

Stochastic DCM of the DMN using resting-state fMRI: test-retest reliability



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Summary

Most analyses of task-free fMRI have focused on functional connectivity using seed-based correlation analysis (SCA) or independent component analysis (ICA).

Advantages of studying effective connectivity using Dynamic Causal Modelling (DCM) include the ability to compare competing network structures, and to characterise the directionality of causal influences.

DCM was originally unsuited for resting-state data; the stochastic formulation (sDCM) opens up this possibility, but has not yet been widely used. The purpose of this work is to determine the test-retest reliability of sDCM, and to compare this to that of functional connectivity.

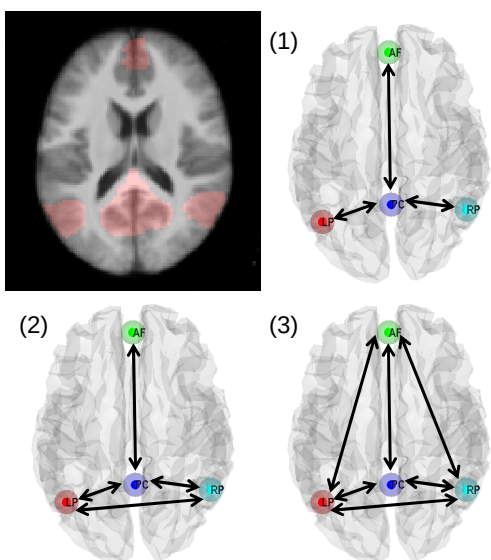


Figure 1. Four clusters from the Default Mode Network independent component from Smith et al. (2009); three candidate DCMs, each progressively more connected.

Background

Resting-state fMRI allows the study of multiple intrinsic connectivity networks without requiring several complex experimental designs. Its simplicity of acquisition, ease of sharing, and applicability to patient studies without risk of task-difficulty issues has created large amounts of data (e.g. Biswal et al., 2010; Van Essen et al., 2012), and generated great interest in clinical utility (Damoiseaux, 2012).

DCM (Friston et al., 2003) is a principled approach for the study of effective connectivity using Free-Energy-based Bayesian inversion of generative dynamical systems models.

DCM has recently been extended with the addition of endogenous stochastic innovations (Li et al., 2011), enabling use on resting-state data; sDCM has the potential to discover subtle effects of group or condition on effective connectivity (Li et al., 2012), but its power (e.g. as a clinical biomarker) will depend on its stability and precision. We therefore investigate its reproducibility using publicly shared test-retest data (Shehzad et al., 2009).

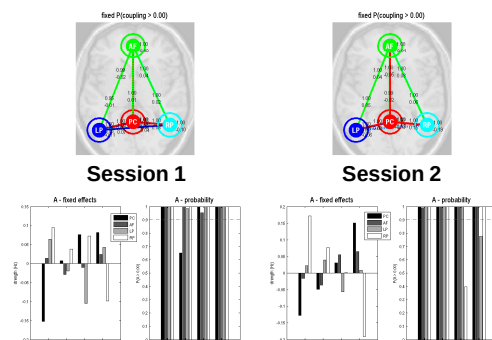


Figure 2. Example sDCM model fits for one subject, using the fully connected model 3.

Methods

25 subjects were scanned 3 times; session 2 was 5-11 months after the first, session 3 was < 45 minutes after 2. Data were processed in SPM8: fMRI data were realigned; anatomical scans underwent unified ("new") segmentation, yielding a bias-corrected skull-stripped image; fMRI data were co-registered to this image; spatial normalisation used warps from unified segmentation; 6mm smoothing was applied.

First-level GLMs contained only realignment parameters; a 128s high-pass filter was used. Eigenvariate were extracted for the 4 largest connected components above a threshold of 3 on the resting-state independent component corresponding to Smith et al's DMN (Fig.1).

DCMs were fitted using SPM12b. Random-effects (RFX) Bayesian model selection (BMS; Stephan et al., 2009) was performed over subjects separately for each session.

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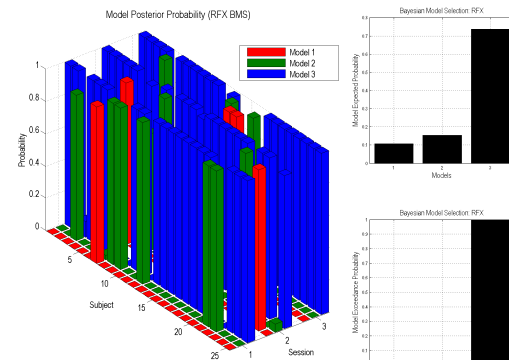


Figure 3. RFX Bayesian Model Comparison.

Results and Discussion

An example of a fitted model (3) is shown in Fig.2. Fig.3 shows BMS results. In all sessions, the model expected probability is >0.68 for model 3, and its exceedance probability is >0.99. However, only 15/25 subjects have consistent model selection in sessions 2 and 3.

Model 3 parameter estimates are summarised in Fig.4. Mean (SD) intraclass correlation coefficient (ICC) between sessions 2 and 3 is 0.321 (0.253), which is comparable to functional connectivity results reported by Shehzad et al. (2009); however, ICCs between session 1 and 2 or 1 and 3 are poor. Overall patterns are similar, but outlier patterns differ, which might indicate convergence to different local optima. This issue could be addressed with techniques such as Gaussian process global optimisation (Lomakina et al., 2012).

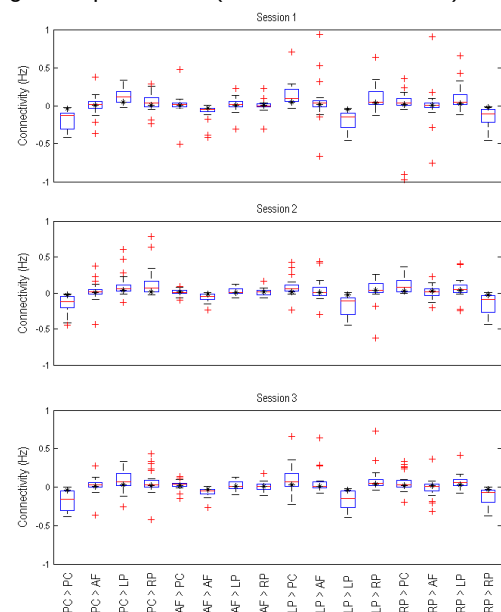


Figure 4. Box-plots (variation over subjects) for posterior mean connectivity strengths.

