A Comparison of Fiber Tracking by Different Numerical Integration Methods

R. Rathore[1], G. Bayu[1], R. Gupta[2], D. K. Rathore[1], A. Purwar[1], R. Trivedi[2], S. Saksena[2], M. K. Sarma[1], A. Singh[1]
[1]Mathematics, Indian Institute of Technology, Kanpur, UP, India, [2]Radiodiagnosis, Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow, UP, India

Introduction: Fiber Tracking by means of DT-MRI is the first non-invasive technique that can provide estimate of white matter tracts in the brain [1]. Accurate mapping of white matter fiber-tracts in relation to brain pathologies is a goal of critical importance to the neurosurgical community [2]. This work discusses comparison of different numerical integration methods for fiber tracking and the fiber tracking results obtained by following the principal eigen vector ($\mathbf{e}_1$) of the tensor with two interpolation methods and different step sizes. The current method which is proposed here has shown clearly the difference between normal and pathological cases.

Material and Methods: 1. The Euler Method (**E**) is a first order method for integrating ordinary differential equations by using a recurrence relation, $w_{i+1} = w_i + hf(t_i ,w_i)$**. 2.** Modified Euler Method (**M**) uses **E** to predict the provisional value w_{i+1} at the next time t_{i+1} and is given by $W_{i+1} = w_i+h[f(t_i,w_i)+f(t_{i+1}+w_{i+1})]/2$ is a second order method**. 3.** Runge-Kutta Method (**R**) is a fourth order method which does four function evaluations per-step. It is given by, $w_{i+1} = w_i + h[k_1+2k_2+2k_3+k_4]/6$, where $k_1= hf(t_i,w_i)$, $k_2= hf(t_i+h/2,w_i+k_1/2)$, $k_3= hf(t_i+h/2,w_i+k_2/2)$, and $k_4= hf(t_{i+1},w_i+k_3)$. Tracking is started at any point of ROI with FA>0.2. Tracking will continue in the direction and opposite direction (for backward tracking) of $\mathbf{e}_1$**.** By using one of the above three integration methods the next point in the volume can be determined. The point obtained may not be an integral point, so by using either nearest neighborhood (**N**) or trilinear interpolation (**T**) one can determine the vector and FA information at that point and continue tracking by checking the stopping criterion. Tracking is stopped if one of the following conditions holds [1,3]: FA< 0.15,or The inner product between two consecutive vectors in the tracking is less than 0.7,or maximum number of voxels is 400. DT-MRI was performed for one normal subject and one pathological case on 1..5 Tesla GE MR Scanner (Echo speed plus) using single-shot echo planar dual spin-echo sequence with ramp sampling at SGPGIMS, Lucknow, India; in-order to test the current method and comparison with different methods. The diffusion weighting b-factor was 1000s/mm^2, TR~8sec, TE~100ms. 36 axial sections, 3mm slice thickness, no gap, FOV= 240 mm x 240 mm and an image matrix of 256x256 (following zero filling). The diffusion tensor encoding used was the balanced, rotationally invariant icosahedral scheme with 10 uniform directions over the unit hemisphere [4]. For checking the validation of tracking, an ROI volume containing corpus callosum using sagittal slices is selected for one pathological and one normal subject, where the tracking reconstructions (Fig. I) are done using integration method **M** with step size h = ½ and interpolation scheme **T**. To compare the methods E, M and R with different step sizes and interpolation schemes, another DTI data set was generated using a normal subject aged 35 yrs. In this case all the trackings were done by an ROI in the corpus callosum at the mid-sagittal level [3].

Results: (a) The images of outer surfaces of the collection of fibers emanating from the corpus callosum from an axial view from the top obtained after tracking one patient and one normal subject are shown in Figure I, where image A is that of the normal subject, and image B that of the pathological case. In the latter, the comparative loss of the fibers is clearly seen. (b) Table I displays the number of extra voxels in the fiber sets of one scheme as compared with another for all cases. It is seen that on the whole as 'h' decreases the relative number of extra voxels in different methods decrease. Indeed, the number of computations increase as 'h' decreases. (c) The first number in each pair of columns of Table-II represents the number of fibers and the second number denotes the total number of voxels comprising the fibers for trilinear and nearest neighbor interpolation schemes. We observe that, on the whole, both the number of fibers and the total fiber volume increase with decreasing h. Moreover the trilinear interpolations generate more fibers as compared with the nearest neighbor. (d) Axial views of the results of the three integration methods **E**, **M** and **R** of tracking, each with four step sizes h=1, h=1/2, h=1/3 and h=1/4 and two interpolation schemes **N** and **T** are shown in Fig. II. Fig III shows a pictorial view of the extra voxels presented in Table I.

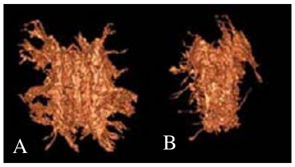

Figure I

Discussion and Conclusions: The tracking results we obtained agree with the anatomy of the corpus callosum. The fiber volume from the Modified Euler method is larger than that by the other two methods for h = 0.5. The functional evaluation at each step in the tracking methods is 1, 2 and 4, for Euler, Modified Euler and Runge-Kutta, respectively. The different results seems to indicate that an identification and verification of the correctness of the fibers has to be taken a little more systematically. Till an optimum method is achieved, the Modified Euler (h = 0.5) with trilinear interpolation is recommended as it generates more fibers data volume.

	Nearest Neighbor								Trilinear							
	h=1		**h=1/2**		**h=1/3**		**h=1/4**		**h=1**		**h=1/2**		**h=1/3**		**h=1/4**	
M vs *E*	2190	2997	2327	2407	1009	1920	864	1696	3138	3244	1569	2282	1063	1714	872	1459
E vs *R*	2618	1273	3159	1886	2725	1562	2618	1273	3875	3342	3435	1888	3087	1336	2834	1151
M vs *R*	3138	1937	2394	1337	2264	1137	2100	845	2539	1140	2330	734	2243	580	2161	528

Table-I: Extra voxels tracked in one method as compared with other for different h and schemes

T	**h=1**		**h=1/2**		**h=1/3**		**h=1/4**	
E	998	23882	1036	32047	1046	33852	1047	33354
M	1010	28024	1043	33005	1044	33631	1042	33193
R	964	21490	1019	26693	1023	27422	1021	27226
N	**h = 1**		**h=1/2**		**h=1/3**		**h=1/4**	
E	910	29812	950	38657	964	40045	974	39679
M	926	22385	942	25361	948	25472	953	25411
R	869	18094	901	21153	908	21484	911	21328

Table-II ; Total fiber volume data tracked from ROI

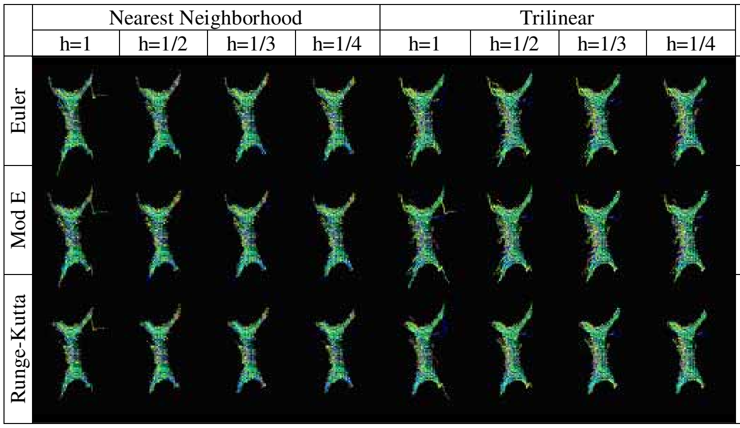

Figure II: Each row depicts one integration method with two interpolations and different step sizes.

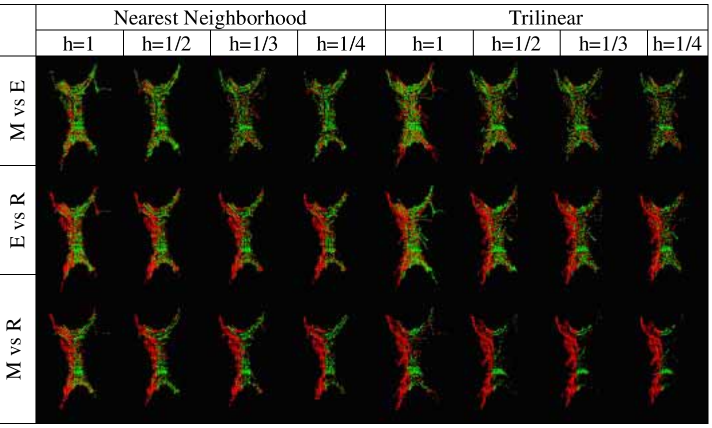

Figure III: Red color represents extra voxels in the first integration method and green extra voxels in the second integration method.

References: [1] Basser PJ, et al.; MRM 2000;44:625-632.[2] M. Guil, et al.; Proc. ISMRM. 2005. [3] Peter C.M, et al.; Radiology 2004; 230:77-87. [4]. Hasan, KM, et al.; JMRI2001; 13:769-780.