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

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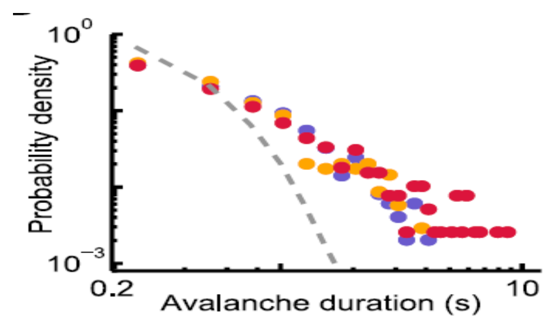
Theoretical research and experiments suggest that the brain operates at or near a **critical state** between sustained activity and an inactive phase, exhibiting optimal computational properties (see: *Beggs & Plenz J. Neurosci. 2003; Chialvo Nat. Phys. 2010; Haimovici et al. PRL 2013*)



Neurons exhibit oscillatory behavior

Quasistatic inhomogneity causes dynamical criticality in Griffiths phases

→ Edge of Synchronization and Griffiths phase in brain models **?**

The Kuramoto oscillator model

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

phases $\theta_i(t)$

global coupling K is the control parameter

weighted adjacency matrix W_{ij}

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

Order parameter : average phase: $R(t) = \frac{1}{N} \left| \sum_{j=1}^{N} e^{i\theta_j(t)} \right|$ freq. spread: $\Omega(t,N) = \frac{1}{N} \sum_{j=1}^{N} (\overline{\omega} - \omega_j)^2$

R(t →) > 0 for *$K > K_c$*,

R(t →) = 0 for *K K_c* as *R* *$(1/N)^{1/2}$*

Initial growth: *$R(t) \sim t^{\eta}$* from incoherent initial states

GPU Cuda, C++ code using VexCL and Boost libraries, Runge-Kutta4, Adaptive ODE

Géza Ódor and Jeffrey Kelling :
Critical synchronization dynamics of the Kuramoto model on connectome and small world graphs
Scientific Reports 9 (2019) 19621
G. O, J.K., R. Juhasz, JSTAT (2019) Kuramoto on Complex networks

Large Human Connectome graphs

Diffusion and structural MRI images with
  $1\ mm^3$ voxel resolution :
  $10^5 – 10^6$ nodes

Hierarchical modular graphs

Top level: *70* brain region (Desikan atlas)

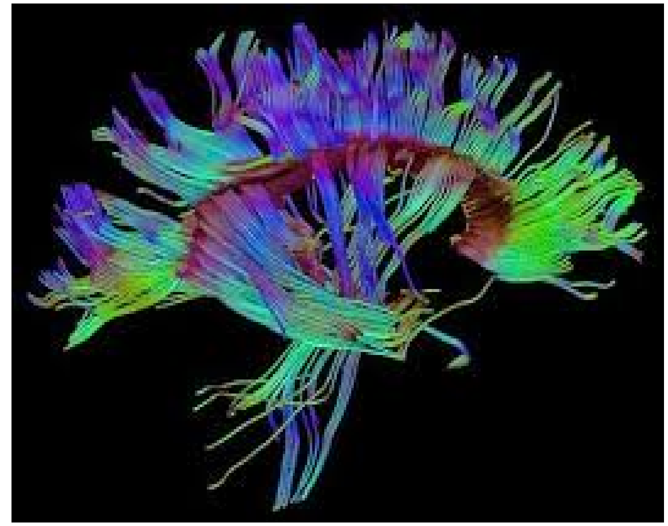
Lower levels obtained by deterministic
  tractography: FACT algorithm

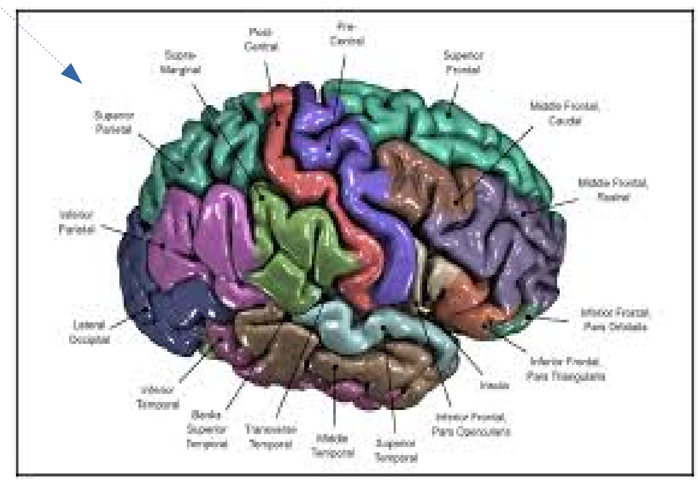
Map : voxel → vertex ($\sim 10^7$)

  fiber → edge ($\sim 10^{10}$)

+ noise reduction → graph

 undirected, weighted





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

Kuramoto solution for the KKI-18 graph with
N= *804 092* nodes and *41 523 908* weighted edges

The synchronization transition point

determined by growth from disorder

KKI-18 has d = *3.05 < 4* →

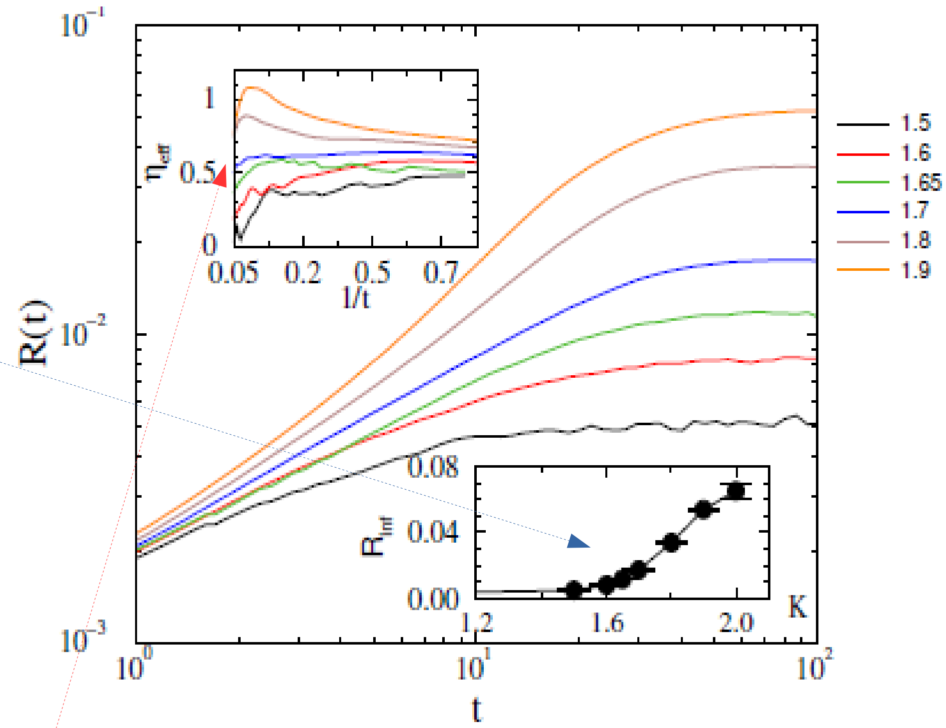
Smooth crossover to partial synch.

Fat-tailed link weight distribution, incoming weight normalization is applied:

$$W'_{i,j} = W_{i,j} / \sum_{j \in \text{neighb.of } i} W_{i,j}$$

to provide local homeostasis (suppress hubs)

K_c =*1.7* and growth exponent: = *0.6(1)*



Determination of the characteristic time exponent: t

Measure characteristic times t_x of first dip below: $R_c = \sqrt{1/N}$

Runs for ~*10.000* random, independent $_i$ realizations

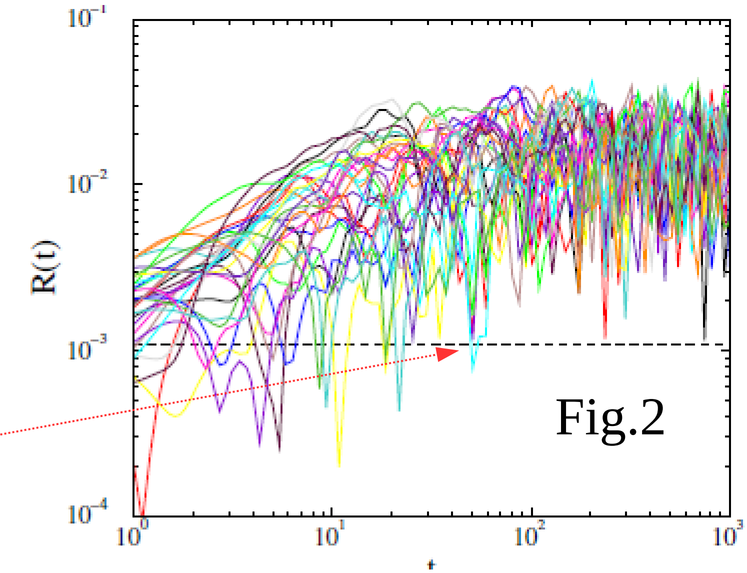
Histogramming of t_x at $K_c = 1.6$

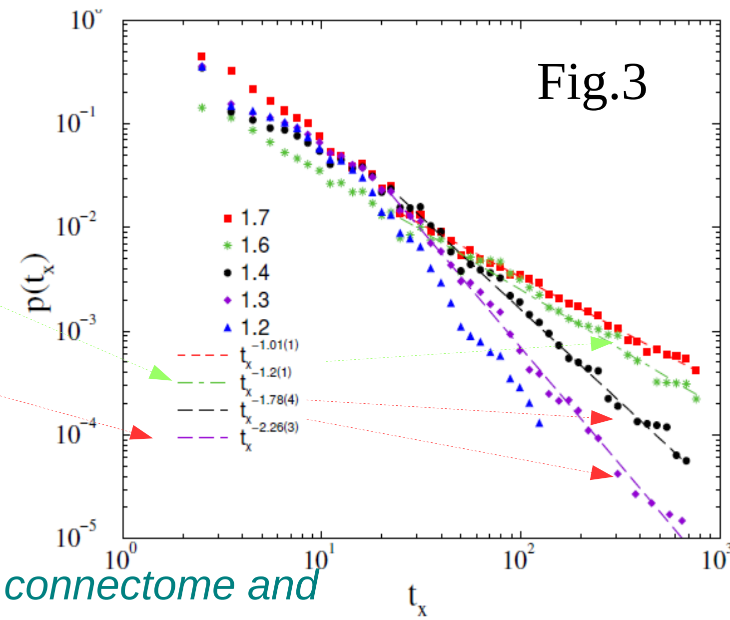
Critical exponent: t

Below the transition point : $K < 1.6$

non-universal power laws in the range of experiments of activity durations :

$1.5 < _t < 2.4$ (Palva et al 2013)





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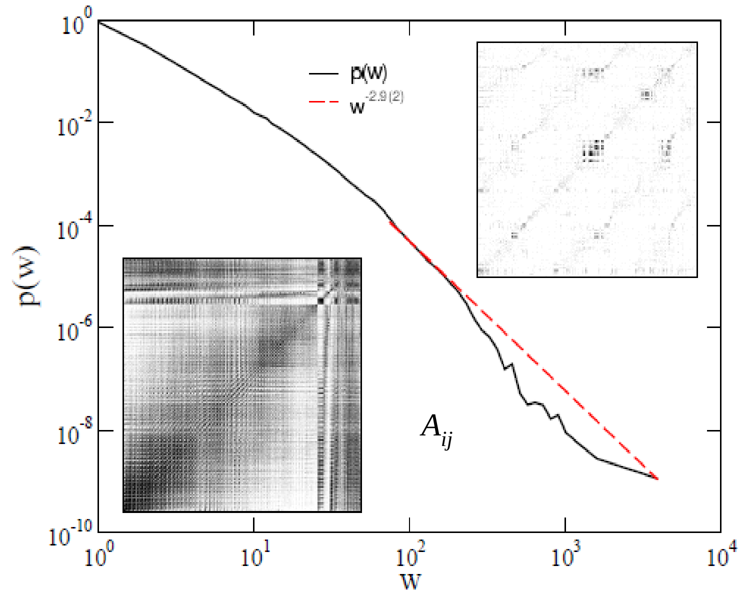
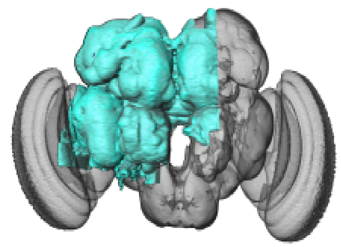
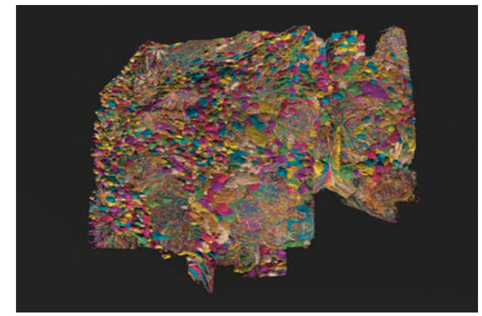
Comparison with the fruit-fly connectome results

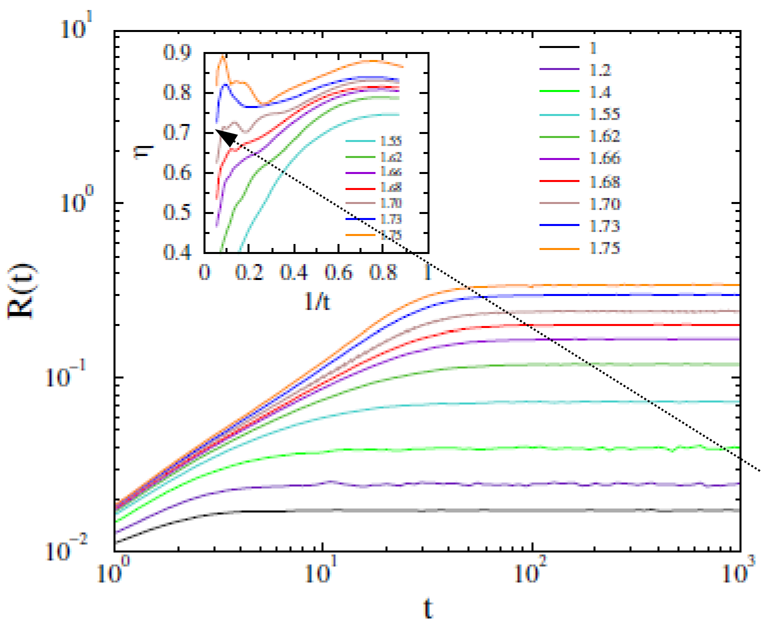






Fruit-fly connectome is the largest exactly known neural network:

N = 21.615, L = 3.410.247, d = 5.4(5)



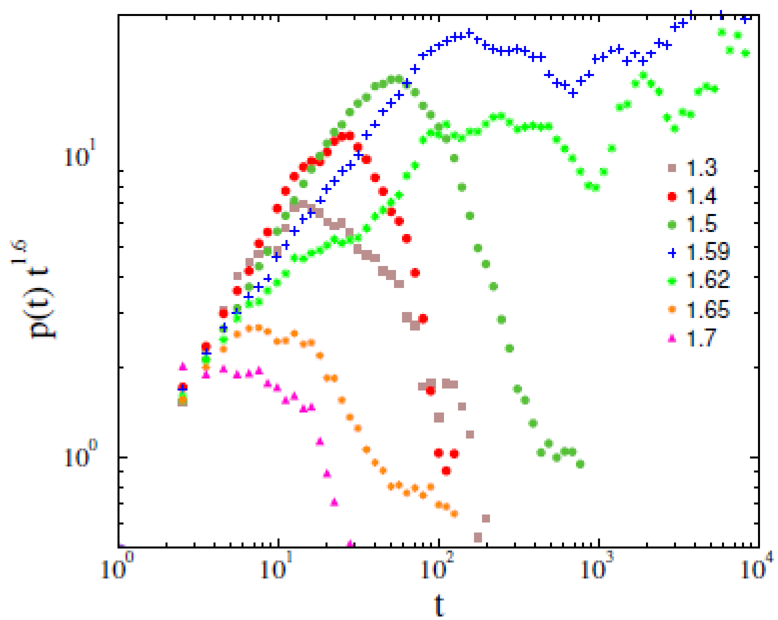
Similar to random Erdős-Rényi (ER) graph, but power-law tailed connection weights

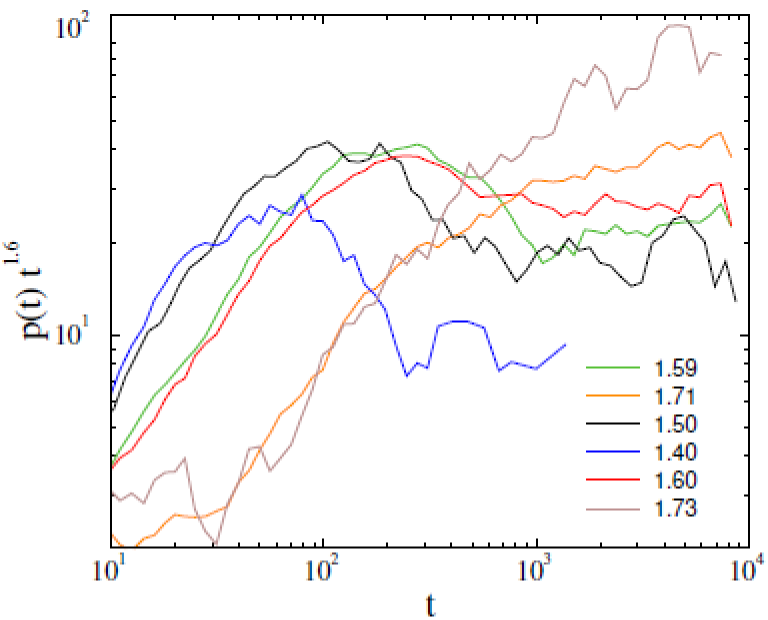
Weakly modular: $Q_{FF} \sim 40\ Q_{KKI\text{-}18}$

Synchronziation transition via *R(t)*
local slopes :   = -d lnR / d lnt

$K_c = 1.60(1)$ (inflexion curve)
Characterized by mean-field growth
Exponent   = *0.7(1)*

Characteristic time exponent $_{t}$ on the fly network





The $p(t_x)$ distros exhibit power-law

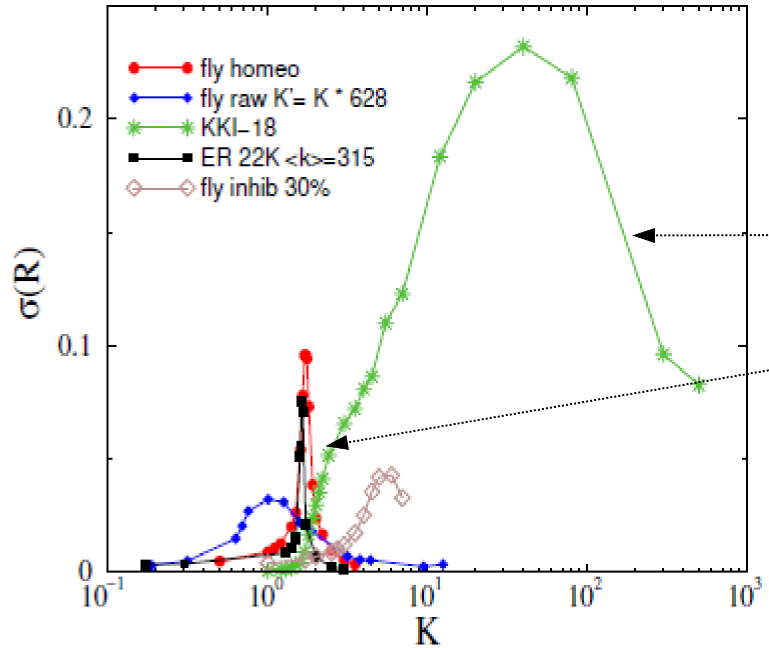
only at the synchronization

Transition point $K_c \sim 1.62$

characterized by mean-field
*e*xponent: $_{t}$ $=1.6$

Similarly as in case of the

random Erdős-Rényi network

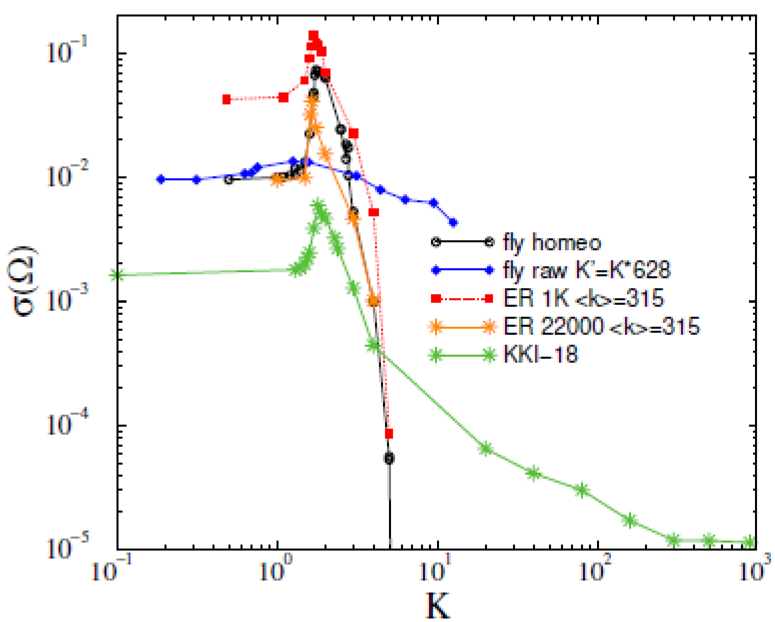


Fluctuations of R show

extended transition for KKI-18

For FF ~ ER like distro

With random inhibitors: wider range



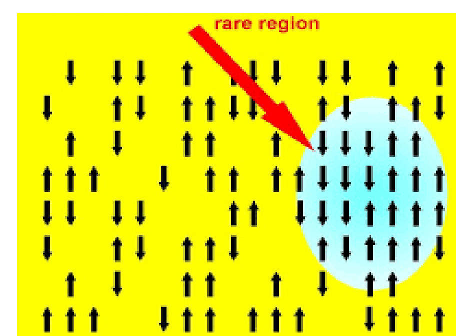
The same is true for fluctuations of □□

HMN structure of KKI-18 is responsible

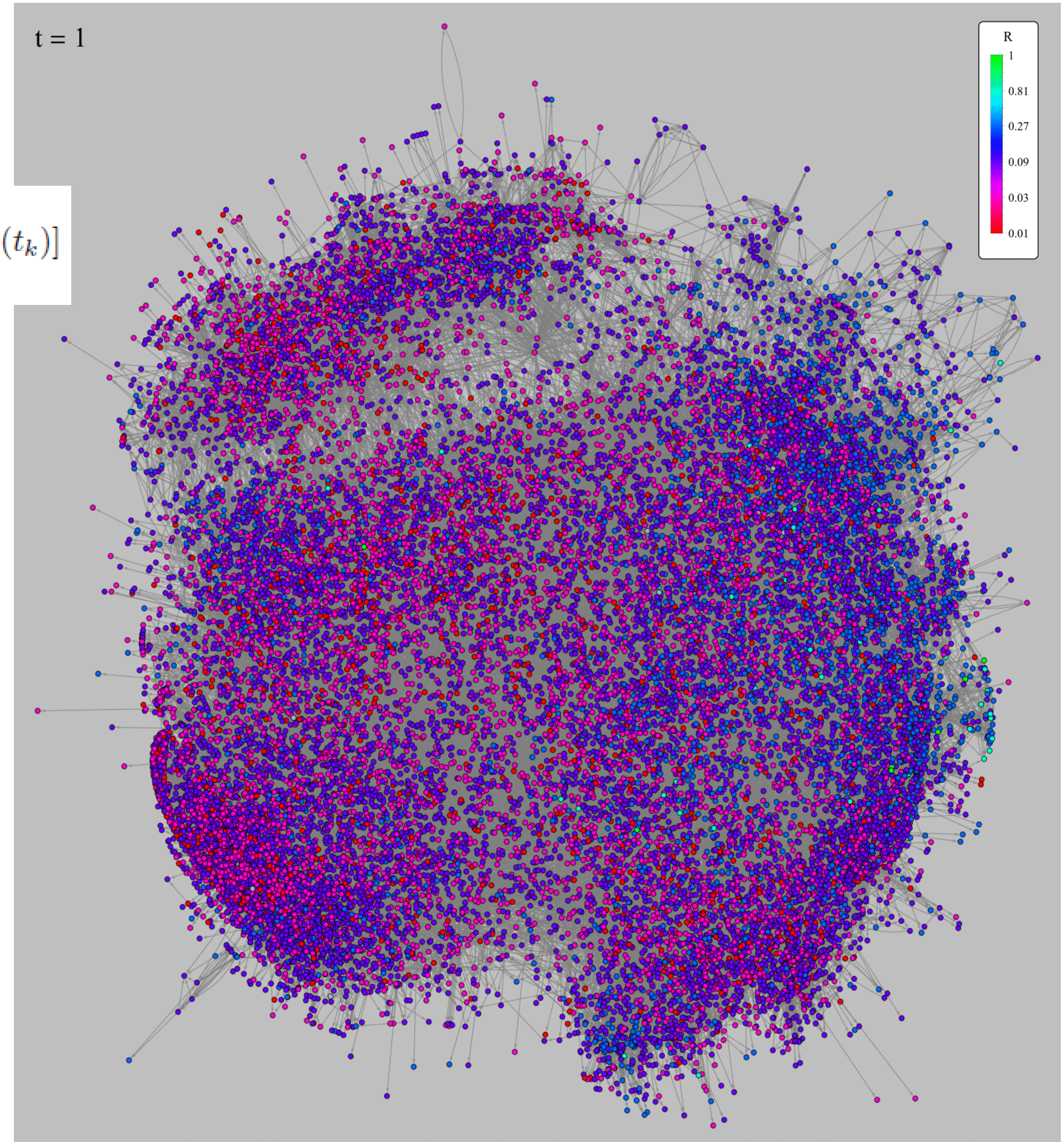
for the extended critical region

and Griffiths Phase of humans

As compared with the fly connectome



$$k_i = 1/N_{neigh.i} \sum_j A_{i,j} \exp\left[i\theta_j(t_k)\right]$$



Local Kuramoto OP. Frustrated synchronization

Visualization: Shengfeng Deng

Conclusions

The almost module-free network of the fruit-fly with $d = 5.4(5) > d_c=4$
Causes mean field like synchronization criticality as for ER

The HMN network of human connectome with $d = 3.1(1) < d_c = 4$
Causes non-mean field transition and an extended region with
Dynamical criticality, with continuously changing exponents
Agreeing with brain LRTC experiments (Palva et al)
GPU speedup ~ 100 x (A100) with respect single Xeon CPU core 3.3GHz

For details see : *Phys. Rev. Res. 4 (2022) 023057,*
Neurocomputing, 461 (2021) 696-704

For a review see: J. Phys. Complex. 2 (2021) 045002

A postdoc and a PhD position is open from September at our Dep.

Thank you for your attention !