Preliminary results of the effects of higher order reconstruction on Diffusion MRI data on our predictive model for tumor recurrence

A. Krishnan[1], S. Chaudhuri[1], D. Davis[2], P. Okunieff[3], and W. G. O'Dell[4]

[1]Department of Biomedical Engineering, University of Rochester, Rochester, New York, United States, [2]Department of Imaging Sciences and Radiation Oncology, University of Rochester, Rochester, New York, United States, [3]Department of Radiation Oncology, University of Rochester, Rochester, New York, United States, [4]Department of Biomedical Engineering and Radiation Oncology, University of Rochester, Rochester, New York, United States

Purpose: The current methods of determining the treatment margins for primary brain Stereotactic Radiotherapy (SRT) are often inadequate as recurrences and secondary tumors frequently occur at or near the boundary of treatment margins. Our hypothesis is that the paths of elevated water diffusion, particularly along white matter tracts, provide a preferred route for migration of cancer cells. If our hypothesis is correct then SRT treatment volumes could be modified to provide elongated margins along the paths of elevated water diffusion; thereby creating a biologically better treatment plan that may reduce the incidence of recurrence. In this study we compare the results of our predictive model of tumor recurrence using one and multi-tensor reconstruction of diffusion MRI data. Our hypothesis is that multi-tensor reconstruction will result in cell migration patterns that are more smooth and continuous, especially through regions of known fiber crossing.

Methods and Materials: We describe herein a method for applying magnetic resonance Diffusion Tensor Imaging (DTI) in patients with aggressive gliomas to predict the spread and recurrence of disease following SRT treatment. Our method involves DTI acquisition and processing, followed by the application of a constrained random walk model for cell migration. DTI was performed using an EPI sequence on a 3.0T Siemens scanner with 70 serial axial images of voxel dimensions: 2.0×2.0×2.0 mm; TR 10.1s; TE 100 ms; 60 diffusion gradient directions and 10 reference (b=0) scans. Three volunteers and four patients with gliomas were imaged. All patients had their primary gliomas surgically resected, followed by SRT to eradicate residual disease. Two patients were scanned post-surgically, one patient was scanned both pre and post-surgically and one patient was scanned pre-surgically. Following SRT, patients are given repeated MRI follow-ups at regular intervals to identify early incidence of tumor recurrence. The random walk of cells is constrained by the local diffusion environment. In our previous implementation the DTI data sets were reconstructed using a one tensor model but it is known that this reconstruction fails in areas of fiber crossing. In the current work we extend our random walk model to incorporate multi-tensor reconstruction of DTI data sets using Camino [1]. The steps involved in the current study are as follows. 1) The dicom images are converted to Analyze format using MRIConvert.2) The DTI data sets are reconstructed with Camino using one and multi-tensor models. 3) Each voxel is classified as one or two tensor based on the relative magnitudes of the diffusion eigen values. 4) In the typical implementation of the cell migration model, seed points are selected on the tumor surface. However, to better evaluate the effect of one versus two tensor reconstruction, for this study seed points are selected in areas of known fiber crossing. In the first scenario the Camino ouput is used to select isolated two-tensor voxels and seed points are selected from the nine voxels surrounding a representative two-tensor voxel. In the second scenario, a hypothetical tumor is placed in the crossing of the corpus callosum and uncinate fasciculus and cells are allowed to migrate from the tumor surface. 5) If the voxel has two tensors then the direction along which the cell migrates is chosen pseudo-randomly, weighted by the volume fraction for each tensor. 6) The uncertainty in the estimation of the principal diffusion direction is determined based on the value of Fractional Anisotropy. This uncertainty is incorporated into the determination of the direction of cell migration, given by theta and phi, the in-plane and out-of-plane solid angles about the estimated principle diffusion direction. For simulations with one tensor, the uncertainty in theta and phi are ±35°, ±20° and ±10° and with two tensors the uncertainty in theta and phi are ±20°, ±10° and ±5° when the FA is 0-0.3, 0.3-0.6 and 0.6-1, respectively. 7) At each step the direction of migration is decided randomly within the uncertainty range. 8) When the cell is on the tumor surface it is constrained to move away from the surface. 9) The probability of cell migration is defined as the number of cells found in or passing through each voxel after a fixed number of steps.

Results and Conclusion: From the results of the predictive model of tumor recurrence using one and multi-tensor reconstruction, we see that the random walk model based on one tensor produces more smooth and continuous paths than that based on multi-tensor reconstruction. Our random walk based on one tensor is also successful in areas of fiber crossing where the inherent greater uncertainty in theta and phi in those voxels partially compensates for the presence of crossing fiber paths. This forces the cells to migrate along many directions and encounter the prominent diffusion direction in that voxel. With our DTI data, the voxel labeling scheme in Camino produced isolated voxels having two tensors. The results of the random walk model based on multi-tensor reconstruction may be improved if a connectivity constraint is imposed on the voxel labeling scheme to better associate isolated voxels. Figure 1 and 2 are the initial results based on a volunteer data set.

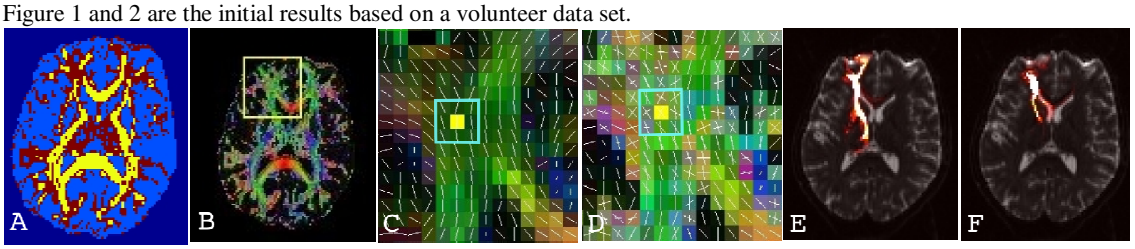

Figure 1: [A] Map of voxel labels. Voxels in yellow have one tensor, red have two tensors and blue are isotropic. The classification is based on eigen values of the one tensor model. [B] Map of Fractional Anisotropy. Yellow square denotes the crossing of the corpus callosum and uncinate fasciculus for the zoomed-in regions [C] and [D] showing the principal diffusion directions of one tensor model [C] and multi-tensor model [D]. The cells were allowed to migrate from the 9 voxels enclosed by the aquamarine square having one tensor [C] and two tensors in multi-tensor fit [D]. The map of cell concentration from our random walk model, based on one tensor model [E] and two tensor model [F]. Voxels in yellow have higher cell concentration and voxels in red have lower cell concentration. The random walk model based on one tensor produces smooth and continuous paths of cell migration.

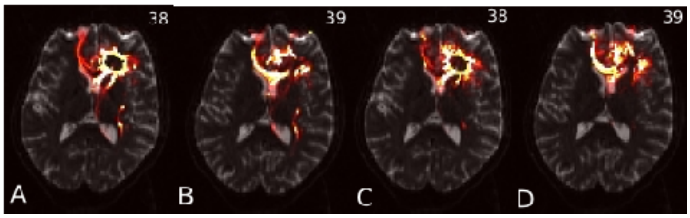

Figure 2: [A] & [B] Map of cell concentration from our random walk model based on one tensor model with cells migrating from the surface of a hypothetical tumor at the crossing of the corpus callosum and uncinate fasciculus. [C] & [D] Map of cell concentration from our random walk model based on multi-tensor model.