the parameters that quantify the linearity of diffusion in tensor fields. We then describe streamtubes and the techniques used to trace streamtubes in tensor fields in section 2.2. This will be followed by the description

of our adaptive seeding algorithm in section 2.3. In section 2.4, we review the two mathematical frameworks for tensor dissimilarity measure which we adopted in our work. We present experimental results of the adaptive seeding algorithm for a synthetic test dataset and brain DT-MRI data in section 3. Section 4 concludes the paper.

#### 2. METHOD

We start by giving a brief overview of diffusion tensor fields that will be followed by discussion of tensor field visualization using streamtubes. Then we describe our adaptive seeding strategy.

#### 2.1. Diffusion Tensor Field Basics

In DT-MR images, the direction of water diffusion at each point is locally modeled by a Gaussian probability density function whose covariance matrix is a  $3 \times 3$  symmetric positive definite diffusion tensor composed of six independent values:

$$T = \left(\begin{array}{ccc} T_{xx} & T_{xy} & T_{xz} \\ T_{xy} & T_{yy} & T_{yz} \\ T_{xz} & T_{yz} & T_{zz} \end{array}\right)$$

The eigenvector decomposition of such a tensor T gives unit length orthogonal eigenvectors  $e_1, e_2, e_3$  with their corresponding eigenvalues  $\lambda_1, \lambda_2, \lambda_3$  such that  $\lambda_1 \ge \lambda_2 \ge \lambda_3 \ge 0$  and  $Te_i = \lambda_i e_i$ , i = 1, 2, 3. The eigenvalues are sorted in decreasing order so that the first eigenvalue  $\lambda_1$  corresponds to the major eigenvector. Moreover the original tensor T can be reconstructed by

$$T = (e_1 \ e_2 \ e_3) \begin{pmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{pmatrix} (e_1 \ e_2 \ e_3)^T$$

Thus in order to visualize all the information encoded in DT-MR images, one needs to simultaneously visualize the eigenvectors and their corresponding eigenvalues. In using streamtubes for DT-MRI visualization, the major eigenvector gives the direction through which to trace the streamtubes and the other two eigenvalues are encoded in the cross-section of the streamtube at each point.

DT-MRI visualization using streamtubes is especially useful to depict fiber structures in the images. This way not only the anisotropy nature of the diffusion is visualized but also the underlying anatomy of biological structures is revealed, which makes it significant for the analysis of fibrous tissues in medical images. In order to characterize the diffusion property, we can define the anisotropy coefficients which correspond to the linear, planar, and spherical (isotropic) diffusion as<sup>5</sup>  $C_l = \frac{\lambda_1 - \lambda_2}{\lambda_1 + \lambda_2 + \lambda_2}$ ,  $C_p = \frac{2(\lambda_2 - \lambda_3)}{\lambda_1 + \lambda_2 + \lambda_2}$ ,  $C_s = \frac{3\lambda_3}{\lambda_1 + \lambda_2 + \lambda_2}$  where  $C_l + C_p + C_s = 1$ .

#### 2.2. Streamtubes

In order to visualize streamtubes at regions of interest, streamtubes are propagated from every seed point. Because eigenvectors are vectors with sign indeterminacy, the propagation follows both forward and backward directions of the major eigenvector of the diffusion tensor. In our work, we employ the  $4^{th}$  order Runge-Kutta integration method for particle tracing and calculating the streamtube trajectory. The cross-section of the streamtubes is stretched to encode the other two eigenvectors and eigenvalues. This way, all the information in DT-MRI is visualized and fiber structure within DT-MR images are depicted.

It is apparent that rendering streamtubes from every point with high linear diffusion  $(C_l)$  results in cluttering affecting the visualization quality. Thus for better visualization results, one needs to render only a few representative streamtubes. This requires selecting representative seed points so that a limited number of streamtubes is rendered as a result. We explain our adaptive seeding approach in the next section.

### 2.3. Adaptive Seeding Algorithm

The proposed adaptive seeding algorithm starts by selecting a seed point with the highest coefficient of linear diffusion  $(C_l)$ . In the subsequent steps, we select a seed tensor with the next highest  $C_l$  and see how close it is to the already used seed points. If it not very close to nearby seed points used, then we trace streamtube starting from this tensor. This allows to display streamtubes that exhibit similar diffusion but are physically far apart. Otherwise we test how similar this tensor is to the nearby seed points already used. In the event that it is dissimilar to the previously used seeds, we trace a streamtube starting from this new seed point. If however it is similar to some of the seed points already used, the streamtube to be generated by this seed point is likely to be the same as, or very close to, those already computed and we may ignore computing such streamtubes. In this way, our algorithm gives rise to a non-uniform seed density. We summarize our method in pseudo code in Algorithm 1.

Algorithm 1 Adaptive Seeding Algorithm
1: Calculate and sort $C_l$ for all tensors
2: Select the seed tensor with the highest $C_l$
3: Trace a streamtube starting from the selected seed tensor
4: while More streamtubes are required <b>do</b>
5: $T \leftarrow$ Tensor voxel with the next highest $C_l$
6: $d_q \leftarrow$ Shortest geometric distance of T from all previous seeds used
7: <b>if</b> $d_q \ge geometric\_distance\_threshold$ <b>then</b>
8: Trace a streamtube starting from this seed tensor
9: else
10: $d_t \leftarrow$ Tensor distance between T and its spatially closest seed tensor used
11: <b>if</b> $d_t \geq tensor\_distance\_threshold$ <b>then</b>
12: Trace a streamtube starting from this seed tensor
13: end if
14: end if
15: end while

It is clear from the above discussion that an appropriate mathematical framework for tensor dissimilarity measure is needed for the adaptive seeding strategy.

## 2.4. Tensor Dissimilarity

We use the recently proposed Log-Euclidean framework calculus<sup>15</sup> and the Affine Invariant tensor distance metric<sup>16</sup> for measuring the dissimilarity of tensors. Both dissimilarity measures were employed and gave similar results. The Log-Euclidean distance,<sup>15</sup>  $d_{LE}$ , between two tensors  $T_i$  and  $T_j$  is given by

$$d_{LE}(T_i, T_j) = \sqrt{tr((logm(T_i) - logm(T_j))^2)}$$

$$\tag{1}$$

where tr(.) denotes the trace of a matrix.  $d_{LE}$  measures the dissimilarity of tensors by noting that a symmetric positive definite tensor T has a unique symmetric matrix logarithm L = logm(T) which verifies T = expm(L), where expm is the matrix exponential. Conversely, each symmetric matrix is associated with a tensor by an exponential. The logarithm of a matrix is computed by decomposing the matrix to its eigenvalues and eigenvectors, taking the logarithms of the eigenvalues, and constructing a matrix from the eigenvectors and the newly computed eigenvalues. Thus the matrix logarithm operation is particularly easy to compute when T is given in terms of its eigenvalues and eigenvectors. We also see that matrices with null or negative eigenvalues are at infinite distance from tensors and will not appear in practical computations.

The Affine Invariant tensor distance metric,  ${}^{16} d_{AI}$ , between two tensors  $T_i$  and  $T_j$  is given by

$$d_{AI}(T_i, T_j) = \frac{1}{2}\sqrt{tr(T_i^{-1}T_j + T_j^{-1}T_i) - 2n}$$
(2)

where n is the dimension of the square matrices  $T_i$  and  $T_j$ .  $d_{AI}$  measures the tensor distance by noting that a DT-MRI tensor T can be interpreted as the covariance matrix of a local Gaussian distribution which characterizes the displacement of water molecules at each lattice point in the image. Thus the Kullback-Leibler (KL) divergence can be used as distance measure which when symmetrized gives the above distance measure. This distance measure is referred to as affine invariant tensor distance measure because it is invariant when the coordinate system where the tensors lie undergoes an affine transformation.

Both tensor distance measures vanish if  $T_i$  is equal to  $T_j$  and the more similar the tensors are the smaller the distance is and vice versa. Thus by examining the distance of neighboring tensors in a given region of interest, we place more seeds if the tensors in the region are dissimilar and fewer seeds if they are similar. The fact that the distance measures incorporate both diffusion magnitudes and directions makes either of them a suitable choice for the proposed adaptive seeding algorithm.

#### 3. RESULTS

#### 3.1. Synthetic Dataset

We first demonstrate our adaptive seeding algorithm with a synthetic DT-MRI data. We generated a  $100 \times 100$  DT-MR image with two distinct diffusion patterns. The dominant major eigenvectors point to the right on the first half part of the image ( $50 \times 100$ ) and upwards on the other half part of the image (figure 1(a)). Without the adaptive seeding algorithm, all the seeds points are distributed uniformly in the image according to the shortest geometric distance threshold used in Algorithm 1. With the adaptive seeding algorithm, however, the result is a non-uniform distribution of seed points due to the dissimilarity of the tensors at the region of separation between the two distinct diffusion patterns.



**Figure 1.** Illustration of visualizing a synthetic 2D DT-MR image with streamtubes utilizing the adaptive seeding algorithm. (a) Diffusion patterns of a DT-MR image visualized with ellipsoids, (b) Tracing streamtubes without seeding algorithm gives rise to uniform distribution of seed points irrespective of diffusion patterns in the image, and (c) The adaptive seeding algorithm results in a non-uniform distribution of seed points with a large number of seed points in regions of different diffusion patterns.

#### 3.2. DT-MRI Brain Dataset

We applied our method to a 3D brain dataset. No regularization, smoothing, or interpolation was performed prior to visualization. Figure 2(a) shows streamtubes from a 3D DT-MRI brain volume without seeding strategy, while figure 2(c) shows streamtubes from the same image using our adaptive seeding strategy. Because the proposed adaptive seeding algorithm leads to more streamtubes compared to a non-adaptive approach for the same geometric distance threshold the result of a non-adaptive seeding approach with the same number of streamtubes as in figure 2(c) is also presented in figure 2(e) for comparison purposes. Iso-surface rendering using linear diffusion coefficients is superimposed in the visualization in order to provide better understanding of the anatomical context. Once again the result is uniform density of seed points when no seeding algorithm is applied. When the adaptive seeding algorithm is utilized, important regions such as the corpus callosum that have varying diffusion patterns<sup>17</sup> end up with a large number of seeds depicting the dissimilarity of diffusion patterns of the intertwined fibres in that region. With no adaptive seeding algorithm, such information is not depicted. Figures 2(b), 2(d), and 2(f) show the zoomed in versions of figures 2(a), 2(c), and 2(e) respectively. Finally we show the top view of the brain in figure 3 once again with both non-adaptive and adaptive seeding approaches in the same order as in figure 2.

## 4. CONCLUSION AND FUTURE WORK

We have developed an adaptive seeding strategy for DT-MRI visualization using streamtubes. While streamtubes have already been studied in great detail, we have noticed that most of the work related to streamtube based visualizations either do not incorporate seeding strategies at all or only make use of the anisotropy quantity for seeding purposes. The latter approach can be problematic because regions with high anisotropy are covered by more seed points; yet these seed points give very similar streamtubes near one another that makes visual clutter more likely. Tensor dissimilarity based seeding strategy helps, (i) avoid the computation of unnecessary streamtubes, which makes the visualization faster, and (ii) adjust the seed density in any given region based on the nature of diffusion both in direction and magnitude in that region. The end result is more representative streamtubes that avoid visual clutter but also reflect the diffusion patterns in the underlying structure as required. We have applied the proposed algorithm to synthetic test data and to a 3D brain DT-MRI data, demonstrating the effect of our seeding strategy and noticed that it results in a better visualization in that only few representative streamtubes are computed. One of the main open problems of our approach is that the seeding strategy is only based on comparing the geometric distance of the newly inserted seed points with previously used seed points. The distance to previously constructed streamtubes could be used to improve the control over the density of streamtubes, by adopting algorithms for evenly spaced streamlines.<sup>10, 13</sup>

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(b)



(c)





Figure 2. Visualization of a brain 3D DT-MR image with streamtubes. (a) Streamtubes generated with no seeding algorithm. Seed points are shown as blue discs. Seed points that are at least 5 grid points apart are accepted and 129 streamtubes are displayed. (b) Zoomed in version of 'a'. (c) Streamtubes generated with the adaptive seeding algorithm. Seed points that are closer than 5 grid points were accepted only if they have tensor dissimilarity measure of at least 1.0 and 272 streamtubes are displayed. (d) Zoomed in version of 'c'. (e) Streamtubes generated with no seeding algorithm but the geometric distance threshold tweaked to 3 grid points so that approximately the same number of streamtubes as in the adaptive seeding algorithm are visualized for comparison purposes. 279 streamtubes are visualized. (f) Zoomed in version of 'e'.



(a)





(c)

(d)



**Figure 3.** Top view visualization of the same brain 3D DT-MR image with streamtubes with the same parameters and results as in figure 2. Close look at the corpus callosum in figures (c) and (d) shows that the proposed adaptive seeding algorithm results in a non-uniform density of streamtubes and reflects appropriately the diffusion patterns in that region. The non-adaptive approach seems to give either very few streamtubes that do not reflect the diffusion patterns as in figures (a) and (b) or to visual clutter as in figures (e) and (f).