DCM for resting-state fMRI

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DEMENTIA RESEARCH CENTRE

Learning objectives

1. When and why should you use resting-state DCM?

2. How does it differ from ‘conventional’ DCM?

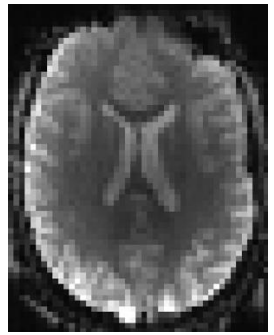
3. What is a spectral DCM?

4. How do you specify a subject level spectral-DCM and test group-level hypotheses? (practical)

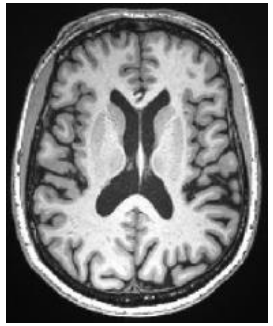
When and why to use resting-state DCM

Why use resting-state DCM?

1. You have / are planning to collect* some resting-state fMRI data



2. You have / are planning to collect some anatomical data

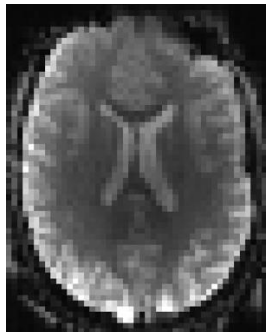


3. **You have a question you want to answer**

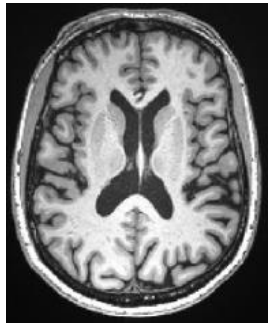
* Would task-based be better for your question?

What do you need?

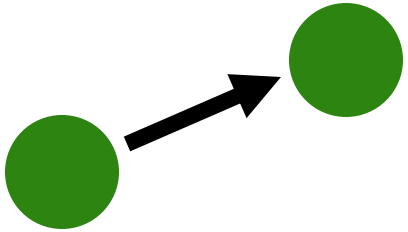
1. Some resting-state fMRI data



2. Some anatomical data



3. **A question you want to answer**
   a) **Some pre-defined regions you are interested in**
   b) **Some hypotheses about how they are communicating with each other**



Defining hypotheses

- DCM is not an exploratory methodology.
- No task – hypotheses are likely to be related to group differences
- Which regions are likely to be important in your group?
- How do you think **directional** connectivity between these regions might change?

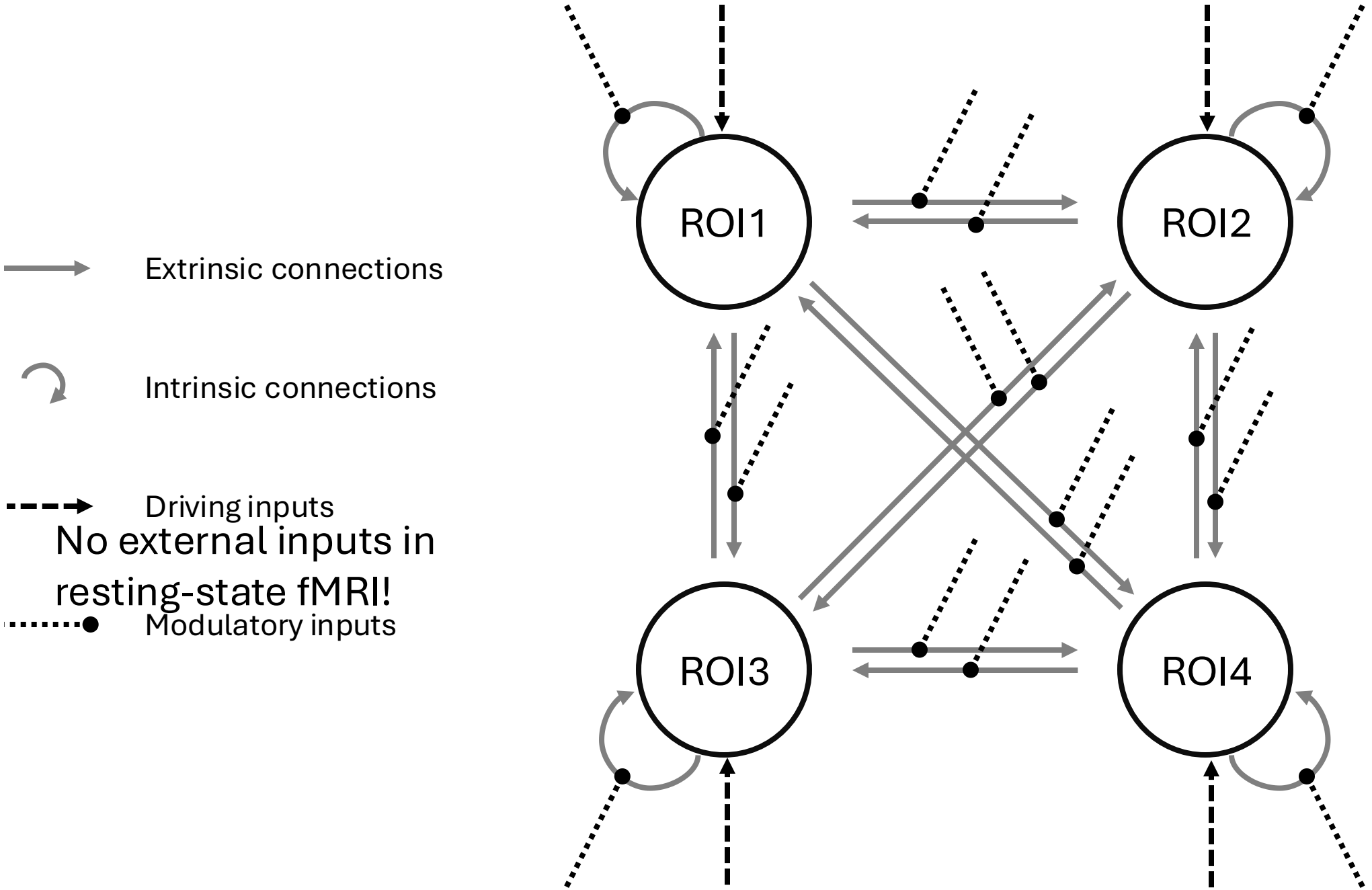
Region selection

- Co-ordinates will not be driven by task activation

- Some other options include:
  - From the literature
  - Structural segmentation
  - Seed-based functional connectivity
  - ICA-type analyses

- **Most importantly – driven by your hypothesis**

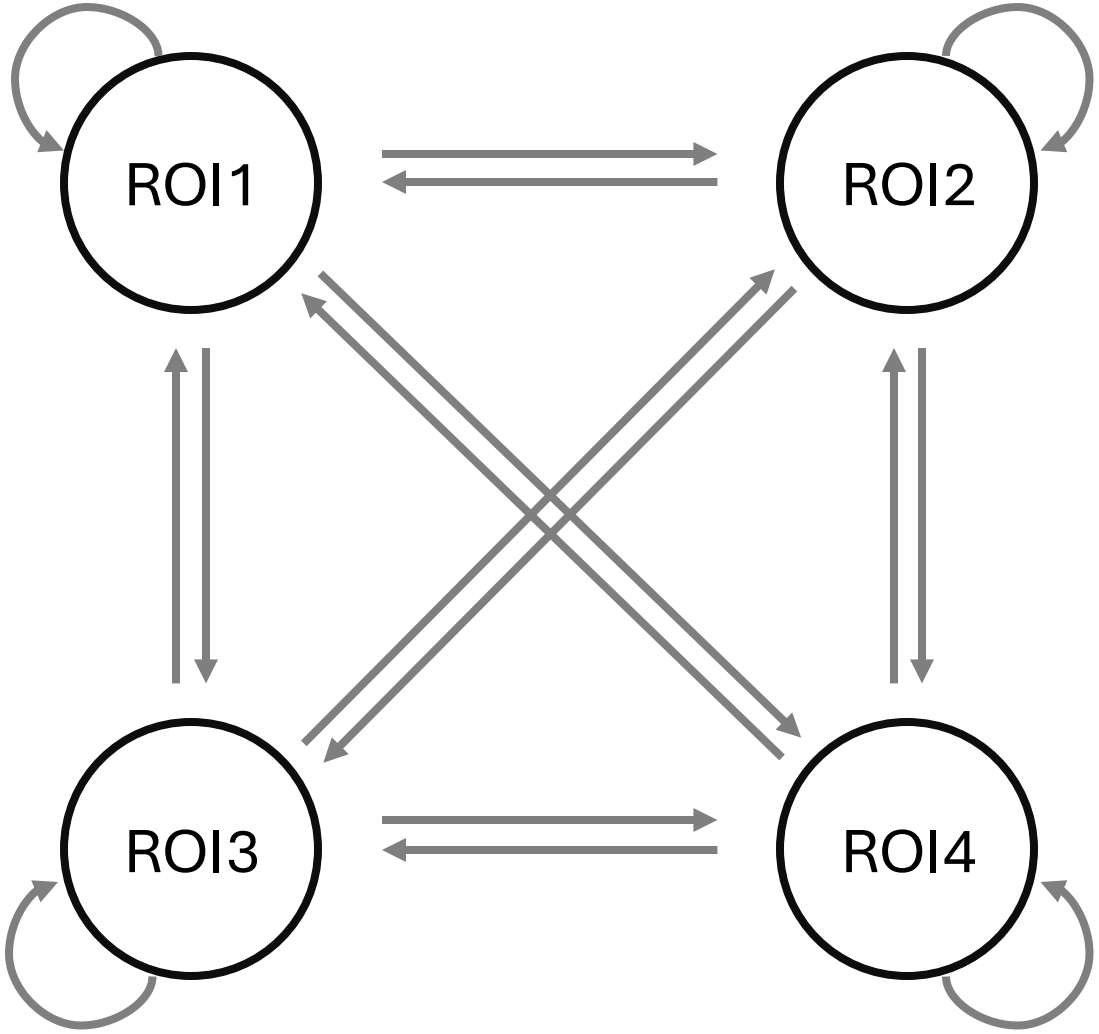
How does resting-state DCM differ from task DCM?


Extrinsic connections
Intrinsic connections
Driving inputs
No external inputs in resting-state fMRI!
Modulatory inputs
ROI1
ROI2
ROI3
ROI4

Extrinsic connections

Intrinsic connections

No external inputs in resting-state fMRI!



$$\dot{z} = Jz$$
$$J = A$$

- No C matrix (driving)
- No B matrix (modulation)
- No inputs (u)
- Just the A matrix (connectivity)

- You just need to define intrinsic and extrinsic connectivity matrices

$$J = \underbrace{-0.5 \cdot \exp(A_I)}_{Intrinsic\ (self-inhibition)} \cdot \underbrace{A_E}_{Extrinsic\ (between-region)}$$

$$A_I = \begin{bmatrix} A_{I\,1} & 0 & 0 & \cdots \\ 0 & A_{I\,2} & 0 & \cdots \\ 0 & 0 & A_{I\,3} & \cdots \\ \vdots & \vdots & \vdots & \ddots \end{bmatrix} \qquad A_E = \begin{bmatrix} 0 & A_{E\,1,2} & A_{E\,1,3} & \cdots \\ A_{E\,2,1} & 0 & A_{E\,2,3} & \cdots \\ A_{E\,3,1} & A_{E\,3,2} & 0 & \cdots \\ \vdots & \vdots & \vdots & \ddots \end{bmatrix}$$

PROBLEM – Nothing is happening!

Zeidman, 2019a, Neuroimage

What drives the system?

$$\dot{z} = f\left(z(t) , \theta^{(n)} \right)$$

Hidden neuronal states

Connectivity parameters

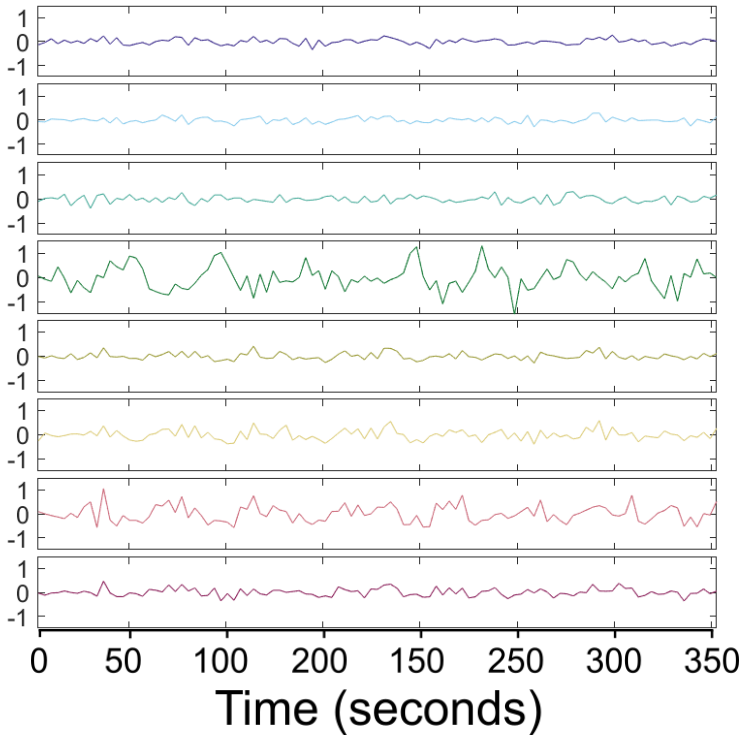
Endogenous neuronal fluctuations

ANOTHER PROBLEM – these fluctuations are time-varying and difficult to estimate

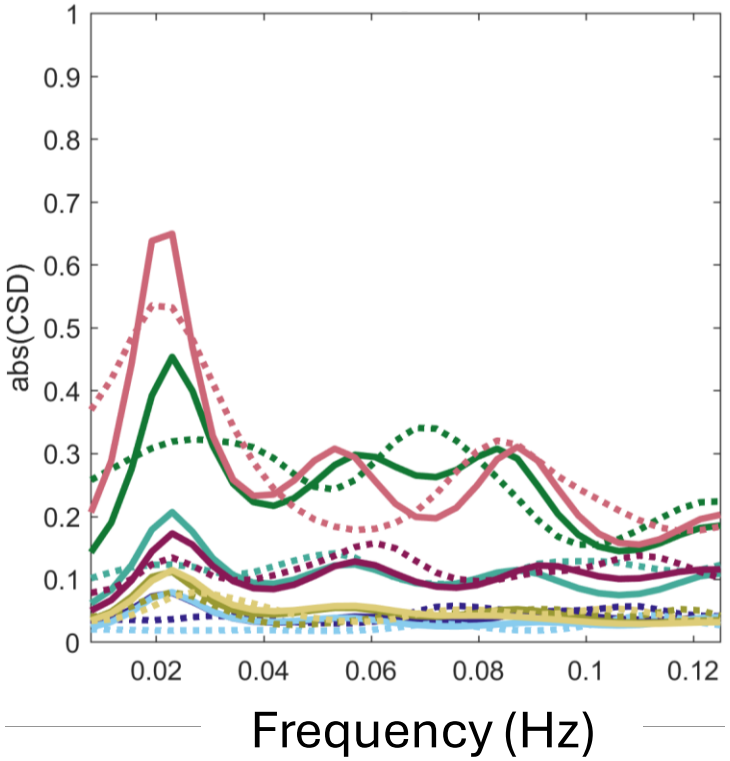
Spectral DCM

Simplifying model inversion

- **Q)** How to simplify computation?
- **A)** Model cross-spectral densities, rather than timeseries



Fourier transform*



* of cross-correlation function

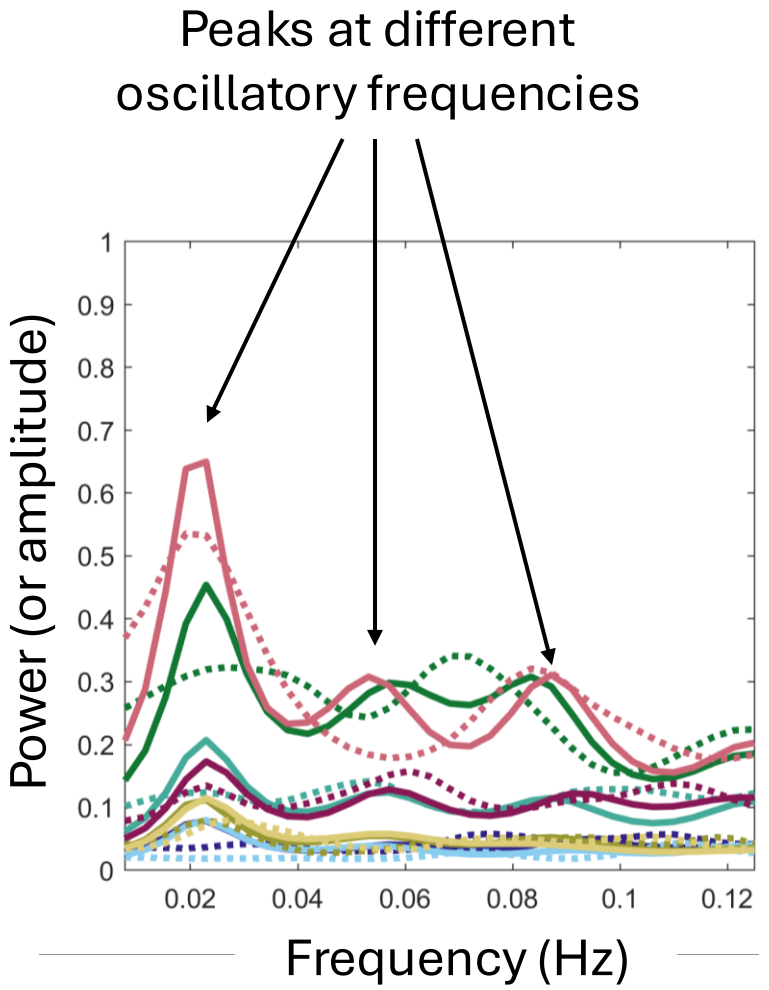
Cross-spectral density

- Correlation in activity between regions (i,j) at different temporal lags (τ)
- At zero lag (τ = 0), this is standard functional connectivity between i,j
- DCM looks at all lags

$$c_{ij}(\tau) = \frac{\rho_{ij}(\tau)}{\sqrt{\rho_{ii}(0) \cdot \rho_{jj}(0)}}$$

Cross-correlation function

Fourier transform



Cross-spectral density

Friston, 2014, Neuroimage

Why is this simpler?

- Move from time to frequency domain
- No longer need to estimate **time-varying** neuronal fluctuations
- Just need to estimate their **time-invariant** covariance

- This can be described by **two** parameters $\{\alpha, \beta\} \subset \theta$:

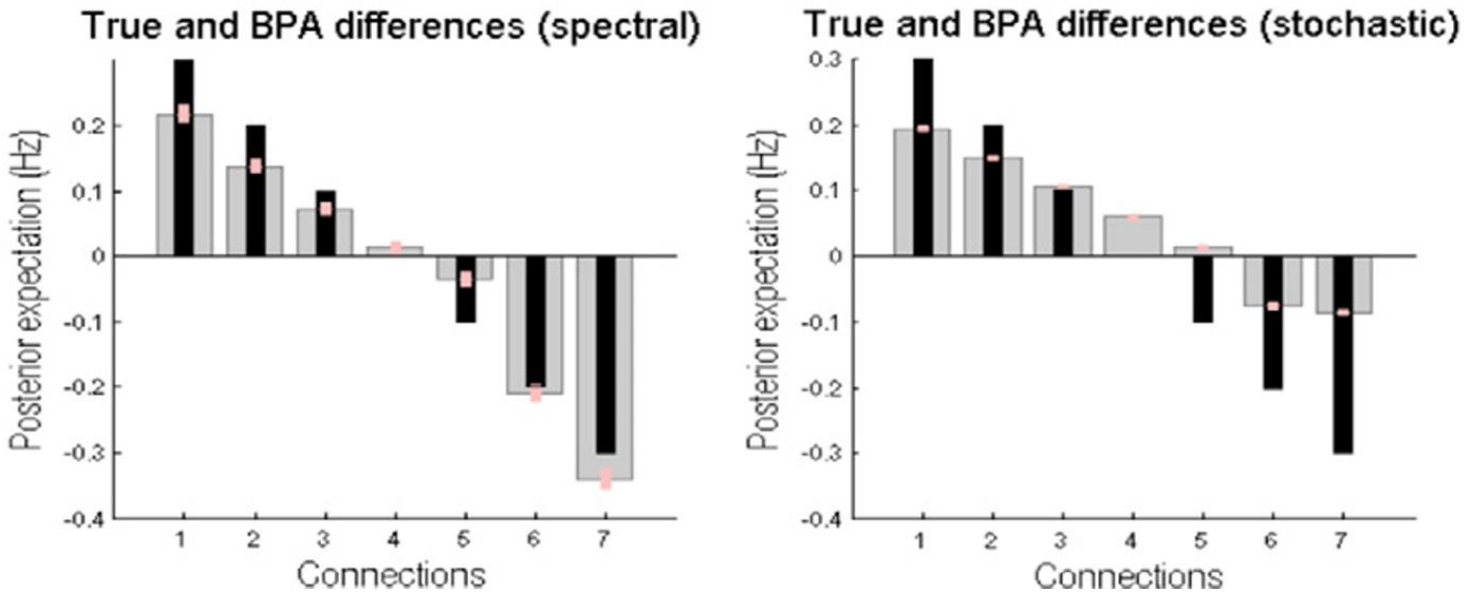
$$g_v(\omega, \theta) = \alpha_v \omega^{-\beta_v}$$

$$g_e(\omega, \theta) = \alpha_e \omega^{-\beta_e}$$

- These describe the amplitudes and exponents of the spectral density of the neuronal fluctuations

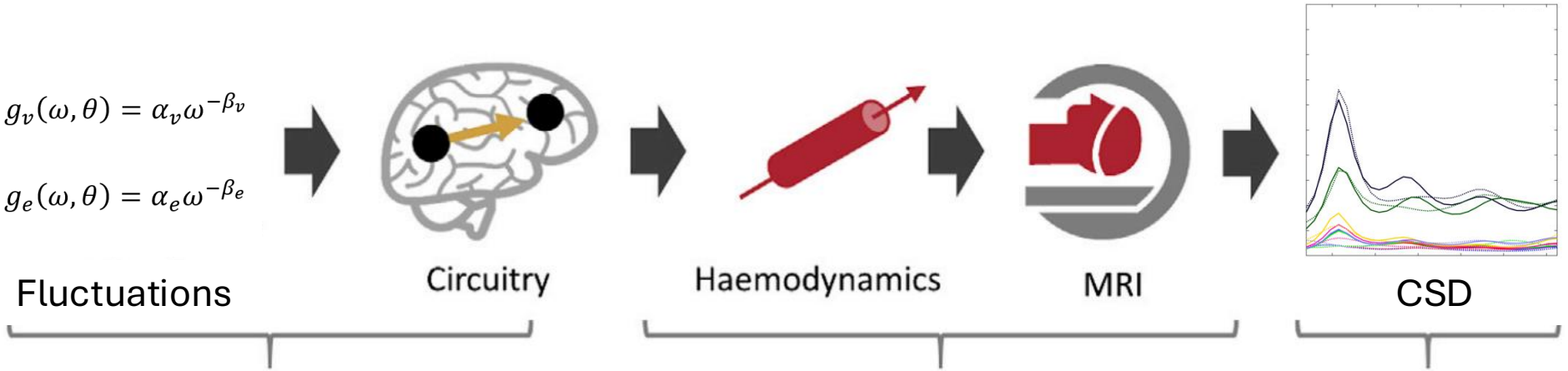
Does it work well? (yes)

- Not just computationally more efficient:



Razi, 2015, Neuroimage

- **BUT:** assumes that effective connectivity is stationary over time



NEURAL

$$\theta^{(n)}$$

OBSERVATION

$$\theta^{(h)}$$

MEASUREMENT

$$\theta^{(\varepsilon)}$$

$$\dot{z} = f\left(z(t) , \theta^{(n)} \right) + v(t)$$

$$\mathrm{y} = g\left(z(t) , \theta^{(h)} \right) + X_0 \beta_0 + \varepsilon(t)$$

Zeidman, 2019a, Neuroimage

Model inversion / testing hypotheses

Model inversion (example in practical)

- Method is identical to that used for 'conventional' DCM
- How well does it explain the data vs how far does it stray from priors?
- Model evidence, $\ln p(y|m)$, approximated by free energy

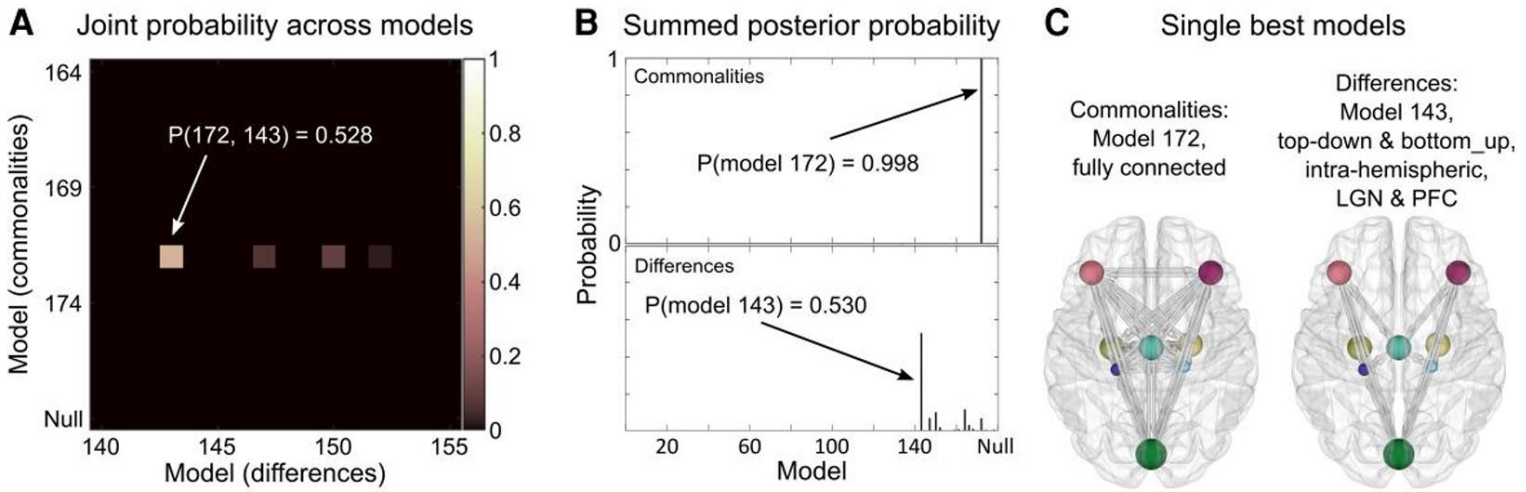
Table 1
Priors on parameters (haemodynamic priors have been omitted for simplicity).

Parameter	Description	Prior mean	Prior variance
$\ln(-A_{ii})$	Inhibitory self connections	$\ln\frac{1}{2}$	$\frac{1}{256}$
A_{ij}	Extrinsic effective connectivity	$\frac{1}{128}$	$\frac{1}{64}$
$\ln(\alpha)$	Amplitude of fluctuations	0	$\frac{1}{64}$
$\ln(\beta)$	Exponent of fluctuations	0	$\frac{1}{64}$

Friston, 2014, Neuroimage

Testing hypotheses (example in practical)

- Again, identical methods to those used for task-based DCM
- Parametric empirical Bayes (PEB) to build a group level model
- Compare group-level models using Bayesian model comparison (BMC) or nested models using Bayesian model reduction (BMR)



Thomas, 2021, Brain Communications

Thanks!

Reading

- Intro to spectral DCM:

Friston, K.J. *et al.* (2014) 'A DCM for resting state fmri', *NeuroImage*, 94, pp. 396–407. doi:10.1016/j.neuroimage.2013.12.009.

- Validation of spectral DCM:

Razi, A. *et al.* (2015) 'Construct validation of a DCM for resting state fmri', *NeuroImage*, 106, pp. 1–14. doi:10.1016/j.neuroimage.2014.11.027.

- Peter Zeidman tutorial papers:

Zeidman, P., Jafarian, A., Corbin, N., *et al.* (2019) 'A guide to group Effective Connectivity Analysis, part 1: First Level Analysis with DCM for fmri', *NeuroImage*, 200, pp. 174–190. doi:10.1016/j.neuroimage.2019.06.031.

Zeidman, P., Jafarian, A., Seghier, M.L., *et al.* (2019) 'A guide to group Effective Connectivity Analysis, part 2: Second level analysis with PEB', *NeuroImage*, 200, pp. 12–25. doi:10.1016/j.neuroimage.2019.06.032.

- Example application in Parkinson's disease:

Thomas, G.E. *et al.* (2022) 'Changes in both top-down and bottom-up effective connectivity drive visual hallucinations in parkinson's disease', *Brain Communications*, 5(1). doi:10.1093/braincomms/fcac329.