Evaluation of pre-defined atlas based ROIs for the analysis of DTI data in Normal Brain Development.

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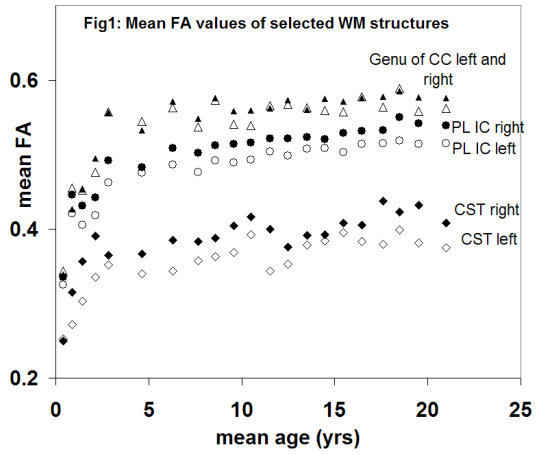
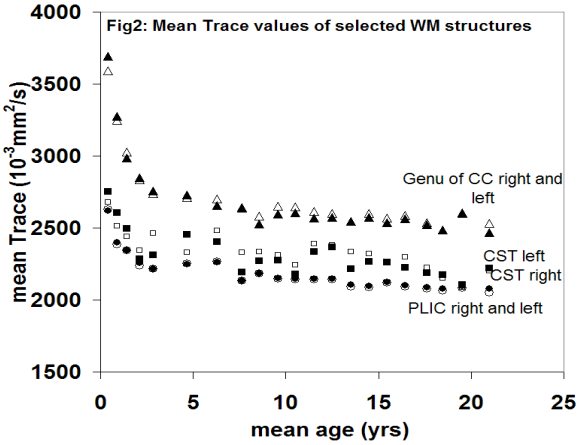
Introduction: Neurodevelopment of healthy pediatric populations has been studied using DTI over various age ranges and with various analysis methods [1-6]. Recently, data from the DTI component of the NIH MRI Study of Normal Brain Development (PedsDTI) have been made available to the public [9]. This study represents the largest prospective DTI study of normal brain covering the entire developmental age range from 0 – 22 years performed to date. We address the issue of evaluating an analysis tool that can be used effectively and efficiently to extract information from this large number of datasets. Atlas based image analysis using Large Deformation Diffeomorphic Metric Mapping (LDDMM) [7] has been previously used in deriving age specific diffusion metrics using an adult template transformed to the subject native space [6]. Here we will assess the feasibility of using these pre-defined regions of interest to extract developmental trajectories of fractional anisotropy (FA) and mean diffusivity (Trace(D)) on age specific group average brains computed from the PedsDTI database.

Method: For the PedsDTI project, subjects were scanned at five imaging centers in the United States on a 1.5T scanner (GE or Siemens). DTI data was acquired with 3mm isotropic resolution, contiguous slices for full brain coverage, slice thickness=3mm, 6 diffusion sensitization directions (b=1000s/mm^2) plus 1 b=0s/mm^2 image repeated 4 times, no averaging, for a total of 28images/slice. DTI data included in the PedsDTI repository were pre-processed using the TORTOISE pipeline [10] and rigorously assessed for quality [11]. In this study, we used age specific average brains (minimum of 10 scans per average) that were created using the non-liner tensor registration software, DTITK[8] from 449 scans of 274 subjects (aged 15 days–22.2 years, 140 female). From each age specific average tensor, average FA and Trace(D) maps were calculated and further processed to enable applying the pre-defined set of 176 ROIs [6,7] using the diffeomap software [http://MRIStudio.org]. Mean FA and Trace(D) values were extracted from the ROIs and plotted as function of mean age.





Results and Discussions: In fig1 and fig2 we present results for representative white matter (WM) regions. The general trend observed is an increase in FA and a decrease in Trace(D) with age, with regional characteristics in agreement with previous DTI studies [1-6]. Therefore, one positive aspect is that the predefined set of ROIs seems able to capture important developmental trends. However, potential limitations of the approach can also be noticed. A puzzling result, for example, is the presence of significant differences in FA values between right and left homologous regions, particularly for small brain structures such as the cortico-spinal tract (CST) or for larger structures that are surrounded by heterogeneous tissue such as the posterior limb of internal capsule (PLIC). In addition, thin structures (eg: CST) show a somewhat jagged trajectory, with large FA and Trace(D) differences from one age point to the next. These behaviors are likely to be attributable to a systematic inaccuracy in the placement of the atlas based ROIs. This conclusion is supported by the fact that these differences were much smaller when we independently drew ROIs on the affected structures. Moreover, our findings with the atlas-based ROI analysis are inconsistent with differences in DTI metrics between left and right structures previously reported in the literature [12].

Conclusion: The use of an independent, previously defined, atlas-based set of ROIs, was successfully applied to a large set of DTI data producing reasonable developmental trajectories. However, bias originating from inaccurate ROI placement can be observed, resulting in exaggerated and spurious differences between left – right homologous structures.

References: [1] P.Mukherjee et al., November 2001 *Radiology,* 221, 349-358, [2] L.Snook: NeuroImage 26 (2005) 1164 – 1173, [3] L. Hermoye et al., NeuroImage Volume 29, Issue 2, 2006, Pages 493-504, [4] C. Lebel et al., NeuroImage Volume 40, Issue 3, 2008, Pages 1044-1055, [5] Westlye et al., Cerebral Cortex 2010; 20:2055-2068, [6] A.Faria et al., Neuroimage 2010 15; 52(2): 415–428, [7] Oishi K et al., Neuroimage 2009; 46(2):486-99, [8] Zhang, H., et al, IEEE Trans on Med Img 2007 [9] www.NIH-pediatricMRI.org [10] C.Pierpaoli et al., ISMRM 18th annual meeting, Stockholm, Sweden, #1597, [11] A.Nayak et al., *Proc. Intl. Soc. Mag. Reson. Med.* 19, p. 2342., [12] J.S.Verhoeven Human Brain Mapping (2010) Volume: 31, Issue: 3, Pages: 470-486.