Parcellation-Independent Framework for Analysing Developing Brain Networks Using Reparametrisation

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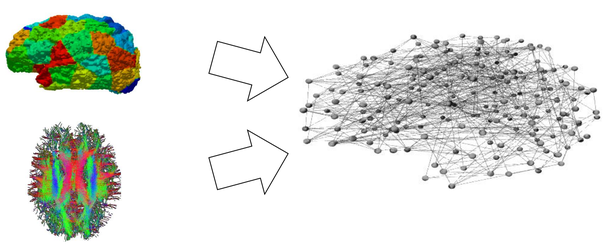
Abstract

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

Divide brain into set of regions

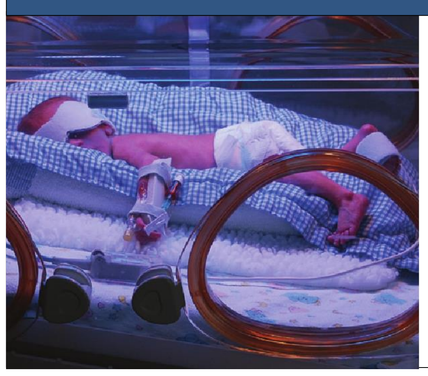


Find connectivity, e.g. diffusion MRI

Network theory is becoming more prevalent in neuro-science, 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

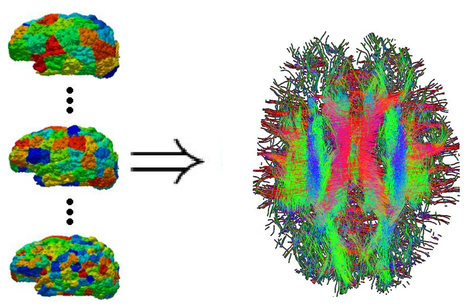
However, no standard set of regions exist for neonates.

→ Stochastic parcellation approaches
- Rely on fewer assumptions
- Need to be repeated multiple times for each subject

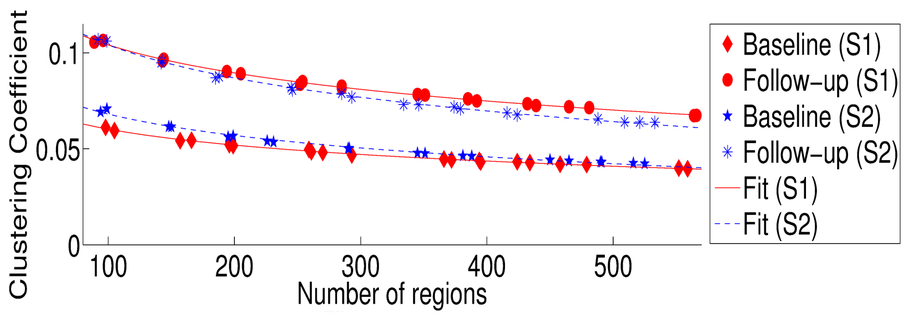
The challenge of comparing networks…

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.

Parcellation scheme	Number of nodes
AAL	70-90
Voxel-based	10^3-10^5
Stochastic	Specified number ± variation

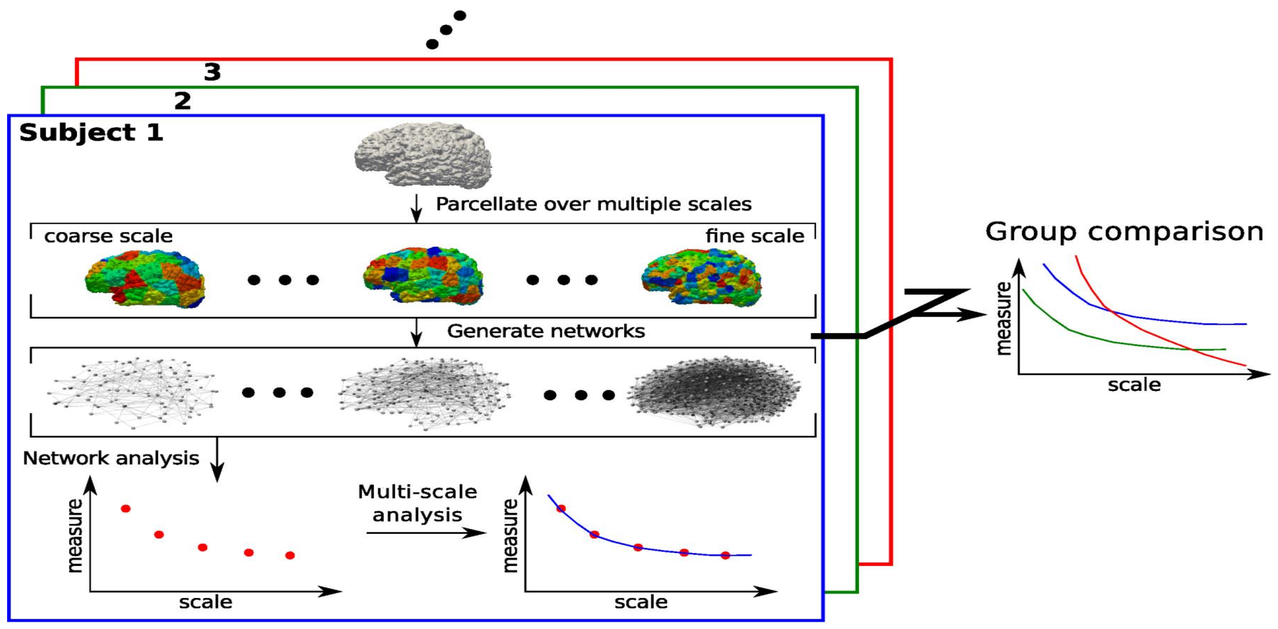
- As a result, comparing across subjects and across studies is difficult.

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

$$m(G) = a * \log(N) + b,$$

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

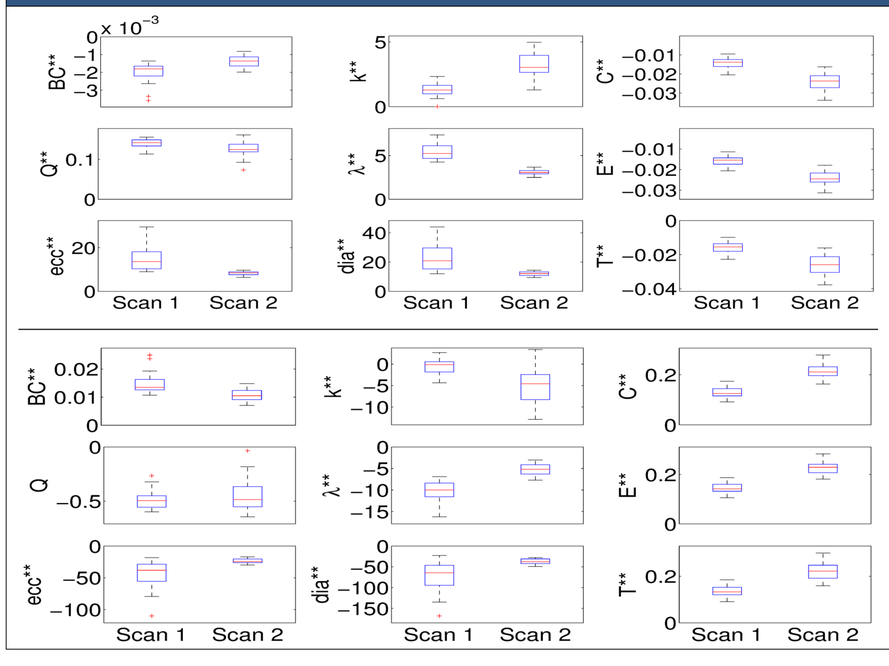


Figure: Box-plots for the model parameters a (left; top) and b (left; bottom) for each measure at both time points. Values represent the group at each scan, where the subjects of scan one and two were 30.8 ± 1.0 and 41.2 ± 1.2 weeks old, correspondingly.

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