DTI Visualization by Fiber Tracking

Final Presentation

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Introduction—Data Outline

• 数据获取:通过对MRI数据计算得到

• 数据格式: NIfTI

• 数据维度: 7 x 148 x 190 x 160

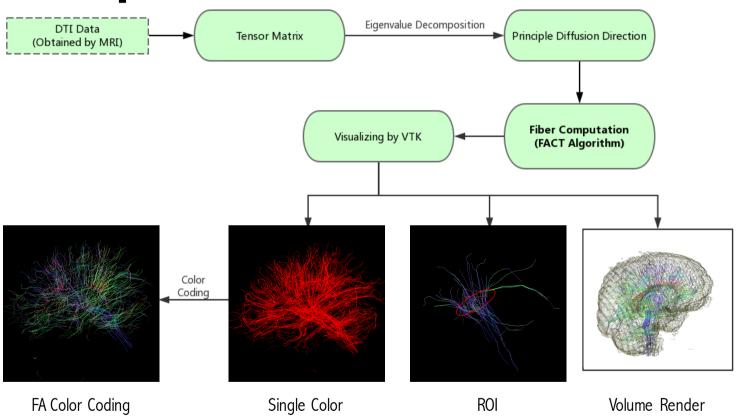
• 张量数据: 空间上每个点都有7维的张量数据,分别对应为

 $D_{xx}, D_{yy}, D_{zz}, D_{xy}, D_{xz}, D_{yz}$ 和 confidence

Introduction—Problem

- 均匀介质中水分子随机运动,在各个方向运动几率相同,具有各向同性 (isotropy)
- 在人体组织中,水分子运动受到组织结构影响,在各个方向弥散程度不同, 具有各向异性(anisotropy)
- 本次使用的DTI数据包含张量数据,刻画一个体素中水分子扩散的各向异性

Operation procedure – Overview



Tensor matrix

$$\mathbf{D} = egin{bmatrix} D_{xx} & D_{xy} & D_{xz} \ D_{yx} & D_{yy} & D_{yz} \ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

$$ar{\mathbf{D}} = [D_{xx}, D_{yy}, D_{zz}, D_{xy}, D_{xz}, D_{yz}]^T$$

Principal direction

• Eigenvalue decomposition

$$egin{aligned} \mathbf{D}\mathbf{v} &= \lambda\mathbf{v} \ \Rightarrow \mathbf{D} egin{bmatrix} ec{v}_1^T \ ec{v}_2^T \ ec{v}_3^T \end{bmatrix} &= egin{bmatrix} \lambda_1 \ \lambda_2 \ \lambda_3 \end{bmatrix} egin{bmatrix} ec{v}_1^T \ ec{v}_2^T \ ec{v}_3^T \end{bmatrix} \end{aligned}$$

Principal direction

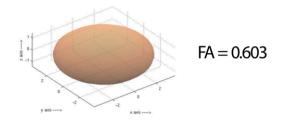
• Principal direction

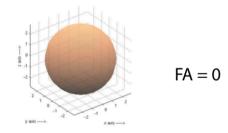
$$\mathbf{D}v_{principal} = \lambda_{max}v_{principal}$$

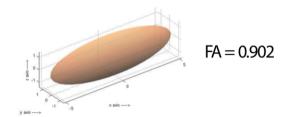
Fractional anisotropy (FA) calculation

$$FA=rac{\sqrt{3}}{\sqrt{2}}rac{\sqrt{(\lambda_1-\lambda)^2+(\lambda_2-\lambda)^2+(\lambda_3-\lambda)^2}}{\sqrt{\lambda_1^2+\lambda_2^2+\lambda_3^2}}$$

$$\lambda = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3}$$



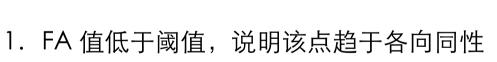




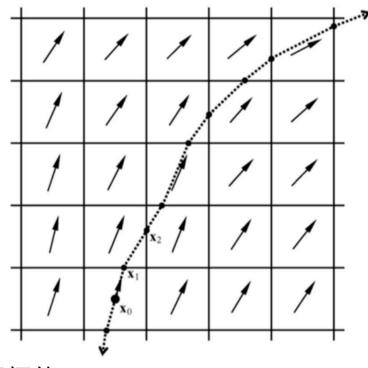
Fiber computation

Tracking Algorithm
Fiber Assignment by Continuous
Tracking (FACT)

• Stop tracking when:



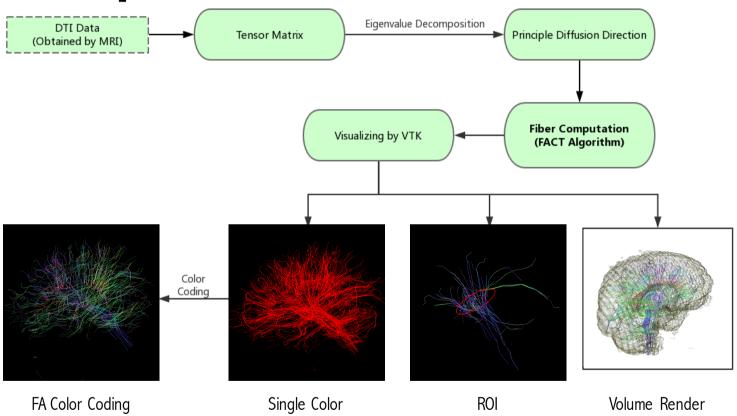
- 2. 当进入新体素运动角度发生的偏折角度大于阈值
- 3. 纤维扩展到了边界体素



Visualize by VTK

- Region of interest(ROI)
 - User defined
- Diffusion anisotropy visualization
 - (R, G, B) represents diffusion anisotropy in each direction (R, G, B) = FA * (v_x , v_y , v_z)
- Volume Rendering
 - Brain tissue structure information

Operation procedure



Reference

1. Jiang H, van Zijl P C, Kim J, et al. DtiStudio: resource program for diffusion tensor computation and fiber bundle tracking.[J]. Computer Methods & Programs in Biomedicine, 2006, 81(2):106-116.

