

# Spiking dynamics and inter-area interactions in a supercomputational model of cortex

Sacha van Albada  
Institute of Neuroscience and Medicine (INM-6),  
Theoretical Neuroanatomy  
Institute for Advanced Simulation (IAS-6),  
Research Centre Juelich, Germany

I will present a spiking multi-area model of all vision-related areas of macaque cortex that relates cortical structure to its dynamics on multiple scales [1]. Each area is represented by a 1 mm<sup>2</sup> microcircuit distinguishing layers 2/3, 4, 5, and 6, with an excitatory and an inhibitory population each. Within each microcircuit, the full density of neurons and synapses is modeled, avoiding distortions of the dynamics due to downscaling [2]. The model definition entails the derivation of a full population-level connectivity matrix based on tracing data from a recent release of the CoCoMac database, quantitative tracing data, and statistical regularities. The model structure is complemented with estimates of area-specific layer thicknesses and population sizes. A statistical mapping of synapses to target cell bodies suggests that layer 4 neurons receive substantial feedback. The model is implemented in NEST and simulated on the JUQUEEN supercomputer. A method using a mean-field reduction of the dynamics enables applying high-level constraints, and stabilizes the model activity at physiological rates [3]. The simulated activity contains slow activity fluctuations propagating across areas and showing correspondences with massively parallel spike train recordings. For intermediate cortico-cortical synaptic strengths, correlations between area-level input traces resemble functional connectivity from resting-state fMRI. The close match between simulated activity and spiking and fMRI data occurs when the model approaches an instability between a low-rate and a high-rate state, suggesting that cortex operates in a metastable regime.

## References

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- [2] van Albada SJ, Helias M, Diesmann M. Scalability of asynchronous networks is limited by one-to-one mapping between effective connectivity and correlations (2015). PLOS CB 11(9):e1004490.
- [3] Schuecker J, Schmidt M, van Albada SJ, Diesmann M, Helias M (2017). Fundamental activity constraints lead to specific interpretations of the connectome. PLOS CB 13(2):e1005179.