

@e_thompson93 elinor.thompson@nottingham.ac.uk

Data-driven Mapping of Structural Connectivity Patterns in the Neonatal Brain

Elinor Thompson¹, Saad Jbabdi², Matteo Bastiani^{1,2}, Stamatios N. Sotiropoulos^{1,2}

1 – Sir Peter Mansfield Imaging Centre, School of Medicine, University of Nottingham, UK 2 – Wellcome Centre for Integrative Neuroimaging – FMRIB, University of Oxford, UK



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Why use data-driven methods?

Standard tractography protocols rely on the delineation of ROIs relative to a template [1]. This is not straightforward to implement in neonatal subjects, due to the rapid brain changes in the first weeks of development. As an alternative, we propose here data-driven methods to identify white matter pathways and their corresponding grey matter networks from whole-brain connectivity matrices [2]. This approach is more immune to the morphological changes that occur during early development and also paves the way for multi-modal data fusion in connectivity analysis (for instance using diffusion and functional MRI jointly to infer connectivity).

Methods

We designed a data-driven framework for the simultaneous extraction of white matter bundles and their corresponding grey matter networks from diffusion MRI data. We first performed probabilistic tractography on data from 36 neonates, from the first release of the developing Human Connectome Project (dHCP) [3,4], to obtain a grey matter to



We used *independent component analysis (ICA)* and *non-negative matrix factorisation (NMF)* [6], as two alternatives for the decomposition. NMF constrains both the mixing matrix and the components to contain positive values, so is a more natural fit for our inherently non-negative structural data. For the matrix decomposition X = WH, the NMF objective function is $F = \frac{1}{2} \|X - WH\|_F + 0.1 \|W\|_{L1} + 0.1 \|H\|_{L1}$, where $\|x\|_F$ is the Frobenius norm and $\|x\|_{L1}$ is the L1 norm, used to increase sparsity. Promoting

sparsity also effectively promotes independence, so the NMF components resembled ICA ones, with the positivity-constraint inherently considered.

Results

Data-driven patterns closely match results from standard tractography

Component scores correlate with age

To obtain subject-specific representations of the components, we performed dual regression [5]. Component scores were calculated as the correlation between the subject-specific components and their group-level equivalent. The scores of two grey matter components increased significantly with subjects' age at scan, indicating a reduction in variability with age, as the white matter connections become better



paired ICA components

paired NMF components





positive













negative









NMF improves interpretability, compared to ICA



Components can be used as features to classify infants born pre-term



The Boruta algorithm [7] shuffles the feature values to generate "shadow features". It then trains a random forest classifier and retains features that perform significantly



better than the shadow features over a number of iterations. NMF features selected:



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References: [1] de Groot et al, Neuroimage (2013). [2] O'Muircheartaigh & Jbabdi, Neuroimage (2017). [3] Hughes et al, Magnetic Resonance in Medicine (2017). [4] Bastiani et al. Neuroimage (2018). [5] Filippini et al PNAS (2009). [6] Lee & Seung, Advances in Neural Information Processing Systems (2001). [7] Kursa & Rudnicki, Journal of Statistical Software (2015). [8] Beckmann & Smith, IEEE Trans. on Medical Imaging (2004)