Novel probabilistic neonatal cortical brain atlas

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Target audience Scientists and clinicians utilising neonatal and developmental neuroimaging

Purpose Understanding infant brain development in healthy and clinical populations helps create and assess interventions that can improve cognitive and functional outcomes throughout life. Critical to investigating structure and function of the infant brain are neuroimaging tools attuned to accommodate tissue types and morphological subtleties that are characteristic of this developmental stage. Such tools should provide accurate parcellation and identification of brain regions, and avoid warping infant brains into an adult template space. The purpose of this project is to provide a freely available, high quality probabilistic neonatal cortical brain atlas, analogous to the commonly used Desikan-Killiany adult brain atlas available in Freesurfer software.

Methods ***Participants*** Initial participants were 3 healthy term-born (≥37 weeks' gestation) control neonates (1 female, 2 male; gestational age at scanning 40.29-43.00 weeks, M = 41.23, SD = 1.52) selected from a cohort of 50 controls with MRI scans that were recruited as part of a preterm study.[1] The subset was selected based on minimal motion or other artifact on T_2-weighted images. ***MRI acquisition*** Imaging was conducted at Royal Childrens Hospital, Melbourne, Australia, on a 3T Siemens Magnetom Trio Tim scanner during infants' natural sleep. A transverse T_2 restore turbo spin echo sequence was used with: 1 mm axial slices, flip angle = 120°, TR = 8910 ms, TE = 152 ms, FOV = 192 x 192 mm, matrix = 384 x 384, in-plane resolution 0.5 mm^2. ***Preprocessing*** T_2 images were AC-PC aligned and resampled to 0.63 mm^3 isotropic voxels. ***Tissue classification*** Automatic tissue classification was performed on the T_2 images using an in-house pipeline. This adapts to the morphological and tissue intensity differences seen in neonates, and is similar to a previously published technique,[2] incorporating the unified segmentation process implemented in SPM8. Cortical grey matter, white matter, cerebrospinal fluid, brainstem, cerebellum, amygdala, hippocampus and deep nuclear grey matter were segmented. The cortical gray matter mask was isolated for further parcellation. ***Manual segmentation*** 33 cortical areas per hemisphere were manually traced (Figure 1a,b), corresponding to those in the Desikan-Killiany[3] adult brain atlas available in Freesurfer, with the addition of insula. Tracing was performed using ITK-SNAP v2.2.0 (www.itksnap.org), based on the T_2 images using a sulcal approach.[3] The Freesurfer atlas was used as a visual reference, and an anatomical atlas[4] was referred to in case of ambiguities. ***Template construction*** A T_2 structural template was generated with ANTS v1.9 (http://stnava.github.io/ANTs), using symmetric diffeomorphic transformation (Figure 1c). Manually segmented images were transformed to the template space per individual, and structure probability maps for each cortical region were constructed.

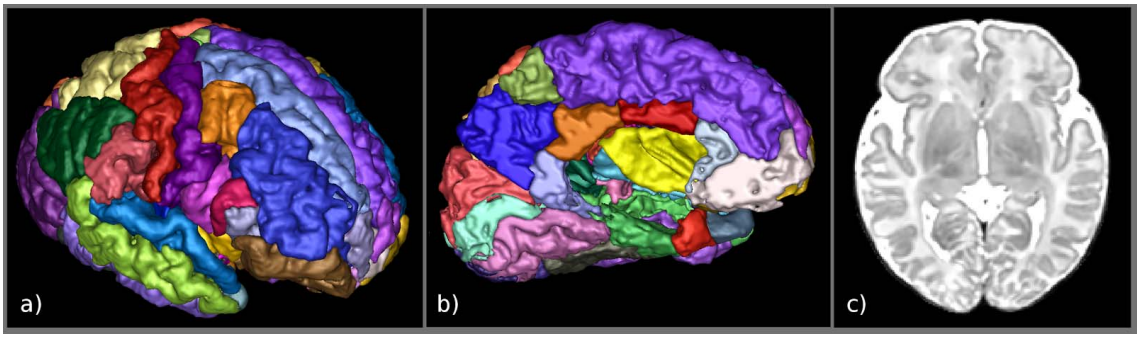

Figure 1. a) lateral and b) medial views of manually traced areas on 3D cortical mesh reconstruction of one representative participant, c) Initial structural T_2 template image.

Discussion & Conclusion This high quality atlas will be incorporated into a freely accessible infant segmentation and parcellation toolbox that will facilitate research into the neonatal brain, furthering the ability to understand brain development at this critical timepoint.

References

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