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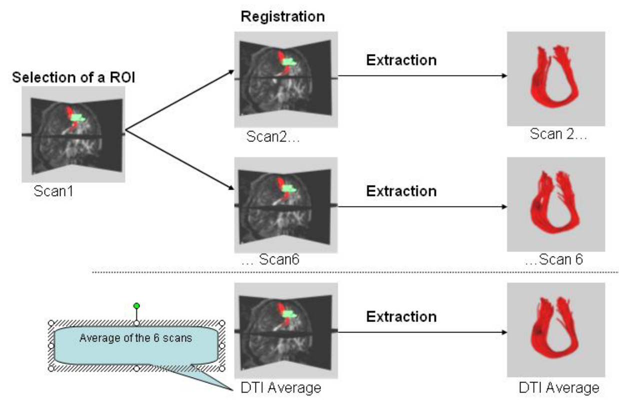
Quantitative Analysis of Diffusion Properties of White Matter Fiber Tracts: A Validation Study

G. Gerig[1], I. Corouge[2,3], C. Vachet[3,4], K. R. Krishnan[5], J. R. MacFall[5]

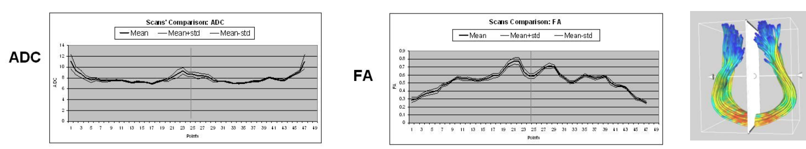
[1]Computer Science and Psychiatry, UNC Chapel Hill, Chapel Hill, NC, United States, [2]Computer Science, UNC Chapel Hill, Chapel Hill, NC, United States, [3]Psychiatry, UNC Chapel Hill, Chapel Hill, NC, United States, [4]CPE, Lyon, France, [5]Psychiatry, Duke University Medical Center, Durham, NC, United States

Introduction: White matter fiber bundles of the human brain form a spatial pattern defined by the anatomical and functional architecture. We have developed an integrated set of tools for novel analysis of diffusion tensor imaging (DTI) that is complementary to region- and voxel-based processing. Using the new methods, statistical analysis of diffusion properties of specific fasciculi of interest can be performed along tracts which form geodesic curves in 3D space. Such complex regions are otherwise not accessible by user-defined region of interest (ROI) analysis. Fiber tracts of interest are extracted from DTI tensor data using existing tractography. The resulting sets of streamlines are further processed by modeling white matter tracts via streamline clustering and arc-length parametrization. Finally, we calculate statistics of diffusion tensor properties within cross-sections and along tracts. A major concern of clinical research is reliability and reproducibility of procedures. We present a validation study of our novel processing based on 6 repeated DTI scans of the same subject, with slight change of head position. An average DTI is calculated by averaging all 6 scans after rigid body alignment. Tensor properties including FA, ADC, and the three eigenvalues λ_1, λ_2, λ_3, are compared. The analysis is applied to 3 callosal bundles and the uncinate fasciculus, but only one callosal bundle is used for illustration below.

Materials and Methods: One subject has been imaged 6 times using slightly different head position. DTI imaging is done on a 3.0 Tesla whole-body MRI system (Trio, Siemens Medical Systems, Malvern, PA, USA) using the 8-channel head coil. Diffusion tensor axial images included 6 diffusion directions with a b value of 1000 sec/mm^2, plus an acquisition where b = 0 sec/mm^2, using the parameters of 25.6 cm FOV; 2 mm slice, 0 gap; Tr = 10000, Te = 80; 1345 Hz/pixel bandwidth; 128 x 128 matrix. The processing pipeline, including tensor calculation, definition of source and target regions of interest for tractography, streamline clustering, and analysis of the diffusion tensors along tracts, is applied to each single scan and the average DTI. The Fiber Tracking Tool [Fillard 2003], developed from a method provided by Susumi Mori [Mori 2002], created the white matter tract images using fractional anisotropy images and the vector field it calculates from the B0 – B6 diffusion images. Sets of streamlines were processed by the new FiberViewer Tool [Corouge2004, Gerig 2004] to provide diffusion properties as a function of arc-length along clustered bundles.



Results: The diagrams illustrate the ADC and FA statistics along the bundle, with origin at the midsagittal plane. The curves show the mean and standard deviation calculated from the 6 scans as a function of arc-length. We also calculated statistics for the three eigenvalues λ_1, λ_2, and λ_3 and compare the means with results from the combined DTI average image. Results at the center, i.e. at the position of the midsagittal plane, are listed in the table. The second row lists the number of streamlines obtained for each experiment. Although the number of streamlines varies due to the instability of tractography, the resulting diffusion tensor statistics are approximately within 5%std for FA and ADC but only 2%std for the first eigenvalue λ_1. The FA of the DTI average (last column) is slightly lower than the 6 case mean.



	Scan 1	Scan 2	Scan 3	Scan 4	Scan 5	Scan 6	Mean	Std	%Std	DTI Average
Nr. of Streamlines	117	119	134	116	132	72				154
FA	0.63	0.64	0.56	0.58	0.55	0.59	0.59	0.03	5.77%	0.56
ADC (mm2/sec)	80.2	81.9	89.1	88.7	91.6	89.1	86.8	4.16	4.79%	88.3
Lambda1 (mm2/sec)	146.8	152.5	152.1	154.2	153.9	156.8	152.7	3.04	1.99%	151.2
Lambda2 (mm2/sec)	54.1	56.4	68.1	66.6	72.1	64.8	63.7	6.40	10.04%	62.2
Lambda3 (mm2/sec)	39.8	36.9	47.0	45.3	48.8	45.7	43.9	4.17	9.48%	51.4

Discussion: Clinical analysis studying fiber tract disruption and integrity requires analysis along tracts and within cross-sections, which is hard to accomplish by conventional region of interest or voxel-based analysis. We have developed and tested a new framework for MR DTI analysis that includes tractography, fiber clustering, and diffusion tensor analysis across and along tracts, potentially leading to better accuracy. The validation study demonstrates the good reproducibility in a test/re-test validation.

References:

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