Social confinement and mesoscopic localization of epidemics on networks

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Recommendations around epidemics tend to focus on individual behaviors, with much less efforts attempting to guide event cancellations and other collective behaviors since most models lack the higher-order structure necessary to describe large gatherings. Through a higher-order description of contagions on networks, we model the impact of a blanket cancellation of events larger than a critical size and find that epidemics can suddenly collapse when interventions operate over groups of individuals rather than at the level of individuals. We relate this phenomenon to the onset of mesoscopic localization, where contagions concentrate around dominant groups.

Standard disease models reduce the complexity of epidemics to simple processes that provide useful insights. In fact, many of the key results of these models provide the foundation for our current understanding and forecasting of novel emerging epidemics [1–3]. The reduction of the complex to the simple is perhaps best embodied by the *mass-action approximation* [4]. This assumption essentially means that we are considering a randomly mixed population, ignoring household structures, social gatherings, and the different behaviors of different individuals. Mass-action models are thus seriously limited, since they focus on the average number of infections caused by each case, the basic reproduction number R_0 [5], and ignore the underlying heterogeneity [6]. There are also conceptual issues with the design of targeted interventions when relying on the mass-action assumption. Where should we target our interventions, and what should be their impact? In this letter, we address these questions through higher-order contact patterns.

Network science provides a natural framework to go beyond the mass-action approximation by considering key features of the structure of contacts among individuals. The simplest generalization is perhaps the *heterogeneous pair approximation*—individuals are nodes categorized by their number of contacts and their state, and the contacts are distinguished by the states of the nodes involved [7]. At this level of sophistication, all pairwise contacts of a given state are still, a priori, equivalent.

One developing area in network science concerns dynamical processes on higher-order representation of networks, i.e., where the network is not simply a conglomerate of pairwise interactions but where interactions occur in a coordinated manner because of a higher-level organization (schools, households, events, etc.) [9]. For dynamics on higher-order networks, one straightforward generalization of the framework just described is the *heterogeneous clique approximation* [10]. Nodes are categorized by their state and *membership*, i.e., the number m of groups to which they belong. The groups are characterized by their size n, and the states of the nodes involved.

Let us consider contagion processes on a simple version of higher-order networks, see Fig. 1. The network is characterized by g_m, the distribution for the memberships m of nodes and p_n, the distribution for the sizes n of groups. We use different heterogeneous distributions for both of them, $g_m \propto m^{-\gamma_m}$ and $p_n \propto n^{-\gamma_n}$, with finite cut-offs $m_{\max}$ and $n_{\max}$ respectively.

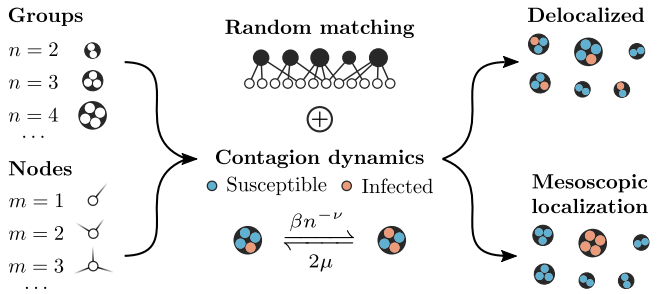

FIG. 1. **Framework for contagions on higher-order networks.** Nodes are assigned to m groups and groups are of various sizes n, distributed according to g_m and p_n. We consider a SIS dynamics where infected nodes transmit the disease in a group of size n at rate $\beta n^{-\nu}$ with $\nu \in [0, 1]$, and recover at rate μ. We characterize the phenomenon of mesoscopic localization, namely the concentration of infected nodes in large groups.

For mathematical convenience, we use a Susceptible-Infected-Susceptible (SIS) dynamics. However, our results have repercussions for a much broader class of dynamical processes, including Susceptible-Infected-Recovered (SIR) dynamics where individuals develop immunity. Infected nodes transmit the disease to susceptible nodes belonging to a same group of size n at rate $\beta n^{-\nu}$ with $\nu \in [0, 1]$, and recover at rate μ. It is equivalent to a standard SIS model on networks formed of cliques [10, 11], but the edges have weights $n^{-\nu}$. We recover an unweighted network for $\nu = 0$. The parameter ν tunes the strength of interactions within groups, which we assume to be decreasing with size. For instance, an individual in a workplace typically interacts with more people than at home, but interactions in a household are stronger.

We track $s_m(t)$, the probability for a node of membership m to be susceptible, and $c_{n,i}(t)$, the probability to observe i infected nodes within a group of size n. Their dynamics are described by the following coupled ordinary differential equa-