Dynamic causal modelling of fMRI with neural mass models

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INTRODUCTION
The aim of this work was to endow dynamic causal models (DCM) for fMRI time series with a greater biological realism. DCM is a natural extension of the convolution models used in the standard analysis of fMRI. DCM models neuronal dynamics in each region and the long-range interactions between different regions. We use a Bayesian inversion scheme to estimate the posterior distributions of the generating parameters. Currently, causal models for fMRI consider only one neuronal state per region. In this work we adopt a more biologically constrained and plausible model, using multiple neuronal sources (subpopulations) per region. Critically, this allows us to place positivity constraints on the connectivity such that the model conforms to the organisation of real cortical hierarchies, whose extrinsic connections are excitatory (glutamatergic). Consequently, we can also model changes in both extrinsic and intrinsic connectivity.

METHODS
Usually, DCMs for fMRI are based upon a bilinear approximation to neuronal dynamics with one state per region. In this work we extend this model to cover two states per region. These states model the activity of an inhibitory and excitatory subpopulation. This has a number of key advantages. First, we can relax the shrinkage priors used to enforce stability in single-state DCMs because the interaction of excitatory-inhibitory pairs confers dynamical stability on the system. Second, we can model both extrinsic and intrinsic connections. Third, we can enforce positivity constraints on the extrinsic connections (i.e., influences of excitatory sub-populations over regions). Finally, this re-parameterisation enables one to model the effect of context or experimental changes, on the coupling as a proportional increase or decrease in connection strength (c.f., the additive bilinear effects used previously). The model and mathematical forms are provided in Figure 1.

EMPIRICAL DEMONSTRATION
We used this new model to assess the site of attention modulation during visual motion processing in an fMRI paradigm previously reported by Buchel and Friston\textsuperscript{2,3}. For the purpose of this experiment we considered three experimental inputs: A ‘photic stimulation’ variable indicates when dots are on a screen, the ‘motion’ variable indicates that the dots are moving and the ‘attention’ variable indicates that the subject is attending to possible velocity changes. We used Bayesian model selection to adjudicate between different two-state and one-state models.

CONCLUSION
Our results indicate that one can estimate area-intrinsic connection strengths using fMRI. On real data, we find that the two-state DCM is a better model than the standard single state DCM. The present analysis demonstrates the usefulness of adopting generative models for fMRI time series that are informed by anatomical and physiological constraints.