Impact of Higher-Order Network Structure on Critical Behaviour in Complex Systems

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Problem

Network structure is known to be an important determinant of criticality. In most studies of its impact on critical behaviour, however, network structure is characterised in terms of simple quantities such as degree distribution and global clustering. Recently [1], we have argued that such quantities can obscure important differences in the prevalence of higher-order structures and that these may impact dynamics in classical epidemic models.


CCM   MDR   BigV
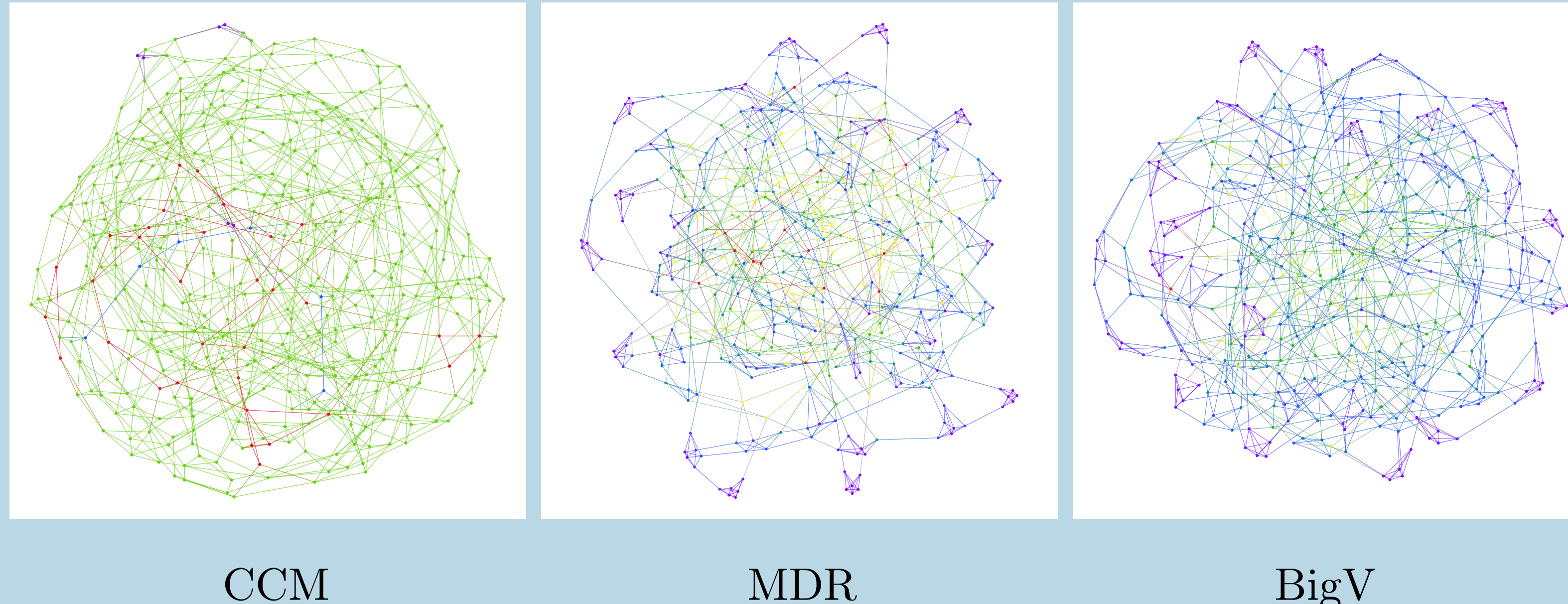
Here, we provide new evidence about how diversity in higher-order subgraphs (for a given degree distribution and global clustering value) can impact the critical behaviour in two other key types of complex systems: complex contagion and the classical Kuramoto model of synchronisation.

Network Generation

To systematically explore the impact of higher-order structure, we used our recently developed method [2] for generating networks with the same degree distribution and global clustering coefficient but different subgraph decomposition. It enables to parametrise networks using arbitrarily chosen subgraphs, e.g., clustering-inducing subgraphs such as △, ☑ or ⊠. Code is available at: https://github.com/martinritchie/Network-generation-algorithms

Evolving for Diversity

We search the space of networks satisfying the same degree distribution and global clustering coefficient through degree- and clustering-preserving operations via resolution of an underdetermined system of Diophantine equations. We optimise for diversity by using a variant of MAP-Elites (arXiv:1504.04909 [cs.AI]).
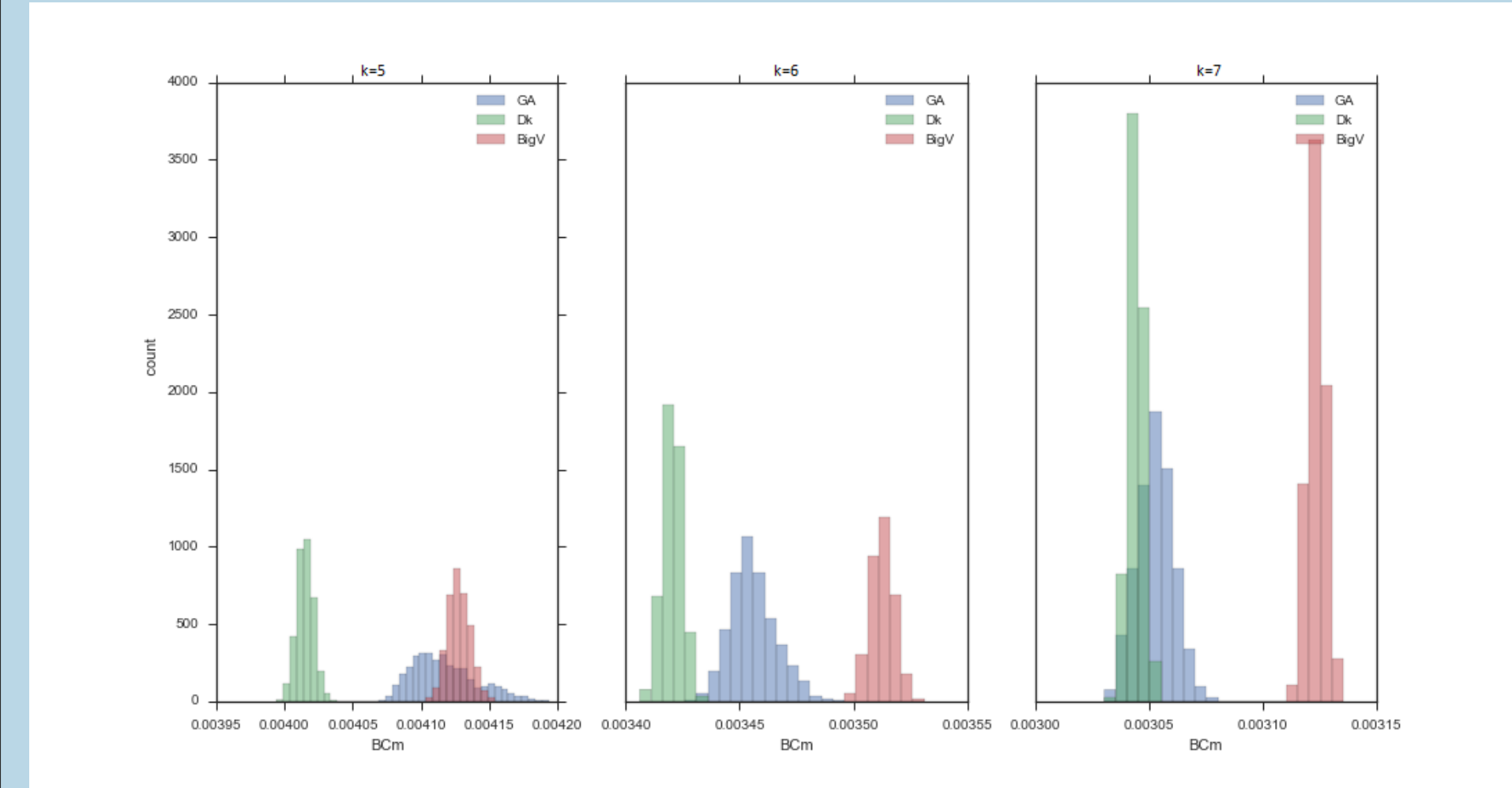

Comparing the histograms of betweenness centrality of networks produced using BigV (red), dK-2.1 (green) and above method (blue) reveals that each method samples from different regions of the parameter space [3].

References

[1] Ritchie, Berthouze, and Kiss. Beyond clustering: Mean-field dynamics on networks with arbitrary subgraph composition. *J Math Biol*, 72(1):255–281, 2016.
[2] Ritchie, Berthouze, and Kiss. Generation of networks with a prescribed degree sequence and subgraph topology: Higher order structure matters. *J Complex Networks*, 5(1):1–31, 2017.
[3] Overbury, Kiss, and Berthouze. A genetic algorithm-based approach to mapping the diversity of networks sharing a given degree distribution and global clustering. In *CompleNet*, pages 223–233, 2016.
[4] Watts and Dodds. Threshold models of social influence. In *The Oxford handbook of analytical sociology*, pages 475–497. 2009.
[5] Miller. Complex contagions and hybrid phase transitions. *J Complex Networks*, 4(2):201–223, 2016.

Complex Contagion
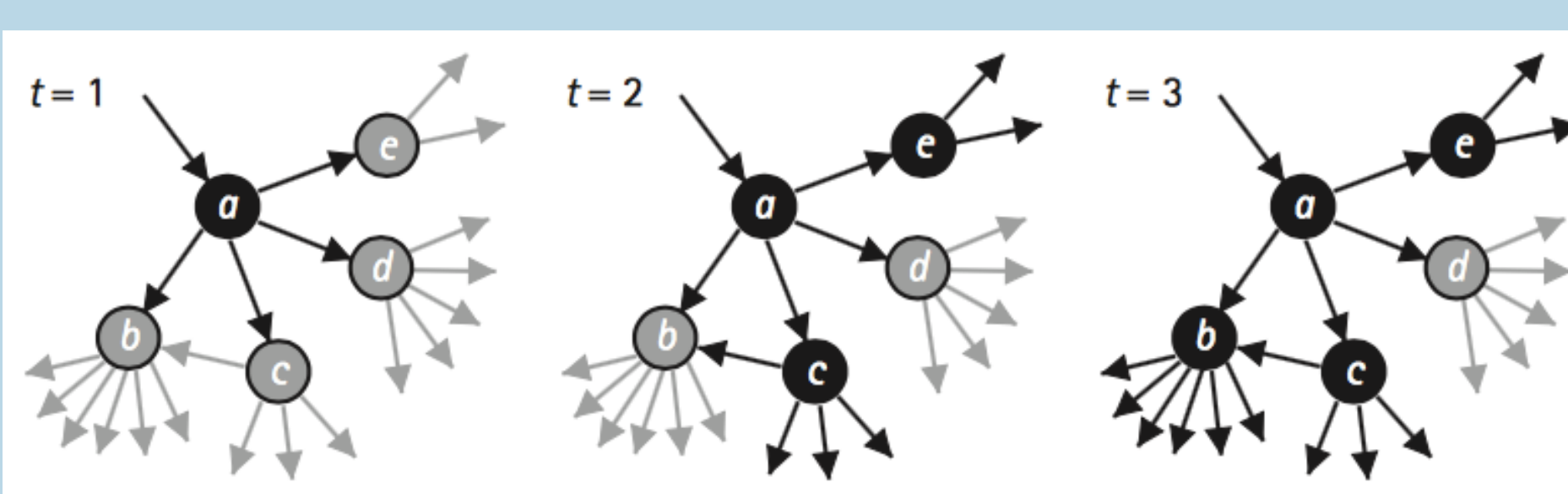
In complex contagion [4] susceptible nodes can only become infected if exposed to **multiple** infectious events. Further, these events must be from different infectious neighbours as only the first infection attempt from an infectious node counts; and infected individuals remain infected for the duration of the epidemic.

Three pairs of network configurations were selected that had the same degree distribution (regular, $N = 1000$, $k = 5$) and global clustering coefficient ($C = 0.4$) but maximising diversity in subgraph decomposition (networks A and B), number of $G_{\boxtimes}$ subgraphs (minC4, maxC4) and mean betweenness centrality (BCmSPmMin, BCmSPmMax). The model was simulated on 100 instances of each configuration.
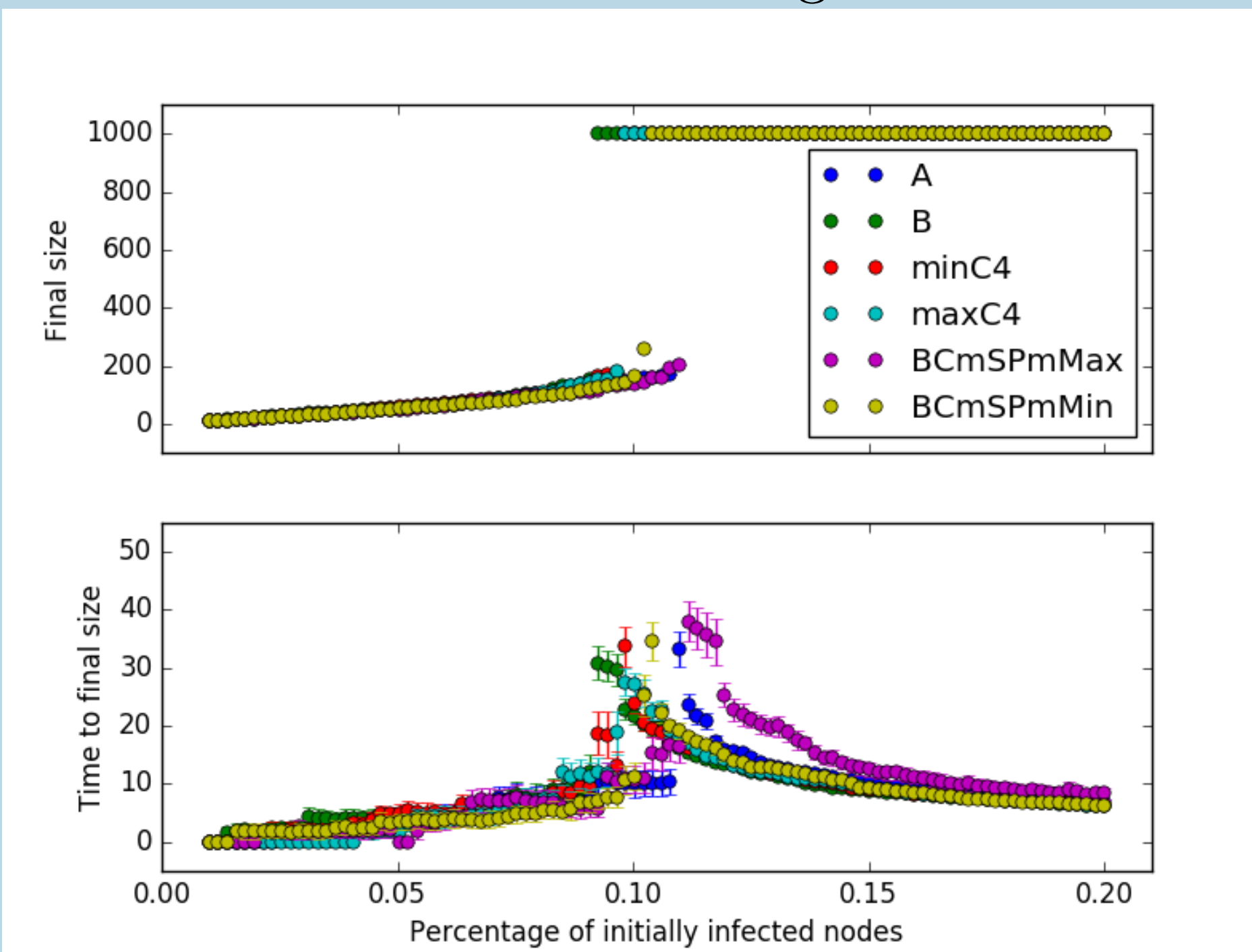
We tracked the mean and standard deviation of final size and time to reach final size when varying the number of initial seeds. We used maximal variability in both quantities as markers of the (hybrid) critical transition [5].

Synchronization

We considered a spatially-embedded version of the Kuramoto model of synchronization, whereby $N = 1000$ self-sustained oscillators (phase ϕ_i) with intrinsic frequency (ω_i) drawn from a unimodal distribution were coupled as follows:

$$\dot{\phi_i}(t) = \omega_i(t) + \frac{K}{N} \sum_{j=1}^{N} C_{ij} \sin(\phi_j(t) - \phi_i(t)) + \eta_i(t)$$

where K is coupling constant, η_i Gaussian noise and C the adjacency matrix of a network realisation. Such system is known to undergo a second-order phase transition at a critical coupling K_c. The model was simulated on the same networks as used with the complex contagion model.

We calculated the order parameter

$$re^{i\psi} = \frac{1}{N} \sum_{j=1}^{N} e^{i\phi_j}$$

when systematically varying the coupling constant K. The transition was identified as the onset of maximum variability in phase synchronization. Data shown is for networks maximising diversity in subgraph decomposition. Results were qualitatively similar for the other pairs (min/max C4 and min/max BC).
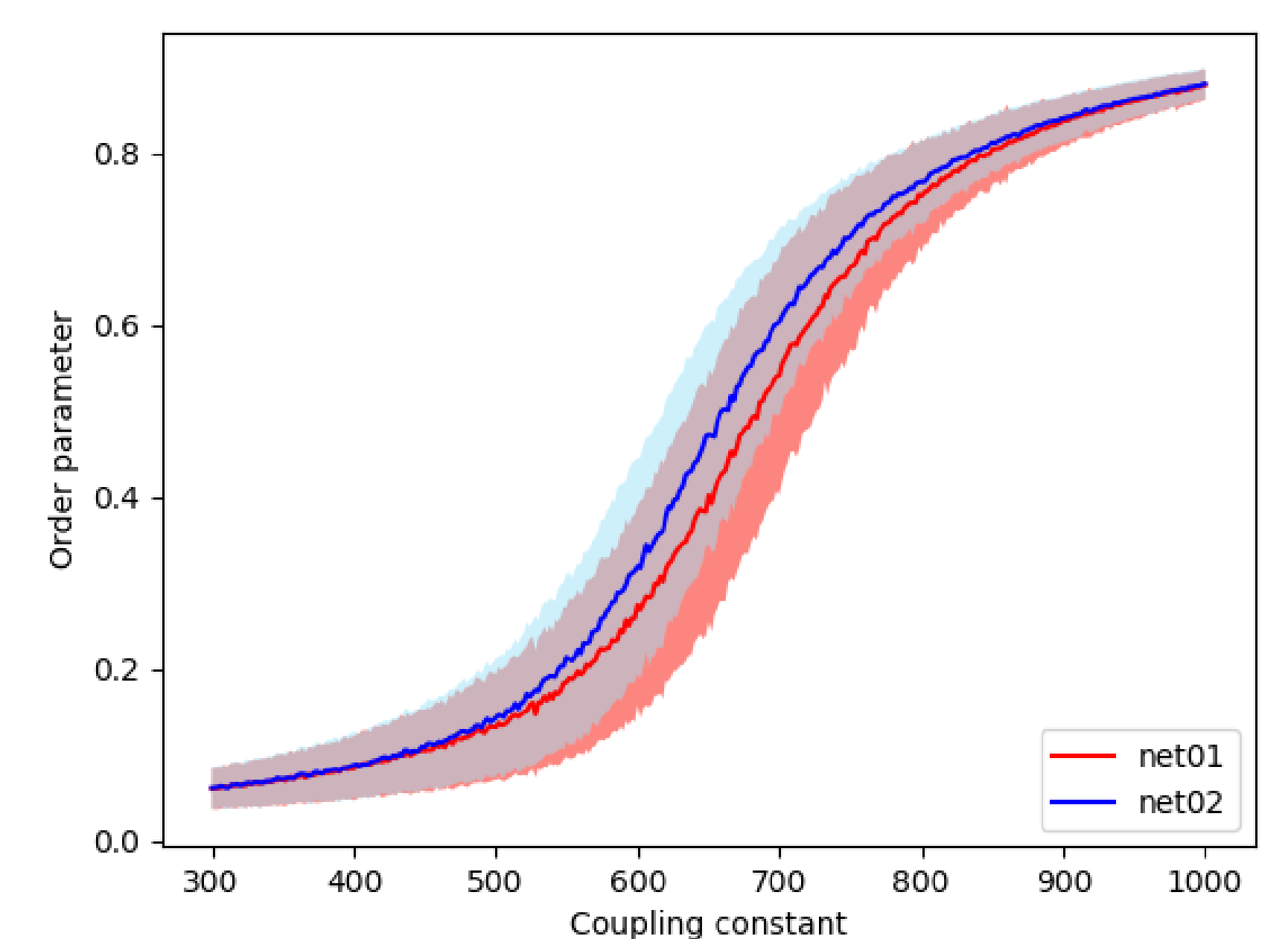
Conclusions

In both models, the value of the order parameter at which the critical transition occurred changed with subgraph decomposition, suggesting that (1) degree distribution and clustering alone have limited predictive power and (2) controlling the prevalence of higher-order subgraphs (i.e., through **local rewiring**) may provide the means to steer networks toward or away from the critical regime. In addition, this work highlights the need for proper **null-models** for clustered networks, including greater understanding (and control) of by-products in finite-size networks.