Towards a Connectome Mapping Pipeline for Neonates Using High-Resolution MP2RAGE and DTI

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Introduction

Exploring the anatomical and functional connectivity between different regions of the brain (the "Connectome") is a core challenge in neuroscience. While robust methods are available for the adult brain, mapping the connectome in neonates is much more complex. The purpose of this pilot study is to present a methodological approach for analyzing structural connectivity of a neonate brain and to exploit the MP2RAGE sequence with its advantageous contrast properties.

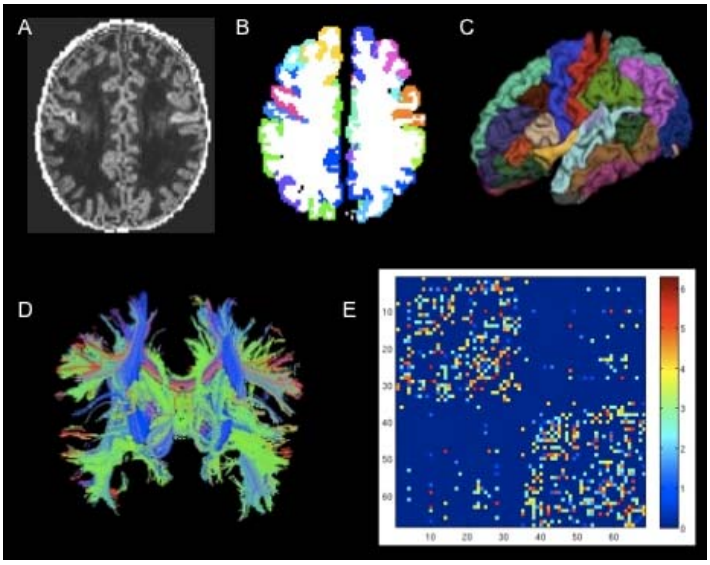
Material and Methods

A prematurely born pilot subject (27 weeks gestational age (GA)) was scanned at term equivalent age. The structural images were obtained with a 3T (MAGNETOM TrioTim, Siemens Healthcare, Germany) and a dedicated 8-channel baby head coil (NOMAG) using a double-echo MP2RAGE sequence with the following parameters: TI1/TI2/TR= 800/2200/5000 ms, TE=4.62 ms, GRAPPA R=2, TA=5:57 min. Per echo time, two image volumes were thus obtained (at the 1st and 2nd inversion time 'INV1' and 'INV2'), from this data two images were reconstructed: a bias-free T1-weighted image (flatImg) and a T1 relaxation map (T1) [1]. Acquisition was sagittal with isotropic voxels of 1.2mm, in plane matrix size of 128x128 and 96 slices. For the MR diffusion images we used a twice-refocused spin echo EPI sequence with TR/TE= 5200/84 ms and a spatial resolution of 2 mm^3 isotropic with a plane matrix of 96x96 and 43 slices. 11 b0-images and 72 diffusion-weighted images with b-value of 1000 s/mm2 were acquired with varying directions.

A brain mask was derived using standard FSL BET2 tool [2] based on the T1 relaxation map. The fractional intensity threshold and its vertical gradient were manipulated to account for the smaller size of the infant brain. For all contrasts, a rigid registration to the preexisting neonate template created by Shi et al. [3] was performed. This was followed by a probabilistic tissue classification in the flatImg contrast using a native SPM segmentation [4] with probabilistic tissue classification maps by Shi et al. [3]. After manually correcting some topological errors in the white matter (WM) mask, we used it as a mask for streamline fiber tractography (Diffusion Toolkit, 35° angle threshold). To identify connected cortical regions, the subcortical surface needs to be extracted and surface parcellation has to be performed. FreeSurfer [5] is providing these two maps, by doing skull stripping and segmentation steps in its default mode. Since we already had created a skull-stripped image and a white matter mask, these initial operations were not necessary. We just fed the INV1 contrast and our previously computed masks upstream into the FreeSurfer surface reconstruction process. The pipeline was able to reconstruct the surface of the grey-white matter junction and to automatically assign neuroanatomical labels to each location on the surface based on Desikan-Killiany Atlas [6]. The surface labels were converted to cortex volume labels to use it as Regions of Interest (ROIs). If fibers with two end points located in their respective ROIs were present, two labels were considered to be connected. As final step a structural connectivity matrix was computed. Each fiber resulting from the tractography process was assigned to a ROI-to-ROI connection, if its two endpoints were located within the two ROIs volumes. In this way two regions are considered connected if it exists at least one fiber connecting them, and the connectivity strength between each pair of regions (values in the connectivity matrix) is given by the number of connecting fibers.

Results

Figures A-E display the different steps in our connectome mapping pipeline. On Fig. A we can see the flatImg contrast after skull-stripping. Fig. B shows the white matter mask and the cortex labels. Fig. C is the surface labeling result of FreeSurfer that we used for cortex parcellation into ROIs. In Fig. D we see the fibers that were calculated during tractography. Fig. E is a plot of our final connectome matrix.



Discussion

There are templates and atlases for neonates that are useful in the segmentation process; furthermore, SPM8 Segmentation tool is able to segment non-conventional contrasts like MP2RAGE in neonates. This contrast is also usable for FreeSurfer to create accurate surfaces and cortex labels. The MP2RAGE sequence provides images of excellent brain tissue differentiation and it is potentially advantageous to T2 weighted contrast in the segmentation process of neonate brains. On the other hand, due to 3D acquisition this sequence is sensitive to head motion.

Conclusion

We developed a connectome mapping pipeline tailored for neonatal images, while exploiting the advantages of MP2RAGE sequence.

References

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