

# MM-DTI: Visualization and segmentation tool for diffusion tensor images

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**Abstract.** *In this paper we present the MM-DTI, a tool that offers diffusion tensor processing functionalities based on mathematical morphology operators. Through a graphic user interface, it is possible to configure and visualize a diffusion tensor image, to compute its tensorial morphological gradient (TMG) and finally, to segment it using the watershed transform. It offers three different visualization modes (tensor glyphs, volume rendering and tracts), three color mappings (FA-based, TMG-based and Segmentation-based) and an extra feature which provides an animation of the movement of water molecules through the interpolation of the objects position on the grid in the orientation and direction of the tensors principal eigenvector.*

## 1. Introduction

Diffusion tensor imaging (DTI) is a relatively new Magnetic Resonance Imaging (MRI) modality able to quantify the anisotropic diffusion of water molecules in highly structured biological tissues [Basser and Pierpaoli 1996]. DTI has been used to demonstrate subtle abnormalities in a variety of diseases (including stroke, multiple sclerosis, dyslexia, Alzheimer and schizophrenia) and is currently becoming part of many routine clinical protocols [Eriksson et al. 2001, Assaf et al. 2003, Symms et al. 2004].

One of the fundamental problems in understanding and working with diffusion tensor data is its three-dimensional and multi-variate nature. Visualizing such tensor fields is not a trivial task. Various techniques for visualizing diffusion tensor data were reported so far [Westin et al. 2002, Zhang et al. 2004, Vilanova et al. 2005] and can be categorized in two groups. One is the series of image-based methods in which each voxel value represents local anisotropy measure or principle direction of diffusion, and the 3D rendering of those images by volume rendering or surface rendering of the isosurface. The other is the group of symbolic (or geometric) display methods by using various types of glyph such as ellipsoids. A few DTI visualization tools have been recently developed and can be found in [Park et al. 2004, Fillard 2005, Jiang et al. 2006, Fillard et al. 2009].

DTI-based segmentation is relatively new and is also a very challenging task. Only in the last decade some approaches for DTI-based segmentation have been proposed [Weldeselassie and Hamarneh 2007, Wang and Vemuri 2005, Awate and Gee 2007].

This work presents the MM-DTI, a free, open source tool that deal with these two important problems of DTI: visualization and segmentation. Its visualization approach

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consists of three different and independent viewing modes and three color mapping options. The segmentation of diffusion tensor fields is performed using mathematical morphology operators, such as the tensorial morphological gradient (TMG) and the watershed transform [Rittner and Lotufo 2008]. The developed tool allows automatic and manual definition of markers as input to the watershed-based segmentation method.

There are a variety of tools which perform similar tasks, but they usually focus on a particular approach of DTI analysis, specially tractography, providing none or a low range of functionalities like DTI-based segmentation. And none of them makes use of mathematical morphology operators and concepts. Some of them are DTI Studio, DoDTI and DTI Track.

In contrast to others similar tools, MM-DTI provides an exclusive animation mode for the tensor glyphs viewing mode, which interpolates the glyph position on the 3D grid in the direction of the principal eigenvector of the tensor. While Section 2 describes the developed tool, Section 3 presents the results and conclusions can be found in Section 4.

## 2. MM-DTI

MM-DTI [Lobo et al. 2009] is a diffusion tensor image processing program running under Windows. It is suitable for tasks such as tensor field visualization, color mapping and DTI-based segmentation. It was developed in C++ and uses only OpenGL for 3D and graphical user interface rendering. Image segmentation is performed through SDC Morphology Toolbox.

As shown in Fig. 1, it provides three viewing modes (tensor glyphs, volume rendering and tracts) and each one of them can reproduce a kind of color mapping (diffusion direction, TMG or segmentation labels). Fig. 2 contains one slice of a synthetic diffusion data (torus) illustrating all nine combinations of viewing modes and color mappings.

Additionally to visualization functionalities, MM-DTI supports advanced techniques of image processing to calculate the TMG and to perform watershed-based segmentation.

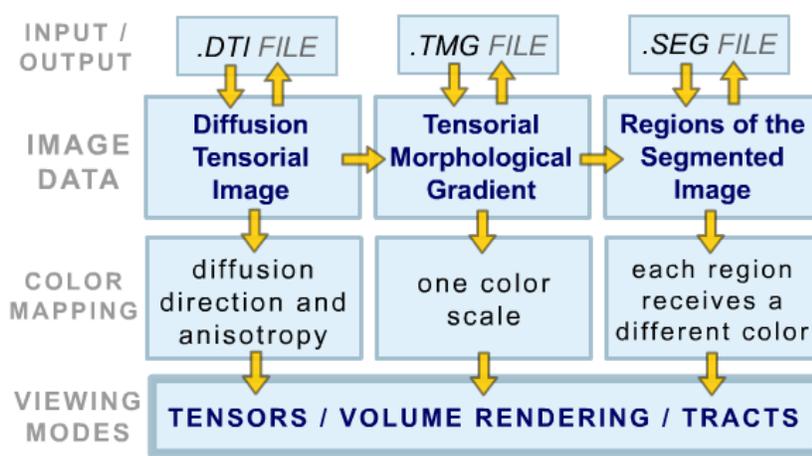


Figure 1. MM-DTI main functionality

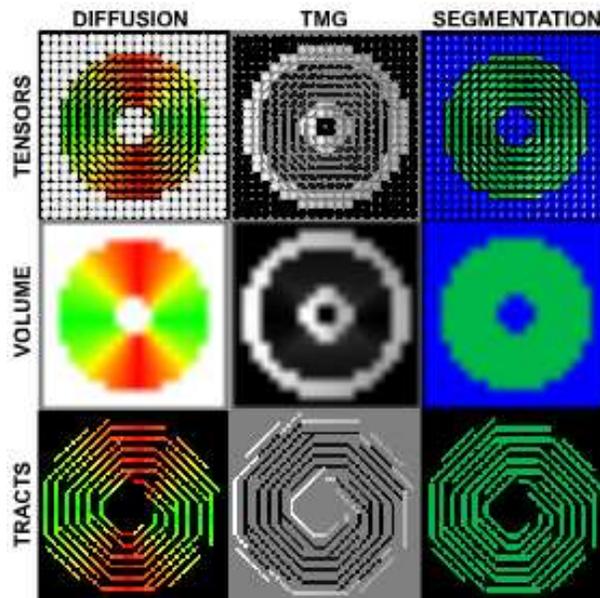


Figure 2. Nine possible combinations of viewing modes and color mapping. Viewing modes at rows and color mapping at columns. The chosen example is one slice of a synthetic torus.

## 2.1. Viewing modes

MM-DTI has three viewing modes: tensor glyphs, volume rendering and tracts. The color assigned to each voxel or region of an image depends on the chosen color mapping.

### *Tensors glyphs*

The program allows the representation of tensors by three types of objects: ellipsoids, boxes and lines. Such objects are arranged in a 3D-grid in the position of the voxel corresponding to each tensor, and are oriented following the direction of the principal eigenvector ( $e_1$ ). The size of an object, in each dimension, is given by the square root of the corresponding eigenvalue ( $\lambda_i$ ). Fig. 3 illustrates such objects.

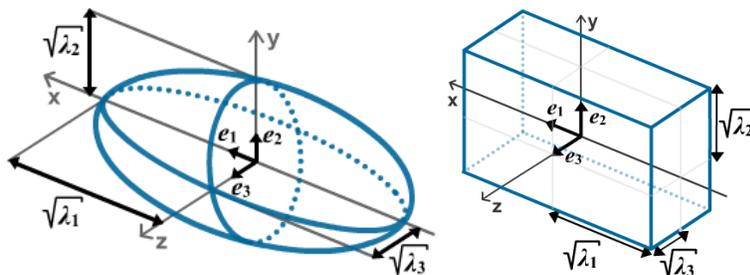


Figure 3. Objects representing a tensor: an ellipsoid and a box. The axes direction are defined by the tensor eigenvectors and the axes sizes are given by the squareroot of the tensor eigenvalues.

### *Volume Rendering*

The volume rendering viewing mode maps the color scheme being displayed on a

3D texture data, allowing the user to see the entire volume rendering or just some textured slices of the image. The slice mode is a feature also available in tensors and tracts viewing modes.

### *Tracts*

The viewing mode by tracts generate tubes (or fibers) connecting a tensor X to other tensor Y, for which X points to. The principal eigenvector orientation of X is used to determine Y. This is done for all tensors of the image, resulting in multiples paths to the movement of water molecules. It is important to notice that a minimum value of FA is used to determine which tensors can generate a path, in order to avoid using tensors that have predominantly isotropic movement. Moreover, the thickness of a tube that represents a path is given by  $1 - FA$ , so thicker tubes represent more isotropic diffusion.

## **2.2. Color mapping**

The tool provides three types of color mapping: main diffusion direction, tensorial morphological gradient (TMG) and segmentation labels.

### *Diffusion*

Several color mapping schemes for diffusion tensor are available in DTI literature [Pajevic and Pierpaoli 1999, He et al. 2004]. Usually, in the diffusion image, the color of each voxel is related to the direction of the principal eigenvector associated to that voxel, as well as its fractional anisotropy (FA). In our system we assign a color (RGB) based on FA, allowing the user to choose the desired FA influence in the color computation:

$$R = e_{1x} + (1 - e_{1x})(1 - FA)^n \quad (1)$$

$$G = e_{1y} + (1 - e_{1y})(1 - FA)^n \quad (2)$$

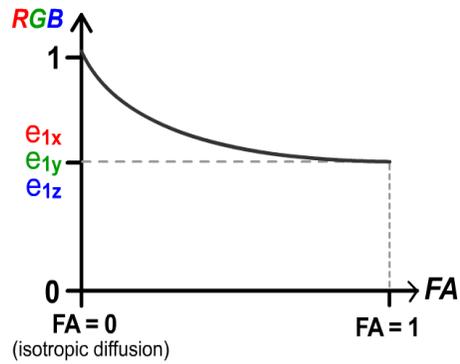
$$B = e_{1z} + (1 - e_{1z})(1 - FA)^n \quad (3)$$

with FA given by:

$$FA = \sqrt{\frac{3}{2} \frac{\sqrt{(\lambda_1 - T_{av})^2 + (\lambda_2 - T_{av})^2 + (\lambda_3 - T_{av})^2}}{\sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}} \quad (4)$$

where  $T_{av}$  is the mean diffusivity [Basser and Pierpaoli 1996].

This method was developed to allow the user to choose the FA influence in tensors color. In Fig. 4, it is possible to see graphically the influence of the characteristics of a tensor in determining its color in a diffusion image. The curvature of the function in the graph is determined by  $n$ , which represents the chromatic sensitivity to FA. For larger values of  $n$ , the value of FA will have less influence on the final color of the object representing the tensor. The opposite is also true, i.e. for lower values of  $n$ , the colors associated with the tensor will be more influenced by the value of FA, tending to white. The traditional linear approach is also available just setting  $n$  to 1. In MM-DTI is also available a variation of the diffusion image color mapping, which assigns colors to tensor using only the fractional anisotropy (FA) value.



**Figure 4. RGB vs FA color function graph with  $n = 2$ . The closer the value of FA is to 0 (isotropic diffusion), more the color will tend to gain a lighter tone, toward the white. The closer the value of FA is to 1, the color tends to be determined predominantly by the principal direction of diffusion**

### *Tensorial morphological gradient (TMG)*

The computation of a tensorial morphological gradient (TMG) is a technique proposed to transform the diffusion tensor image into a scalar map with meaningful values at edges of structures whose segmentation is desired [Rittner and Lotufo 2008]. The TMG uses diffusion intervoxel measures and combines them to compute a gradient using concepts from mathematical morphology. The MM-DTI implements the TMG computation based on four similarity functions: dot product (DP), tensorial dot product (TDP), Frobenius norm (FN) and J-Divergence (J-Div) [Pierpaoli and Basser 1996, Alexander et al. 1999]. It is also possible to choose the structuring element used in TMG computation, and to choose the colors to be assigned to the minimum and maximum values of TMG. It is important to note that the computed TMG serves as input data for the segmentation function.

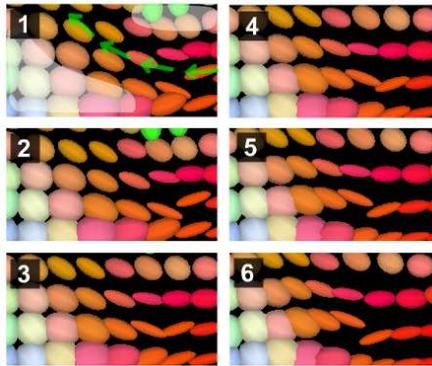
### *Segmentation labels*

The watershed-based segmentation method is applied to the results of the TMG calculation to divide the original image into regions with similar diffusion characteristics [Rittner and Lotufo 2008]. Each region is identified by a label, and then a common color is assigned to voxels belonging to the same region. The user chooses between manual or automatic markers placement for the watershed segmentation, and can also configure the assignment of colors to each label of the segmented image.

## **2.3. Animation**

The tensor glyphs viewing mode has an extra feature (non-existent in other viewing modes), which provides an animation of the movement of water molecules through the interpolation of the object's position on the grid in the orientation and direction of the principal eigenvector [Lobo et al. 2009]. Since the original data of a diffusion tensorial image provide only the orientation of the eigenvector, and not the direction, we created a method that gives coherence to the animation by assigning direction to a tensor based on its neighbors (Fig. 5). This method does a breadth-first search in the image, starting from a seed voxel, and determines the direction of each tensor in the image based on its

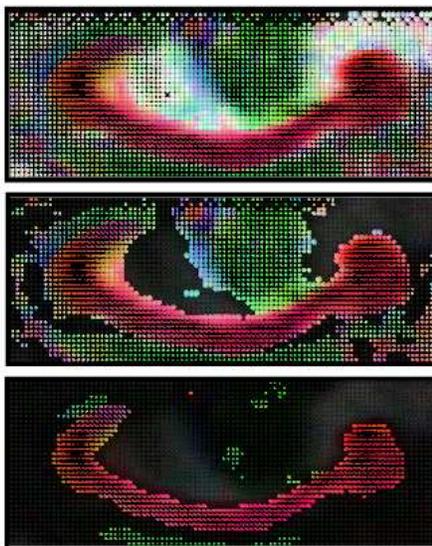
neighbors which have had their direction defined in order to minimize inconsistencies in the movement.



**Figure 5.** A diffusion tensorial image which has been animated. The six frames shows the same part of the image in different periods of time. In the first frame, the green arrows follow the main direction of diffusion in the area, while the whitened areas indicate regions with predominantly isotropic diffusion.

#### 2.4. Mask and filters

MM-DTI defines a mechanism that allows the user to import a binary mask file, which can be used to remove from visualization pre-defined voxels marked as invisible in the mask. These mask files can be created in Matlab and then exported to a MM-DTI friendly format file. The tool also allows the user to apply the mask permanently to the image and save as another modified image, which will have null tensors in the positions filtered by the mask.



**Figure 6.** Three images showing the same slice of the corpus callosum with different FA filters. The top image was not filtered, the middle image set the minimum FA to 0.22 and the bottom image set this same parameter to 0.51. In all images, the filtered areas are showed with 5 percent of transparency.

The tool also provides three types of dynamic filters applicable to any kind of combination of viewing mode and color mapping. The first one is the FA filter, which allows the user to set the level of transparency of tensors with FA between some defined interval of values. It is usually useful to hide some tensors which compose a FA uniform image background. An example of the use of this kind of filter can be seen in Fig. 6.

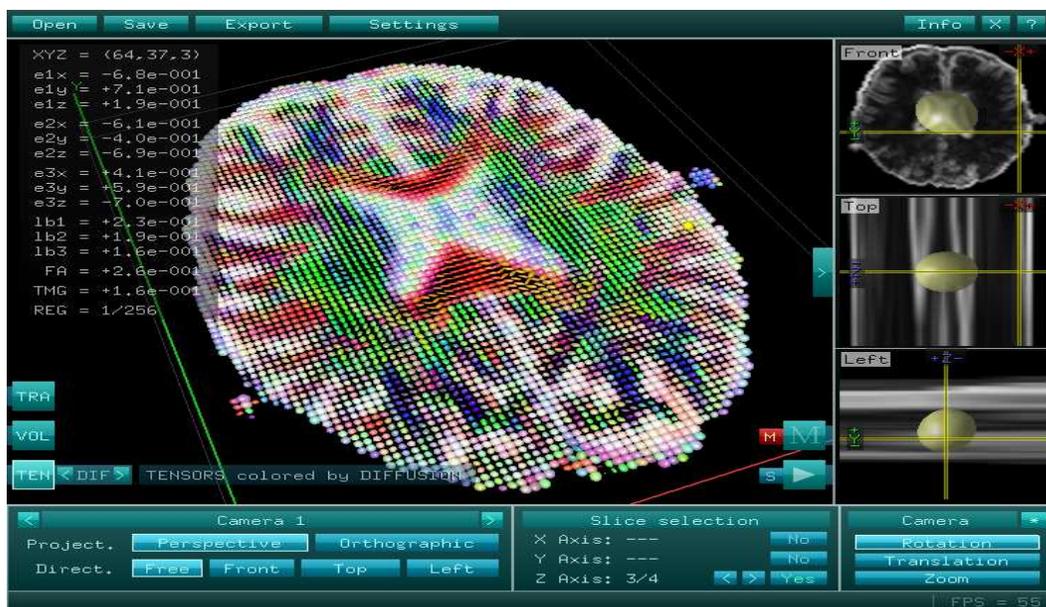
The second filter allows the user to select which regions defined by the segmentation process will be visible, increasing the focus on the desired view area through the exclusion of other regions that do not interest.

Finally, the third filter is the slice filter, which provides a mechanism to select orthogonal slices in the tridimensional grid of objects being viewed.

### 3. Results

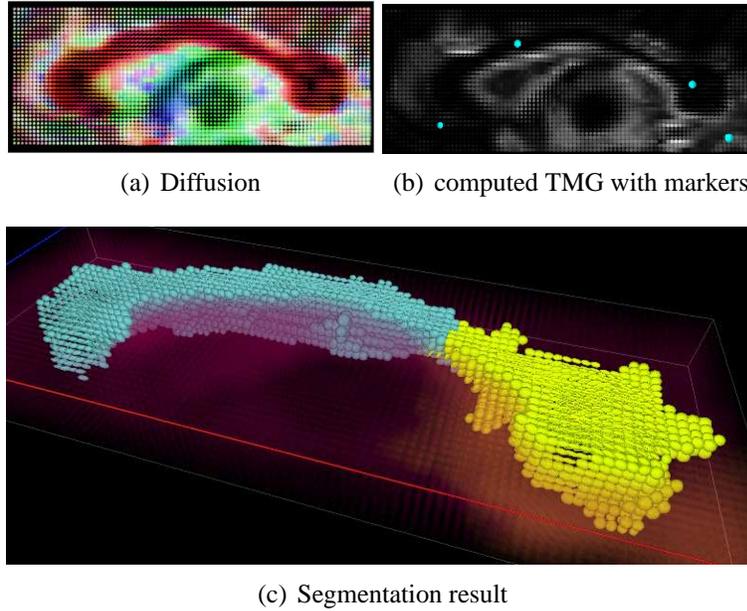
Fig. 7 shows the MM-DTI graphical user interface, with a slice of a diffusion tensorial image of a human brain on the center. The user interface allows camera operations, tensor/slice selection and simultaneous viewing modes. Through the “Settings” panel it is possible to configure preferences in visualization and image processing.

Fig. 8 illustrates the segmentation functionality of the MM-DTI. Fig. 8(a) shows an original DTI data set, cropped around the corpus callosum. Although only one slice is shown, the data set is composed by 7 slices. Fig. 8(b) contains the computed TMG using the FN as similarity measure and a 6-connected structuring element, where the borders of the corpus callosum can be observed. The markers to be used in the watershed segmentation can also be observed in blue. Fig. 8(c) depicts the segmentation result using the watershed from markers.



**Figure 7. MM-DTI user interface. In the main window the diffusion data is shown, according to the chosen viewing mode (ellipsoids) and the color mapping (diffusion direction). The right panel shows a slice/tensor selection mechanism**

Table 1 lists a group of popular DTI tools, including the tool presented in this work (MM-DTI), and summarizes the visualization modes and algorithms used by these



**Figure 8. Steps for segmenting the corpus callosum. While Fig. 8(a) shows ellipsoids colored by FA, Fig. 8(b) shows ellipsoids colored by TMG and the markers placed by the user. Fig. 8(c) depicts the segmentation result, making transparent the regions outside the corpus callosum.**

**Table 1. Comparison between MRI visualization tools**

Name	Visualization	Segmentation	Fiber tracking	Other features	OS
MM-DTI	<ul style="list-style-type: none"> <li>- Interactive display for tensor glyphs, volume rendering and tracts</li> <li>- FA sensitive color scheme</li> </ul>	Automatic segmentation through mathematical morphology	<i>(Not available)</i>	<ul style="list-style-type: none"> <li>- Animation</li> <li>- Filtering</li> <li>- Automatic region of interesting selection</li> <li>- Tensor selection</li> </ul>	Windows
FSL	Interactive display for 3D data	Automatic brain segmentation	<ul style="list-style-type: none"> <li>- Probabilistic tractography</li> <li>- Crossing-fiber modeling</li> </ul>	<ul style="list-style-type: none"> <li>- Image registration</li> <li>- Image processing (including noise reduction)</li> </ul>	Windows Mac OS X Linux
DTI-Studio	Interactive display for tensor glyphs and volume rendering	<i>(Not available)</i>	<ul style="list-style-type: none"> <li>- Stream-line tracking</li> <li>- Probability tracking</li> </ul>	<ul style="list-style-type: none"> <li>- DWI reconstruction</li> <li>- Along tract quantitative analysis</li> </ul>	Windows
3D Slicer	Interactive display for tensor glyphs and volume rendering	Atlas based medical image segmentation	Fiber clustering module	<ul style="list-style-type: none"> <li>- Manual region of interest selection</li> <li>- Filtering</li> </ul>	Windows Mac OS X Linux
OsiriX	Interactive display for volume and surface rendering	Growing region segmentation for regions of interest merging	<i>(Not available)</i>	<ul style="list-style-type: none"> <li>- Multiplanar reconstruction</li> <li>- Image blending</li> <li>- Manual region of interest selection</li> </ul>	Mac OS X
BioImage Suite	Interactive display for tensor glyphs and volume rendering	Semi-interactive surface segmentation	<ul style="list-style-type: none"> <li>- Stream-line tracking</li> <li>- Anisotropic front propagation</li> </ul>	<ul style="list-style-type: none"> <li>- Image registration</li> <li>- Region of interest analysis</li> </ul>	Windows Mac OS X Linux

tools to perform segmentation and fiber tracking. Additional features and the operational system required to run each tool were also presented.

Finally, the developed tool was efficient in relation to the computational time demanded for opening and pre-processing of DTI data, and has low rendering time even for various modes of visualization combined at the same time.

#### 4. Conclusions

This paper presents the MM-DTI, a visualization and segmentation tool for diffusion tensor images. The MM-DTI visualization approach, which separates the data information in two independent groups, named color mapping and viewing modes, allows the user to choose the best combination of visual information for each study case. In the segmentation functionality, the proposed method requires no manual seed placement and/or initial surface delineation, and is possible to control the number of regions into which the image should be segmented. Finally, the tensor animation mode, which provides the possibility of dynamically viewing a DT field, renders a digital representation of the data closer to the diffusion phenomenon.

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