Loops, not groups: Long loops are responsible for discontinuous phase transitions in higher-order network contagions

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Extended Abstract

Discontinuous phase transitions are commonly observed in dynamics on higher-order networks, where they are not for the corresponding dynamics on dyadic networks [1, 2]. It is often claimed that it is the group structure that gives rise to the discontinuous phase transition in the size of the largest connected component. In this talk, we argue that the impact of groups on the phase transition is more nuanced, and we show that transmission trajectories looping back on themselves are essential for these discontinuous phase transitions. To demonstrate this, we disentangle the impact of groups from the impact of loops (separate transmission chains entering the same group). Here, we deal with a class of networks that is fully composed of independent edges, connecting pairs of nodes, and triangles (or *3-cliques*), connecting groups of 3 nodes together [3, 4].

We extend the models of Newman and Miller [3, 4] who separately proposed models for simple contagion dynamics on clustered networks (networks with a high density of triangles) by solving a self-consistent set of probability-generating functions. In the simple-contagion models of Newman and Miller, which have a single transmission probability T. The same equations capture both the fractional size of the largest connected component and the probability that a node seeds a *global cascade*. This is because for simple contagion, both of these quantities are equal (see Figure 1(a)).

For higher-order contagion, we consider that the second node to be activated in a triangle can have a higher probability of transmitting to the one remaining inactive node. Under certain conditions (e.g., Figure 1(d)) this can lead to a discontinuous phase transition in the expected size of the largest connected component, but not in the probability of a global cascade. For complex contagion, the symmetry between the size of the largest connected component and the probability of a seed triggering a global cascade is broken, and thus we extend the percolation theory for simple contagion to two separate systems for size and probability for complex contagion.

We aim to understand whether the discontinuous phase transition is coming from transmission internal to the triangle, from two separate paths of transmission meeting in the triangle, or from both. We thus consider the probabilities of activating a third node in a triangle from a single transmission path in the triangle (i.e., first node in triangle transmits to second node transmits to third node with probability T_{Δ}), and from two separate paths (i.e., one node in triangle gets activated, attempts to activate two other nodes in triangle and fails to activate both, then the second node becomes active through a second external transmission path and activates the third node with probability $T_{\curvearrowright}$). In Figure 1 we show the four possible situations where (a) $T = T_{\Delta} = T_{\curvearrowright}$, (b) $T_{\Delta} > T$ and $T_{\curvearrowright} = T$, (c) $T_{\Delta} = T$ and $T_{\curvearrowright} > T$, and (d) $T_{\Delta} = T_{\curvearrowright} > T$. We find the discontinuous phase transition in expected size of the largest connected component only when $T_{\curvearrowright} > T$, which indicates that the group structure alone is not sufficient to trigger the discontinuous phase transition, and that allowing for multiple chains of transmission to meet at the groups is necessary for triggering a discontinuous phase transition.

References

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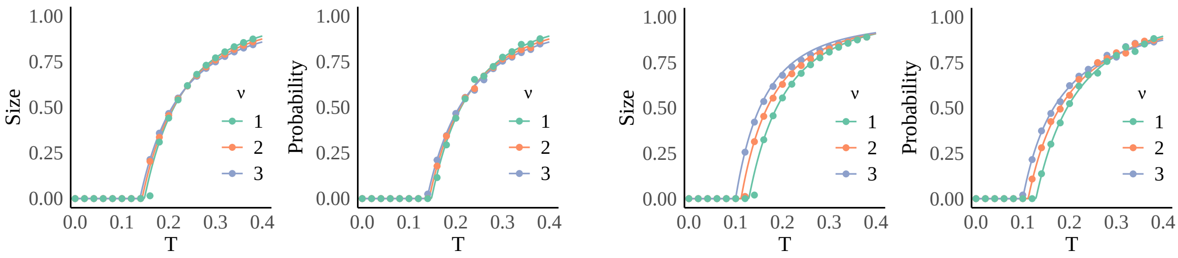
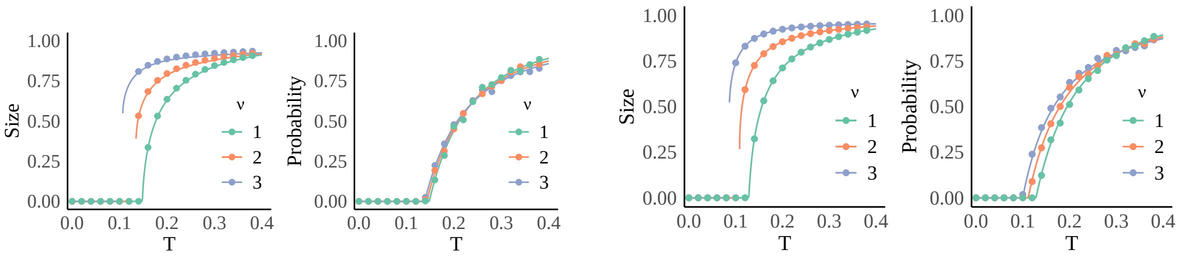


(a) No loops, no groups (simple contagion)

(b) Groups, no loops



(c) Loops, no groups

(d) Loops and groups

Figure 1: The fractional size of the largest connected component and the probability of a uniformly-randomly selected node seeding a global cascade for networks that follow a doubly-Poisson distribution with mean number of triangles per node ν, and mean number of single links per node $\mu = 6.5 - 2\nu$. In each of the panels (a)–(d), we vary the values of T_Δ and $T_\curvearrowright$ such that in (a) $T = T_\Delta = T_\curvearrowright$, in (b) $T_\Delta = 1-(1-T)^\alpha > T$ and $T_\curvearrowright = T$, in (c) $T_\Delta = T$ and $T_\curvearrowright = 1-(1-T)^\alpha > T$. In all of these figures, $\alpha = 10$, the solid curves are the numerical solutions to our self-consistent set of equations, and the points represent the mean values of the size of the largest connected component (for size) and the fraction of cascades that occupy more than 1% of the network (for probability) of 1000 simulations each on networks with 100,000 nodes.