

# Towards the "Baby Connectome": Mapping the Structural Connectivity of the Newborn Brain

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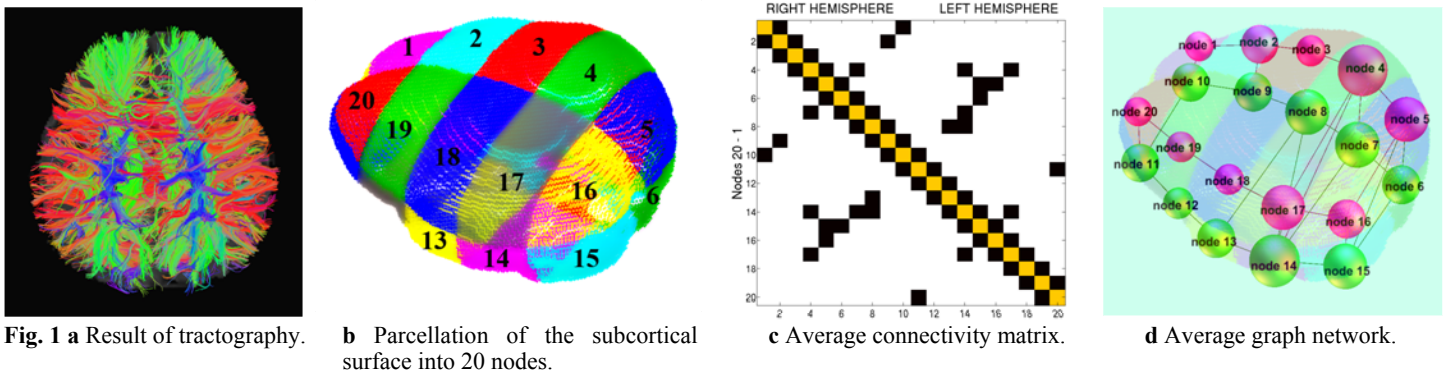
**Introduction.** Defining the structural and functional connectivity of the human brain (the human "connectome") is a basic challenge in neuroscience. Recently, techniques for noninvasively characterizing structural connectivity networks in the adult brain have been developed using diffusion MRI [1-3]. The purpose of this study was to establish a robust framework for assessing structural connectivity in the newborn brain and to study network properties in a clinical cohort of six month old infants.

**Methods.** As part of a study on neonatal encephalopathy, DTI was performed on 10 term-born neonates at the age of six months who had transient encephalopathy at birth, but no evidence of brain injury. The babies were scanned on a 3T GE EXCITE MR scanner using half-Fourier SE EPI with a FOV of 24 cm, 128x128 matrix zero-filled to 256x256, min TE, 30 directions, b-value = 700 s/mm<sup>2</sup>. Data were processed and used to construct structural networks using the following steps in Matlab, FSL [4], and Diffusion Toolkit [5]:

- To insure data quality, an automated rejection algorithm was first employed to identify and discard directionally-encoded measurements distorted by motion. Images, which demonstrated intensity ripples or signal loss due to the k-space center displacement in half-Fourier imaging [6], were identified as outliers.
- The modified raw diffusion data were corrected for eddy current distortions and affine head motion. Tensor-based reconstruction and deterministic whole-brain streamline fiber tractography was undertaken on the resulting data using standard techniques.
- The algorithm for assembling the structural network included subcortical surface extraction, surface parcellation, identification of white matter tracts connecting individual nodes, and finally, assembling the connectivity matrix. Network nodes were defined by partitioning the subcortical surface into spatial regions of equal spatial extent along x, y and z. This approach differs from template-based techniques in that nodes were not anatomically predefined. This equal partition approach is straightforward and more suitable for the rapidly changing newborn brain.
- Binary connectivity matrices were built for each subject by thresholding the weighted matrices. The average matrix across all 10 subjects was analyzed and visualized using the brain connectivity toolbox [7] and network graph analysis software Gephi [8].

**Results.** Figs. 1a and 1b show examples of the tractography and parcellation of one subject's brain into 20 distinct cortical nodes. Figs. 1c and 1d show the average connectivity matrix and graph network. The size of the nodes in the graph network (Fig. 1d) corresponds to the degree of the node. The average clustering coefficient (a measure of segregation) was 0.15, and the characteristic path length (a measure of integration) was 2.81. The infant network showed small-world properties.

**Discussion.** We have developed a robust technique to study the structural connectivity of the newborn brain using diffusion MRI, and used this approach to characterize the common axonal connectivity pattern of the cortex across 10 six month old babies. The procedure can be applied to newborns of different age, including premature babies, and thereby provide a novel tool for studying structural maturation of the brain. Previously, developmental trajectories could only be studied by measuring anatomy and analyzing separate DTI tracks using tract- or region-of-interest based analysis. The proposed approach allows automated, unbiased study of the network properties of the brain using graph theoretic analysis. The baby connectome will significantly increase our understanding of how brain structure and resulting functionality mature, and will provide insights into how functionality is affected when normal network structure is disrupted.



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**References.** [1] Hagmann P et al (2007) PLoS ONE 2:e597. [2] Iturria-Medina Y et al (2008) Neuroimage 40(3):1064-1076. [3] Gong G et al (2009) Cereb. Cortex 19(3):524-536 [4] Smith SM et al (2004) NeuroImage, 23(S1):208-219. [5] Wang R et al (2007) Proc ISMRM, #3720. [6] Storey P et al (2007) MRM 57:614-19. [7] Rubinov M & Sporns O (2010) NeuroImage 52:1059-1069. [8] Bastian M et al (2009) Proc. AAAI ICWSM.