Brain network model dynamical simulations

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Numerical simulations of threshold models have been performed on a human brain network with N = 836 733 connected nodes available from the Open Connectome Project. Variable threshold models exhibit extended critical dynamical scaling regions in an extended control parameter region, suggesting Griffiths phases due to the heterogenities [1].

The simulations have been done using a stochastic cellular automaton model, which enables efficient parallelization over GPU nodes using CUDA [2]. The speedup on NVIDIA Kepler K40 cards is about x10 with respect to an Intel Xeon X5650 @2.67GHz CPU core. This is a crucial factor, because the simulations require extremely large computing times and opens up the possibility to take into account more complex neuro-physiological effects.

[1] Géza Ódor, Critical dynamics on a large human Open Connectome network,
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[2] Vince Varga, A rendezetlenség hatásának vizsgálata hálózati modellekben, BSc thesis BME 2016