Generating a human neonatal brain atlas for superior normalization accuracy

Yajing Zhang[1], Linda Chang[2], Thomas Ernst[2], Jon Skranes[3], Steven Buchthal[2], Daniel Alicata[2], Heather Johansen[2], Antonette Hernandez[2], Robyn Yamakawa[2], Lillian Fujimoto[4], Michael Miller[1], Susumu Mori[5], and Kenichi Oishi[5]

[1]Department of Biomedical Engineering, Johns Hopkins University, Baltimore, Maryland, United States, [2]University of Hawaii at Manoa, Honolulu, Hawaii, United States, [3]Department of Laboratory Medicine, Children's & Women's Health, Norwegian Univ. of Science and Technology, Trondheim, Norway, [4]Straub Mililani Clinic, Mililani, Hawaii, United States, [5]Department of Radiology, School of Medicine, Johns Hopkins University, Baltimore, Maryland, United States

Target audience: Clinical researchers, including neonatologists, pediatricians, and neuroradiologists, who are interested in MRI-based markers of normal brain development and developmental abnormalities.

Purpose: To introduce a technology to create a study-specific neonatal brain DTI atlas with a detailed parcellation map of neuroanatomical structures, to achieve accurate measurement of structure-specific neurodevelopment. A neonatal brain template in the general space (JHU-neonate atlas) has been developed for analyses of T1w, T2w and DTI images of neonatal brains. Although the accuracy of the structural segmentation based on the JHU-neonate atlas[1], combined with diffeomorphic image transformation, is substantially high, studies from adult brain MRI have suggested that a study-specific template for the neonate could achieve higher image transformation accuracy, especially when targeting diseased brains. In this paper, a method to create a study-specific neonatal brain DTI atlas, based on Bayesian estimation[2], is introduced and validated. Using this method, users could avoid manual drawing of three-dimensional regions-of-interests, which is prohibitively labor-intensive.

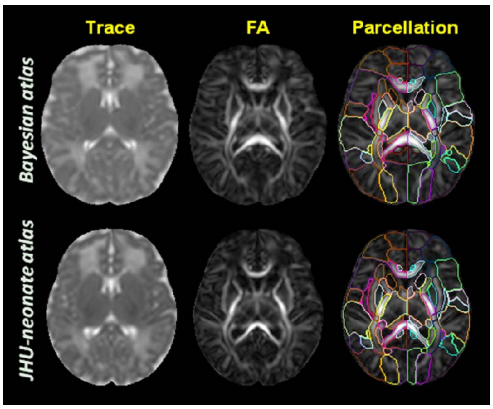

Fig.1. The study-specific Bayesian atlas (upper row) and the JHU-neonate atlas (bottom row). The Bayesian atlas adjusted the brain shape based on the studied population.

Methods: Nine DTI scans of normal neonates, 39~42 weeks of age, were acquired at the Queen's Medical Center, University of Hawaii (matrix size: 80 x 80 x 40, FOV: 160 mm x 160 mm, slice thickness: 2.5 mm). The FA and TRACE contrasts were calculated, and the images were skull-stripped and rigidly aligned according to the AC-PC line. The high-resolution JHU-neonate atlas (matrix size: 180 x 220 x 180, with 0.6 mm isotropic resolution) served as the initial template, and the clinical images were re-sampled to match its dimensions. A Bayesian atlas and its parcellation map were generated through the template estimation algorithm[1]. Nine tissue structures were manually delineated in the Bayesian atlas. Image registration accuracy using the two atlases was examined by Dice overlap[3].

Results: The Bayesian neonate atlas is shown in Fig.1. There were 122 structural parcellations automatically acquired from the initial template. The brain shape was adjusted to the studied population, e.g., the frontal lobe appears bigger than the JHU-neonate atlas. The registration performances for all subjects are shown in Fig.2. The new atlas achieved higher registration accuracy in the corpus callosum, the core deep gray matter structures (such as the thalamus and the lenticular nucleus), and the peripheral structures (such as the pre-central white matter and the superior temporal white matter). Using the Bayesian atlas, improved registration was observed in all structures. Two-way ANOVA showed statistical significance for the use of the two atlases for segmentation ($p<<0.05$). Fig.3 showcased the automated segmentation results from the JHU-neonate atlas and the Bayesian atlas. The result from the JHU-neonate atlas segmented a larger lenticular nucleus and a smaller thalamus region than the manual delineation.

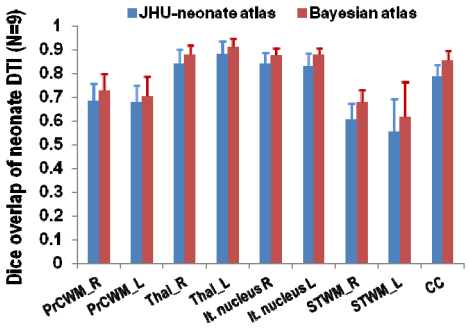

Fig.2. The registration performance of the JHU-neonate atlas (blue) and our Bayesian atlas (red) on the dataset.

Discussion: The study-specific Bayesian atlas provided better image normalization than the general JHU-neonate atlas in all measured structures, probably because it is a better representation of the average features of the study population.

Conclusion: The relevance of this study is that it provides an automated framework to create a study-specific neonatal brain atlas with neuroanatomical parcellation for use in future studies of neonatal pathology. Improvement in registration accuracy in major deep gray matter and peripheral white matter structures has potential impact in detecting subtle abnormalities related to developmental abnormalities. The neuroanatomical parcellation is based on that of the JHU-neonatal atlas, but was customized to the study population. Thus, the results of the atlas-based analyses can be reported in a consistent way among the research community.

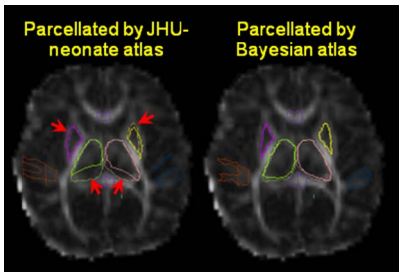

Fig.3. Automated parcellation using the two atlases for one representative neonate brain. Manual delineation overlaid (dashed lines).

References: **1.** K. Oishi, et al. Multi-contrast human neonatal brain atlas: Application to normal neonate development analysis. Neuroimage 2011: 56(1); 8-20. **2.** Y. Zhang, et al. Creation of a population-representative brain atlas with clear anatomical definition. Proc. Intl. Soc. Mag. Reson. Med. 19 (2011), pp.135. **3.** T. Ratnanather, et al. Validation of semiautomated methods for quantifying cingulate corticalmetrics in schizophrenia. Psychiatry Res. 2004: 132: 53–68. **Grant support:** NIH grants R01HD065955, U54NS/DA056883, K02DA16991, and K24DA16170