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

Géza Ódor MTA-EK-MFA Complex Systems, Budapest
Jeffrey Kelling HZDR, Dresden

Theoretical research and experiments suggest that the brain operates at or near a critical state between sustained activity and an inactive phase, exhibiting optimal computational properties (see: *PRL 110, 178101 (2013)*)

Individual neurons emit periodic signals (*PNAS 113 (2016) 3341*) → criticality at the synchronization transition point
Kuramoto oscillator model (1975)

Order parameter: average phase:

Non-zero, above critical coupling strength $K > K_c$,
tends to zero for $K \leq K_c$ as $R \propto (1/N)^{1/2}$

or exhibits an initial growth: $R(t,N) = N^{-1/2}t^{\eta}f_+(t/N^{\bar{z}})$ for incoherent initial state

Critical synchronization transition for $D > 4$ spatial dimensions,
which is mean-field like: i.e. $D \longrightarrow \infty$ (full graph)

The dynamical behavior suffers very strong corrections to scaling and chaoticity, see:

Róbert Juhász, Jeffrey Kelling and Géza Ódor:
Critical dynamics of the Kuramoto model on sparse random networks
Test of Kuramoto model on sparse synthetic networks

2D lattices of linear size $L = 6000$, periodic boundary conditions, + extra random long link between connecting any edges: $<k> = 5$, 90,000,000 edges

Growth runs from random initial state Runge-Kutta-4 parallelized for GPUs Maximum time: $t_{\text{max}} = 1000$, average over: 10000 independent $\omega_i$ realizations

Critical point located at $K = 0.4773$

Critical exponent: $\eta = 0.55$ (10)
Determination of desynchronization avalanche exponent $\tau_t$

Measure characteristic times $t_x$ of first dip below: $R_c = (1/N)^{1/2}$

average over: 10,000 independent $\omega_i$ realizations

Histogramming of $t_x$ at the critical point

Critical exponent: $\tau_t = 1.6 \,(1)$ obtained by fitting for the PL tails
What do we know about neuron networks?

The largest precisely explored structural networks contains ~302 neurons (C. Elegans) (very recently fruit fly is reported)

Connectomes, obtained by approximative methods like diffusion MRI contain < $10^6$ nodes (voxels)

Recently DMRI tractography was confirmed by tract-tracing in ferret
Open Connectome Large Human graphs

Diffusion and structural MRI images with
1 mm³ voxel resolution:
$10^5 - 10^6$ nodes

Hierarchical modular graphs

Top level: 70 brain region (Desikan atlas)

Lower levels: Deterministic tractography:
Fiber Assignment by Continuous Tracking (FACT) algorithm

Map: voxel $\rightarrow$ vertex ($\sim 10^7$)
fiber $\rightarrow$ edge ($\sim 10^{10}$)

+ noise reduction $\rightarrow$ graph
undirected, weighted
The structural human connectome (i.e. the network of fiber connections in the brain) can be analyzed at ever finer spatial resolution thanks to advances in neuroimaging. Here we analyze several large data sets for the human brain network made available by the Open Connectome Project. We apply statistical model selection to characterize the degree distributions of graphs containing up to $\approx 10^6$ nodes and $\approx 10^8$ edges. A three-parameter generalized Weibull (also known as a stretched exponential) distribution is a good fit to most of the observed degree distributions. For almost all networks, simple power laws cannot fit the data, but in some cases there is statistical support for power laws with an exponential cutoff. We also calculate the topological (graph) dimension $D$ and the small-world coefficient $\sigma$ of these networks. While $\sigma$ suggests a small-world topology, we found that $D < 4$ showing that long-distance connections provide only a small correction to the topology of the embedding three-dimensional space.

Small world, still finite dimensional, non-scale free, universal modular graphs
Kuramoto solution for the KKI-18 graph with $N = 836,733$ nodes and $41,523,931$ weighted edges

The synchronization transition point determined by growth as before.

KKI-18 has $D = 3.05 < 4 \rightarrow$ No real phase transition, crossover.

Due to the fat-tailed link weight distribution, incoming weight normalization is applied:

$$W_{i,j}' = \frac{W_{i,j}}{\sum_{j \in \text{neigh. of } i} W_{i,j}}$$

$K_c = 1.7$ and growth exponent: $\eta = 0.6(1)$
Duration distribution for the KKI-18 graph

Measure characteristic times $t_x$ of first dip below: $R_c = (1/N)^{1/2}$

average over: 10,000 independent $\omega_i$ realizations

Histogramming of $t_x$ at the critical point

Critical exponent: $\tau_t = 1.2 \,(1)$

obtained by fitting for the PL tails

Out of range of experiments:

$1.5 < \tau_t < 2.4$ (Palva et al 2013)
Inhibitory (negative) links compared to experiments

Inhibitions: 5-20% of nodes: $w_{ij} \rightarrow -w_{ij}$ randomly

Scaling exponent within experimental range: $1.5 < \tau_t < 2.4$

*J.M. Palva et al PNAS 110 (2013) 3585*
Conclusions

Heterogeneity effects are considered on large human connectomes and 2d + long range lattices of extremely large sizes.

Kuramoto synchronization equation is solved by 4\textsuperscript{th} order Runge-Kutte method, implemented on parallel \textbf{GPU-s}.

In case of 2d + long range lattices we determined the temporal mean-field like solution, with very strong corrections to scaling.

De-synchronization characteristic exponent is found: $\tau_t = 1.6 (1)$

On the normalized, weighted \textbf{KKI-18} graph, describing variable node sensitivity, $\tau_t = 1.2 (1)$, out of experimental range.

On the normalized, inhibitory \textbf{KKI-18} graph $\tau_t = 1.8 (2)$, within experimental range.

\textbf{Frustrated} synchronization sub-critically!

Insensitivity to 5 - 20% link sign reversal, \textbf{robustness}.


HPC support from Hungarian HPC infra: KIFU is acknowledged.