

Critical synchronization dynamics of the Kuramoto model on connectome and small world graphs

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The hypothesis, that cortical dynamics operates near criticality also suggests, that it exhibits universal critical exponents which marks the Kuramoto equation, a fundamental model for synchronization, as a prime candidate for an underlying universal model. Here, we determined the synchronization behavior of this model by solving it numerically on a large, weighted human connectome network in an assumed homeostatic state. Since this graph has a topological dimension $d < 4$, a real synchronization phase transition is not possible in the thermodynamic limit, still we could locate a transition between partially synchronized and desynchronized states. At this crossover point we observe power-law-tailed synchronization durations, with $\tau \sim 1.2(1)$, away from experimental values for the brain. However, mimicking a network with inhibitory interactions by flipping the signs of the outgoing weights of a randomly selected 20% of nodes, we found $\tau \sim 1.9(2)$, which is in the range of human brain experiments. This implies that inhibitory interactions in brain models are necessary to describe experimental values. We provide results on a large two-dimensional lattice, having additional random, long-range links, finding a critical exponent $\tau \sim 1.6(1)$ for comparison.