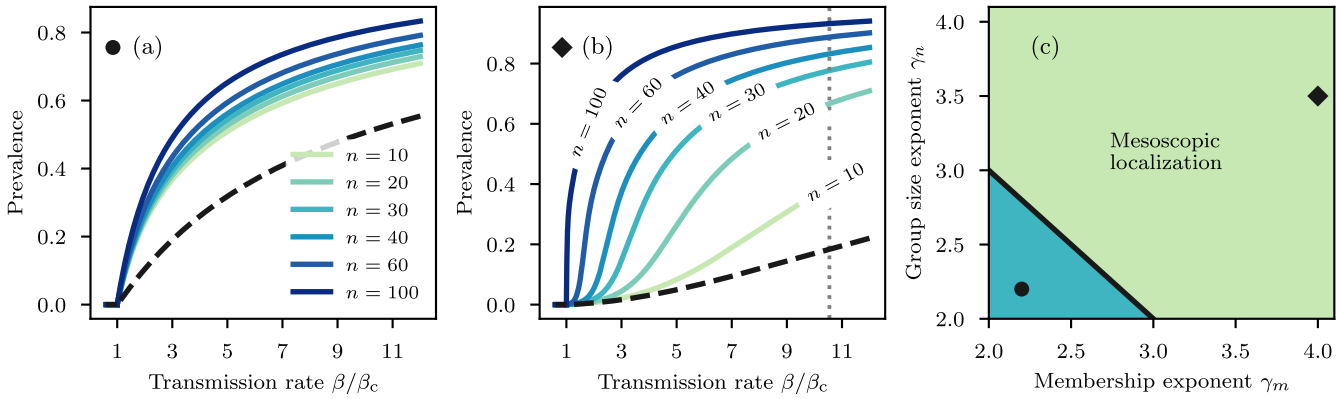

FIG. 2. **Epidemic localization in networks with heterogeneous higher-order structures.** We use $\nu = 0$ for all panels and power-law distributions for the memberships $g_m \propto m^{-\gamma_m}$ and group sizes $p_n \propto n^{-\gamma_n}$. (a)-(b) Solid lines represent the stationary group prevalence and dashed lines represent the stationary global prevalence. (a) For strongly coupled groups ($\gamma_m = \gamma_n = 2.2$), we find a collective phase transition. (b) For weakly coupled groups ($\gamma_m = 4, \gamma_n = 3.5$), we find a phenomenon of mesoscopic localization. While the global prevalence in the population can remain extremely low, larger groups can self-sustain the epidemic. The vertical dotted line is an estimation of the *delocalization* threshold, where the epidemic invades the whole network (see Ref. [8]). (c) Mesoscopic localization is the rule rather than the exception. The solid line, $\gamma_m + \gamma_n = 5$, separates the *delocalized regime* (blue area of strong group coupling) from the *mesoscopic localization regime* (green area of weak group coupling), obtained from Eqs. (8a-b). The circle and diamond markers correspond to the networks in panels (a)-(b).

tions [10],

$$\frac{\mathrm{d}s_m}{\mathrm{d}t} = \mu(1 - s_m) - mrs_m \,, \tag{1a}$$

$$\frac{\mathrm{d}c_{n,i}}{\mathrm{d}t} = \mu(i+1)c_{n,i+1} - \mu i c_{n,i} + (n-i+1)\{\beta n^{-\nu}(i-1) + \rho\}c_{n,i-1} - (n-i)\{\beta n^{-\nu} i + \rho\}c_{n,i} \,, \tag{1b}$$

with the mean fields $r(t)$ and $\rho(t)$ defined as

$$r(t) = \frac{\sum_{n,i} \beta n^{-\nu} i\ (n-i)c_{n,i}(t)p_n}{\sum_{n,i}(n-i)c_{n,i}(t)p_n} \,, \tag{2a}$$

$$\rho(t) = r(t)\frac{\sum_m (m-1)\, m s_m(t) g_m}{\sum_m m s_m(t) g_m} \,. \tag{2b}$$

If we take a susceptible node and select a random group to which it belongs, $r(t)$ is the mean infection rate associated to that group. Now if we pick a susceptible node in a group, $\rho(t)$ is the mean infection rate received from all external groups (i.e., excluding the one we picked the node from). Without loss of generality, we set $\mu = 1$ hereafter.

An important feature of this framework is that Eq. (1b) is an *approximate master equation* : it describes the full range of possible states for groups of size n, while assuming a mean-field coupling between them. As we show in Ref. [8], the agreement with Monte-Carlo simulations is excellent. The global prevalence in the network—the average fraction of infected nodes—is then

$$I(t) = \sum_m \left[1 - s_m(t)\right] g_m \,, \tag{3}$$

and the group prevalence is

$$I_n(t) = \sum_i \frac{i}{n} c_{n,i}(t) \,. \tag{4}$$

In Fig. 2(a) and Fig. 2(b), we show the stationary prevalence (global and within groups) for two different networks, obtained using Eq. (1). As expected from standard models, there exists an epidemic threshold β_c for the transmission rate below which epidemics cannot be sustained (see Ref. [8] for an analytical expression of β_c). Above β_c, the disease-free equilibrium of the dynamics becomes unstable, driving the epidemic to invade the network.

What is less expected are the sequential local transitions observed in the second panel [Fig. 2(b)]. For any value of the transmission rate, the outbreak thrives only in groups above a certain size. The epidemic is *self-sustained* locally, and the global prevalence reaches its highest growth rate with β well above the epidemic threshold, a defining feature of *smeared* phase transitions [12, 13]. This is reminiscent of certain infections, such as the bacteria *C. difficile*, mainly found in hospitals with large susceptible populations in close contact [14].

To get some insights on the emergence of this localization phenomenon, we examine the stationary group prevalence, I_n^*, near the absorbing-state. Using a saddle-point approximation valid for large n, we obtain [8]

$$I_n^* \sim \begin{cases} \dfrac{1}{1 - \beta n^{1-\nu}} & \text{if } \beta < n^{\nu-1} \\ n^{1/2}\ (\beta n^{1-\nu})^n\ e^{-n+n^\nu/\beta} & \text{if } \beta \geq n^{\nu-1} \,. \end{cases} \tag{5}$$

For $\beta > n^{\nu-1}$, this implies $I_n^* = O\left(n^{1/2} e^{bn}\right)$ with $b > 0$. Therefore, if $\beta_c \to n_{\max}^{\nu-1}$, the group prevalence increases exponentially with n above the epidemic threshold, and the outbreak is *localized* in large groups, as observed in Fig. 2(b). In other words, the behavior of the epidemic threshold dictates whether or not localization is possible for a given network organization.

In Ref. [8], we show that for power-law distributions of