

Mesoscopic localization of spreading processes on networks

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In the context of spreading processes on networks, an epidemic is localized if the infected (or affected) nodes mostly belong to a certain subgraph (the *localization set*). A better grasp of this phenomenon for realistic network structures contributes to a sound understanding of spreading processes, for it has important applications, e.g. targeted immunization strategies are very sensitive to the localization regime [1].

Using spectral analysis [1] or compartmental formalism on random networks [2], it is possible to distinguish the different localization regimes. The former approach suggests that the localization set for real networks often corresponds either to the star subgraph associated with the maximal degree node, or to the maximum K -core in a K -core decomposition. However, as far as we know, the role of ubiquitous mesoscopic structures—such as clusters of densely connected communities—remains virtually unexplored, theoretically or otherwise, with regards to localization.

We revisit the SIS model on random networks with heterogeneous cluster sizes [3] and leverage the analytical tractability of the compartmental formalism to identify a dichotomy for the localization, dependent only on the structural properties [see Fig. 1(c)]. In the delocalized regime [Fig. 1(a)], all clusters participate to the epidemic, leading to a clean phase transition; in the *mesoscopic localization* regime [Fig. 1(b)], the phase transition is smeared, with the epidemic mostly localized in the largest clusters at the critical point.

Our work establishes the concept of mesoscopic localization in a coherent mathematical formalism and paves the way for the investigation of this phenomenon under various conditions, e.g. non-Markovian and complex contagions. It further suggests that mesoscopic localizations (and the associated localization sets) could be identified in real systems and exploited in targeted immunization strategies.

[1] R. Pastor-Satorras and C. Castellano, J. Stat. Phys. 173, 1110-1123 (2018)

[2] G. St-Onge *et al.*, Phys. Rev. E 97, 022305 (2018)

[3] L. Hébert-Dufresne *et al.*, Phys. Rev. E 82, 036115 (2010)

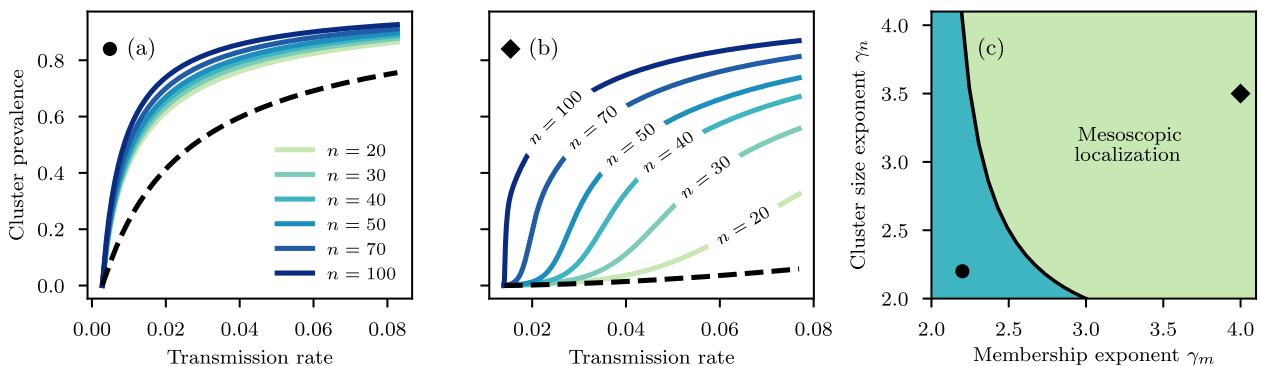


Figure 1: Localization regimes for the SIS model on clustered random networks, in the thermodynamic limit. (a)-(b) Solid lines represent the mean stationary fraction of infected nodes in a cluster of n nodes; dashed lines represent the global mean fraction of infected nodes. Both are obtained through a system ordinary differential equations, and consider a power law distribution of cluster size $p_n \sim n^{-\gamma_n}$ and membership to m cluster $p_m \sim m^{-\gamma_m}$ with cut-offs $n_{\max} = m_{\max} = 100$ (see Ref. [3]). (a) Delocalized regime ($\gamma_n = \gamma_m = 2.2$). (b) Mesoscopic localization regime ($\gamma_n = 3.5, \gamma_m = 4$). (c) Clear separation of the two regimes in the space of structural exponents (γ_n, γ_m). The circle and diamond markers indicate parameters used for panels (a) and (b) respectively.