Parcellation-Independent Framework for Analysing Developing Brain Networks Using Reparametrisation

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Abstract
Brain connectivity may be studied with diffusion MR (dMR), tractography and network theory. However, the lack of a standard for parcellating the neonatal brain leads to the use of atlas- and random-based methods, and thus to the unresolved challenge of comparing graphs with varying numbers and an unknown correspondence of nodes. We propose a parcellation-independent multi-scale analysis of network measures and show its potential in describing developmental changes in neonatal serial dMRI data.

Network theory in brains
- Network theory is becoming more prevalent in neuroscience, as it:
  - Allows to analyse complex systems
  - Finds connections in data
  - Defines properties of data points

Preterm and neonatal subjects
- High prematurity rate (worldwide ~ 10%)
- Prematurity linked to adverse developmental outcome (~50%)
- Early intervention and targeted support is desirable

The challenge of comparing networks...

Different sets of regions of the same brain

Same structural connectivity

Varying results depending on number of nodes

- Network measures are highly dependent on set of regions parcellation method.

<table>
<thead>
<tr>
<th>Parcellation scheme</th>
<th>Number of nodes</th>
</tr>
</thead>
<tbody>
<tr>
<td>AAL</td>
<td>70-90</td>
</tr>
<tr>
<td>Voxel-based</td>
<td>10^2-10^4</td>
</tr>
<tr>
<td>Stochastic</td>
<td>Specified number ± variation</td>
</tr>
</tbody>
</table>

Parcellation-independent Framework

Figure: A framework for parcellation-independent multi-scale analysis. Each brain image is parcellated at multiple scales from a coarse (larger regions) to a fine scale. Subsequent estimates of structural networks are based on the subjects’ dMRI data. For each network, the fitted models for global network measures over multiple scales, given by

\[ m(G) = a \times \log(N) + b, \]

where \( m(G) \) is a network measure taken on graph \( G \), \( N \) is the number of nodes and \( a \) and \( b \) are the model parameters which are used for group comparison.

Results

Figure: Box-plots for the model parameters \( a \) (left; top) and \( b \) (left; bottom) for each measure at both time points. Values represent the group at each scan, where the subjects of scan one and two were 30.8 ± 1.0 and 41.2 ± 1.2 weeks old, correspondingly.

One and two stars next to the measure name represents \( P \)-values of \( P < 0.01 \) and \( P < 0.001 \), correspondingly.

Conclusion

+ Results independent of specific parcellation
+ Multi-scale analysis, circumventing number of nodes bias

- Fitting function is parameter of framework
- Direct interpretation of results is difficult