Comparison of the synchronization transition of the Kuramoto model on fruit-fly versus a large human connectome

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Oscillatory behavior of neural systems +
Quasistatic inhomogneity causes dynamical criticality in Griffiths phases: *Phys. Rev. Lett. 105, 128701 (2010)*
→ Frustrated edge of synchronization in brain models **?**

Kuramoto oscillator model, with Hopf synchronization transition:

$$\dot{\theta}_i(t) = \omega_{i,0} + K \sum_j W_{ij} \sin[\theta_j(t) - \theta_i(t)]$$

$\omega_{i,0}$ is the intrinsic frequency of the i-th oscillator,

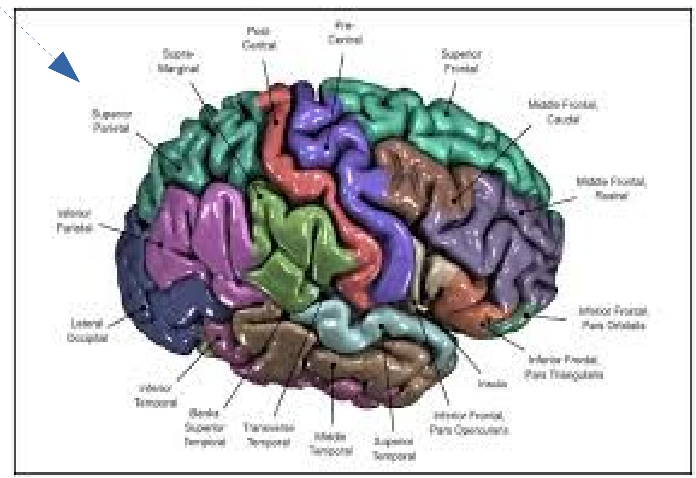
Quenched heterogeneity in self-frequencies and network topology

Large Human Connectome 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 obtained by deterministic
tractography: FACT algorithm

Map : voxel → vertex (~ 10^7)

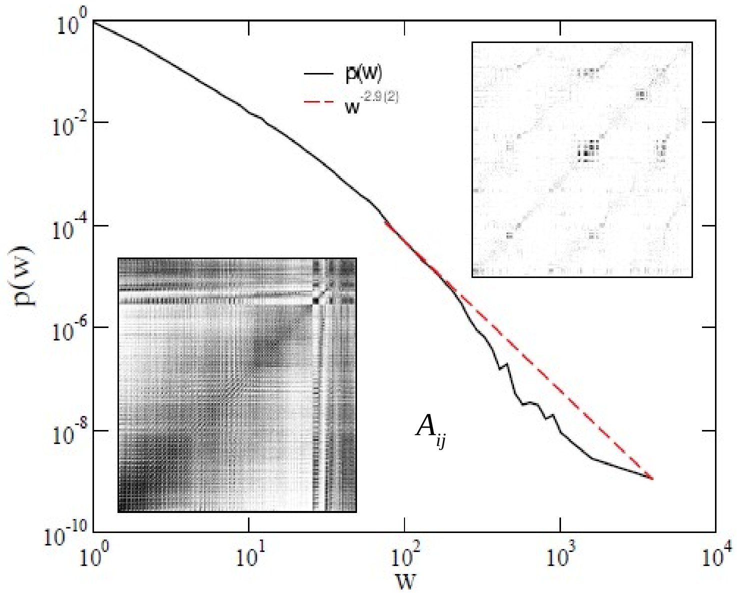
fiber → edge (~ 10^{10})

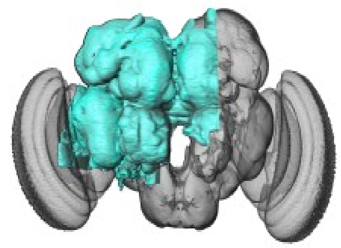
+ noise reduction → graph

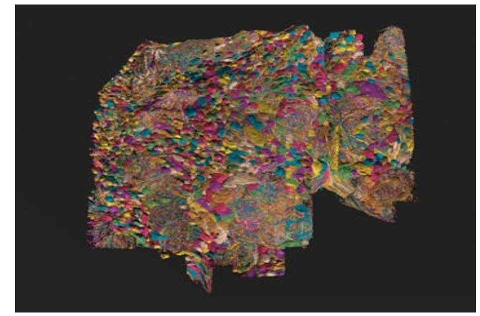
undirected, weighted, *dim < 4 !*

Structural graphs of nodes (containing ~10^4 neurons) and power-law weight distributed edges see : *Michael T. Gastner and Géza Ódor, Scientific Reports 6 (2016) 27249*

Comparison with the fruit-fly connecome results

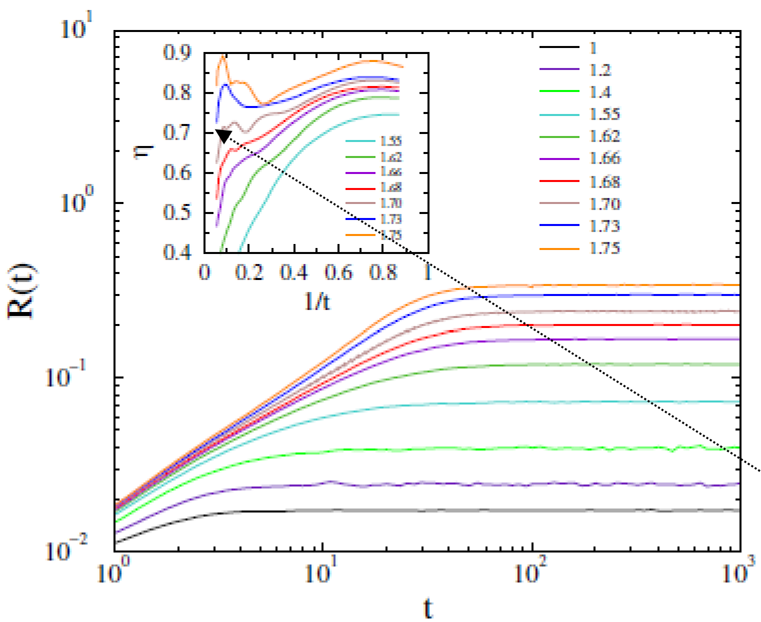






Fruit-fly connectome is the largest exactly known neural network:

N = 21.615, L = 3.410.247, dim > 5

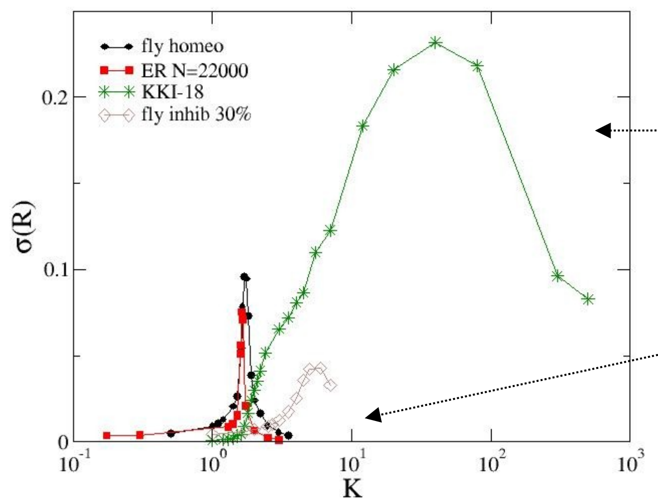


Similar to random Erdős-Rényi (ER) graph, but power-law tailed connection weights

Weakly modular: $Q_{FF} \sim 40\, Q_{KKI-18}$

Synchronziation transition via *R(t)*
local slopes : $\eta = -d \ln R / d \ln t$

K = 1.60(1) (inflexion curve)
Characterized by mean-field growth
Exponent $\eta = 0.7(1)$

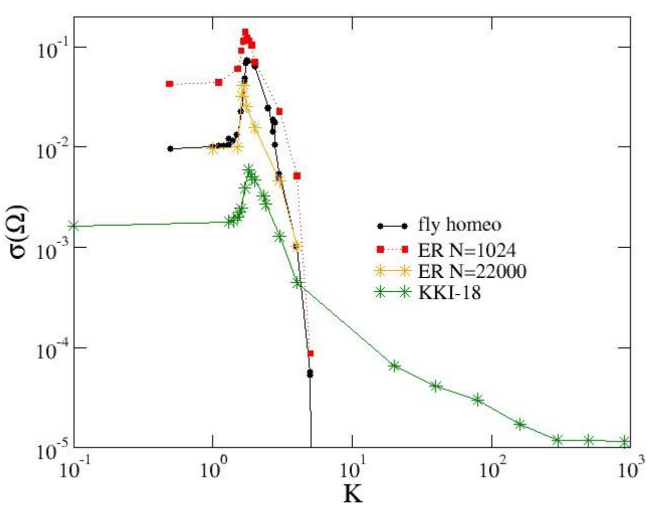


Fluctuations of: $R(t) = \frac{1}{N}\left|\sum_{j=1}^{N} e^{i\theta_j(t)}\right|$ show

extended transition for KKI-18

For FF ~ ER like prob. distribution

With random inhibitors: wider range



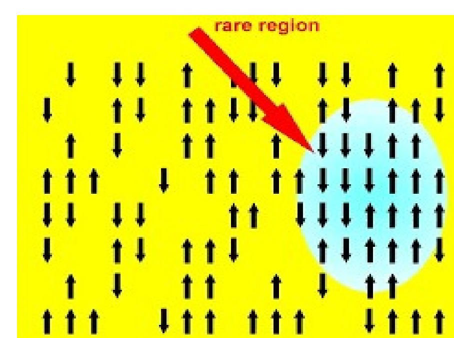
For fluctuations of: $\Omega(t,N) = \frac{1}{N}\sum_{j=1}^{N}(\overline{\omega} - \omega_j)^2$

HMN+lower dim. of KKI-18 is responsible

for the extended critical region

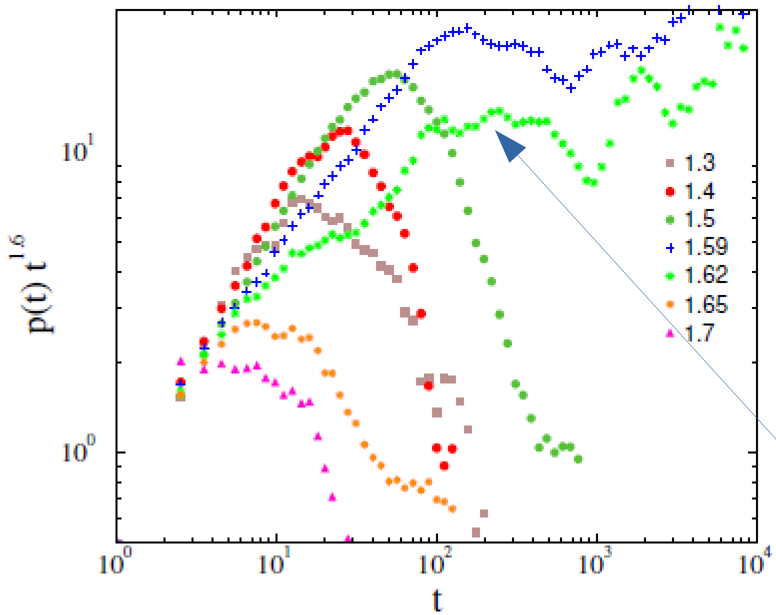
and the Griffiths Phase of humans

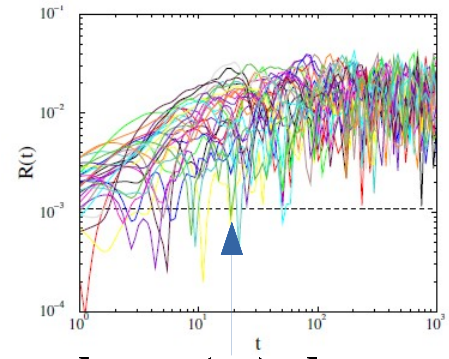
As compared to the fly connectome



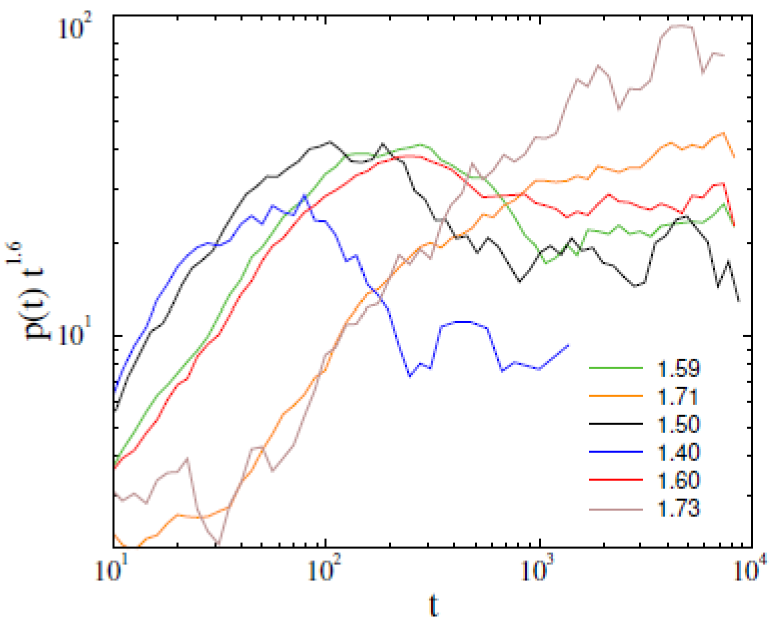
GÓ, G. Deco and J. Kelling, Differences in the critical dynamics underlying the human and fruit-fly connectome Phys. Rev. Res. 4 (2022) 023057.

Characteristic time exponent τ_t on the fly network





The $p(t_x)$ distros exhibit power-law only at the synchronization transition point $K_c \sim 1.6$ characterized by a mean-field exponent: *1.6*



Similarly as in case of the random Erdős-Rényi network

Géza Ódor and Jeffrey Kelling :
Critical synchronization dynamics of the Kuramoto model on connectome and small world graphs Scientific Reports 9 (2019) 19621