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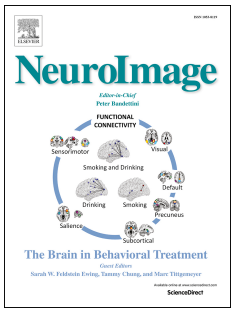


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ACCEPTED MANUSCRIPT

# Multi-subject hierarchical inverse covariance modelling improves estimation of functional brain networks

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## Abstract

A Bayesian model for sparse, hierarchical inverse covariance estimation is presented, and applied to multi-subject functional connectivity estimation in the human brain. It enables simultaneous inference of the strength of connectivity between brain regions at both subject and population level, and is applicable to fMRI, MEG and EEG data. Two versions of the model can encourage sparse connectivity, either using continuous priors to suppress irrelevant connections, or using an explicit description of the network structure to estimate the connection probability between each pair of regions. A large evaluation of this model, and thirteen methods that represent the state of the art of inverse covariance modelling, is conducted using both simulated and resting-state functional imaging datasets. Our novel Bayesian approach has similar performance to the best extant alternative, Ng *et al.*'s Sparse Group Gaussian Graphical Model algorithm, which also is based on a hierarchical structure. Using data from the Human Connectome Project, we show that these hierarchical models are able to reduce the measurement error in MEG beta-band functional networks by 10%, producing concomitant increases in estimates of the genetic influence on functional connectivity.

KEY WORDS: fMRI; MEG; *functional connectivity; Gaussian graphical models; hierarchical Bayesian models; concentration graph; precision model; inverse covariance model;* MCMC.

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