Supplementary Information

Model description

Facing the outbreak of the epidemic, each subpopulation can generate resources for fighting against the disease at each time step. In reality, infected individuals consume various medical resources, but susceptible individuals are responsible for resource production. So we reasonably assume that the amount of resources produced by one subpopulation are positively correlated to its current proportion of susceptible individuals. Accordingly, we define the resources production $r_i(t)$ of subpopulation i at time t as follows:

$$r_i(t) = \theta[1-\rho_i(\mathrm{t})], \tag{S1}$$

where $\rho_i(\mathrm{t})$ is the ratio of infected individuals in subpopulation i at time t, and θ (≥1) is the coefficient denoted as resource production strength. Higher θ means a faster speed on resource production.

With the emergence of infected individuals in neighboring subpopulations of subpopulation i, subpopulation i would release resources to suppress the disease. Usually, not all resources could be donated because of the need for self-protection. Besides, we consider the amount of resources that one of its neighboring subpopulation j can receive at time t is proportional to its number of infected individuals among all neighbors. Accordingly, the resource donation $\omega_{i\to j}(\mathrm{t})$ that subpopulation i releases to j at time t can be denoted as follows:

$$\omega_{i\to j}(\mathrm{t}) = r_i(t) \bullet q_i(t) \bullet \frac{I_j(\mathrm{t})}{\Sigma_{k\in V(i)} I_k(\mathrm{t})}, \tag{S2}$$

where $\Sigma_{k\in V(i)} I_k(\mathrm{t})$ is the total number of infected individuals in the neighboring subpopulation set V(i) of subpopulation i, $I_j(t)$ is the number of infected individuals belonging to neighbor j, and $q_i(\mathrm{t})$ is donation will of subpopulation i at time t.

When an epidemic breaks out, one subpopulation i can perceive this threat intuitively by acquiring the information from neighbors. So, to quantify the response strength of a subpopulation to the information of disease, a parameter $\alpha \in [0,1]$ denoting awareness is introduced, and a higher α means less resources will be donated. Usually, the more infected individuals around a subpopulation, the more resources are supposed to be donated to them. Hence, we assume that the donation will of subpopulation i increases with the ratio of infected individuals around it. Based on the above description, we define donation will $q_i(\mathrm{t})$ of subpopulation i at time t as follows:

$$q_i(t) = q_0 \bullet (1-\alpha) \bullet \frac{1}{1+e^{-\beta(m_i(t)-0.5)}}, \tag{S3}$$

where q_0 is basic donation factor, $m_i(\mathrm{t})$ is the ratio of infected individuals in all neighboring subpopulations of i at time t, and coefficient β (≥0) represents the donation sensitivity. The third

submultiple on the right side of Eq. (S3) is a sigmoid function which represents donation sensitivity to the infection. A smaller β means the subpopulation is more sensitive to degree of infection around the neighboring subpopulations. The smaller β indicates that donation will gets a higher initial value and increases steadily with $m_i(t)$ with a less slope., and particularly the sigmoid function keeps a fixed value of 0.5 if β=0 (see Fig. S1). Besides, the constant 0.5 in the sigmoid function restricts its value in the range [0, 1]. The function obtains 0.5 when $m_i(t)=0.5$, and when $m_i(t)<0.5$, the function is less than 0.5, and vice versa. That is, how many resources will be donated depends on the value of $m_i(t)$. Naturally, $m_i(t)$ is expressed as follows:

$$m_i(t) = \frac{\Sigma_{k\in V(i)} I_k(t)}{\Sigma_{k\in V(i)} N_k}, \quad \text{(S4)}$$

where $\Sigma_{k\in V(i)} N_k$ is the total number of individuals traversing neighboring subpopulation set V(i) of subpopulation i, and $\Sigma_{k\in V(i)} I_k(t)$ has been mentioned above.

When infected individuals emerge around subpopulation i, it intends to donate resources to neighbors to suppress diseases, and protects itself from infection as well. However, donating resources may lead to an increasing risk of infection due to the lack of sufficient resources for self-protection. Hence, we consider a penalty coefficient c (≥1) for modified infection rate, $\lambda_i(t)$, of subpopulation i after donating resources at time t, and $\lambda_i(t)$ is expressed as

$$\lambda_i(t) = q_i(t)c\lambda + [1-q_i(t)]\lambda, \quad \text{(S5)}$$

where λ is the basic infection rate, and $q_i(t)$ is donation will at time t as mentioned above. From Eq. (S5), the infection rate recovers a constant λ if c=1, i.e., there is no impact when donating resources to others. On the contrary, if c>1, there is a relatively higher infection rate when donating resources. The above definition means that the infection rate usually varies from subpopulation to subpopulation with time.

In general, a subpopulation can generate resources by itself or receive from others. So, the resources that a subpopulation i holds at time t are expressed as follows

$$\omega_i(t) = r_i(t)\bullet[1-q_i(t)] + \sum_{j\in V(i)} \omega_{j\to i}(t), \quad \text{(S6)}$$

where the first term denotes its remaining resources after donating resources and the second denotes the resources received from others. Generally, a subpopulation has a higher recovery rate if it holds more resources. So, the recovery rate of subpopulation i at time t, $\mu_i(t)$, can be defined as

$$\mu_i(t) = 1-(1-\mu)^{1+\varepsilon\omega_i(t)}, \quad \text{(S7)}$$

where μ is the basic recovery rate, and $\varepsilon\in[0,1]$ is resource utilization rate. From Eq. (S7), we can see that recovery rate of subpopulation i keeps the basic recovery rate μ if ε=0 or without resources; otherwise, the recovery rate increases with the growth of holding resources $\omega_i(t)$, and the recovery rate $\mu_i(t)\to 1$ when $\omega_i(t)$ is sufficiently large. Similarly, the recovery rate generally varies from subpopulation to subpopulation with time.

Supplementary Table 1. Involved parameters in the MIR metapopulation network model

Parameter	Definition	Default value
λ	Basic infection rate	-
μ	Basic recovery rate	0.2
p	Migration probability	0.2
c	Penalty coefficient for infection rate after donation	2.0
ε	Resource utilization rate	0.6
q_0	Basic donation factor	0.8
θ	Resource production strength	-
α	Resource donation awareness	-
β	Resource donation sensitivity	-

Unless extra specifications, the default values of other parameters are set as μ=0.2, q_0=0.8, ε=0.6, c=2.0, and p=0.2.

Microscopic Markov chain method and threshold analysis

Based on the above mode description, we construct a metapopulation network model composed a total of N subpopulations. Each subpopulation i has a number of n_i individuals, $\forall$i=1, 2, …, N. At the migration stage, an individual leaves its resident subpopulation i with probability p, and migrates to one of its neighboring subpopulations j in terms of the transition matrix **R**, whose entries are $R_{ij}=\frac{W_{ij}}{\sum_{j=1}^{N}W_{ij}}$, where W_{ij} denotes the weight between subpopulation i and j. Then, once individuals have moved, they interact in a well-mixed way in each subpopulation i and change their epidemic status in terms of current infection rate $\lambda_i(t)$ and recovery rate $\mu_i(t)$ at time t based on SIS model. Finally, they return to their resident subpopulation and next time step starts.

There are N variables $\rho_i(t)$ denoting the ratio of infected individuals associated with subpopulation i at time t. The time evolution of $\rho_i(t)$ can be written as follows

$$\rho_i(t+1)=\rho_i(t)\left[(1-p)(1-\mu_i(t))+p\sum_{j=1}^{N}R_{ij}(1-\mu_j(t))\right]+(1-\rho_i(t))\Gamma_i(t), \qquad \text{(S8)}$$

where the first term on the right side is the fraction of infected individuals who do not recover. The infected individuals are those who remain in subpopulation i and those who migrate to neighboring subpopulations and then return back to subpopulation i. The second term on the right side accounts for the ratio of susceptible individuals associated with subpopulation i that are infected at time t. In this second term, $\Gamma_i(t)$ denotes the probability that a susceptible individual associated with subpopulation i becomes infected at time t, and reads

$$\Gamma_i(t) = (1-p)P_i(t) + p\sum_{j=1}^{N} R_{ij}P_j(t)\,, \tag{S9}$$

where the first term on the right side is the probability that susceptible individuals, who do not move, get infected in the resident subpopulation i at time t, and the second term denotes the probability that individuals get infected when migrating to any neighboring subpopulation. And $P_i(t)$ is denoted as

$$P_i(t) = 1-\prod_{j=1}^{N}(1-\lambda_i(t)\rho_j(t))^{n_{j\to i}}\,, \tag{S10}$$

where $n_{j\to i}$ denotes the population flux moving from subpopulation j to subpopulation i, and reads

$$n_{j\to i} = \delta_{ij}\left(1-p\right)n_i + pR_{ji}n_j\,, \tag{S11}$$

with $\delta_{ij}=1$ if i=j and otherwise $\delta_{ij}=0$.

To analyze the steady state of the dynamics when $t\to\infty$, namely $\rho_i(t+1) = \rho_i(t) = \rho_i$, we can simplify Eq.(S7) as:

$$[1-(1-p)(1-\mu_i) - p\sum_{j}^{N} \mathrm{R}_{ij}(1-\mu_j)]\rho_i = (1-\rho_i)\Gamma_i\,, \tag{S12}$$

where ρ_i is the steady density of infected individuals associated to subpopulation i.

When close to the critical point, let's denote $\rho_i = \varepsilon_i^* << 1$ for any subpopulation i. We estimate $\mu_i = \mu(1+\varepsilon\omega_i)$ neglecting second order terms from Eq. (S6), and $\omega_i \approx \theta[1+\frac{k_i q_0(1-\alpha)}{1+\mathrm{e}^{0.5\beta}}]$.
We denote left side of Eq. (S12) as follows:

$$[1-(1-p)(1-\mu_i) - p\sum_{j}^{N} \mathrm{R}_{ij}(1-\mu_j)]\varepsilon_i^* = T\varepsilon_i^*\,, \tag{S13}$$

where $T=1-(1-p)(1-\mu_0[1+\varepsilon\theta(1+\frac{k_i q_0(1-\alpha)}{1+\mathrm{e}^{0.5\beta}})]) - p\sum_{j}^{N} \mathrm{R}_{ij}(1-\mu_0[1+\varepsilon\theta(1+\frac{k_i q_0(1-\alpha)}{1+\mathrm{e}^{0.5\beta}})])$.

On the right side of Eq. (S12), we have

$$P_i(t) \approx \sum_{j=1}^{\mathrm{N}} \lambda_i\rho_j n_{j\to i}\,,$$

$$n_{j\to i} = \delta_{ij}\left(1-p\right)n_i + p_d R_{ji}n_j\,,$$

$\Gamma_i \approx (1-p)\sum_{j=1}^{\mathrm{N}}\lambda_i\rho_j n_{j\to i} + p\sum_{j=1}^{N}R_{ij}\sum_{l=1}^{\mathrm{N}}\lambda_j\rho_l n_{l\to j}$, so

$$\Gamma_i=\lambda\sum_{j=1}^{N}\left\{(1-p)^2\delta_{ij}n_j+p(1-p)R_{ji}n_j+p(1-p)\theta[\frac{q_0(1-\alpha)}{1+e^{0.5\beta}}(c-1)+1]R_{ij}n_j+p^2\theta[\frac{q_0(1-\alpha)}{1+e^{0.5\beta}}(c-1)+1](\mathbf{R}\bullet\mathbf{R}^T)_{ij}n_j\right\}\varepsilon_j^*.$$

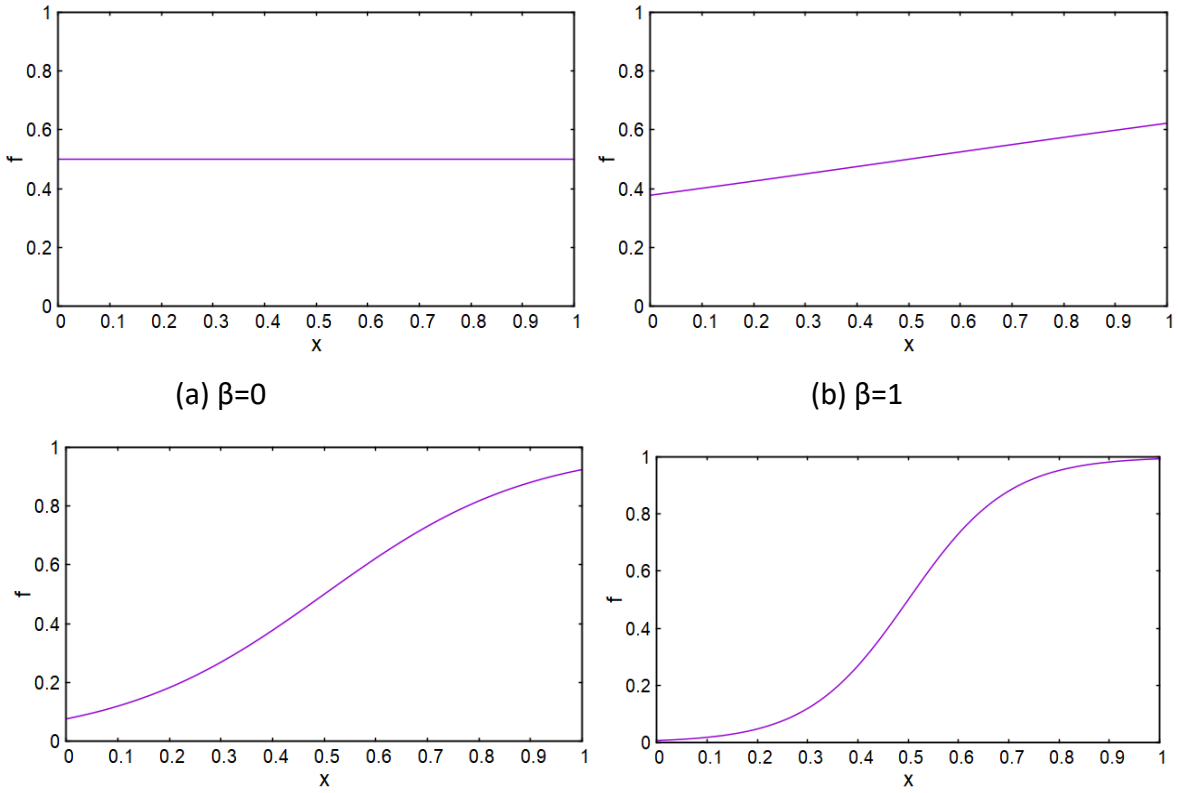
We denote $\mathbf{M}_{ij}=(1-p)^2\delta_{ij}n_j+p(1-p)R_{ji}n_j+p(1-p)\theta[\frac{q_0(1-\alpha)}{1+e^{0.5\beta}}(c-1)+1]R_{ij}n_j+p^2\theta[\frac{q_0(1-\alpha)}{1+e^{0.5\beta}}(c-1)+1](\mathbf{R}\bullet\mathbf{R}^T)_{ij}n_j$

Accordingly, we derive epidemic threshold λ_c as follows:

$$\lambda_c=\frac{T}{\Lambda_{\max}(\mathbf{M})}, \qquad \text{(S14)}$$

where $\Lambda_{\max}(\mathbf{M})$ is the maximum eigenvalue of the matrix M. Unfortunately, the detailed expression for the maximum eigenvalue of the matrix **M** is impossible. Nevertheless, we can get the epidemic threshold by numerical iteration.

Sigmoid function



(a) β=0 (b) β=1

(c) β=5 (d) β=10

Fig. S1 Sigmoid function $f(x)=\frac{1}{1+e^{-\beta(x-0.5)}}$ corresponding to various values of parameter β. The function become constant 0.5 when β=0. The lower β presents a more steady growth with a higher initial function value.

Effects of the parameter α

The time evolution of the epidemic under HOD and HED

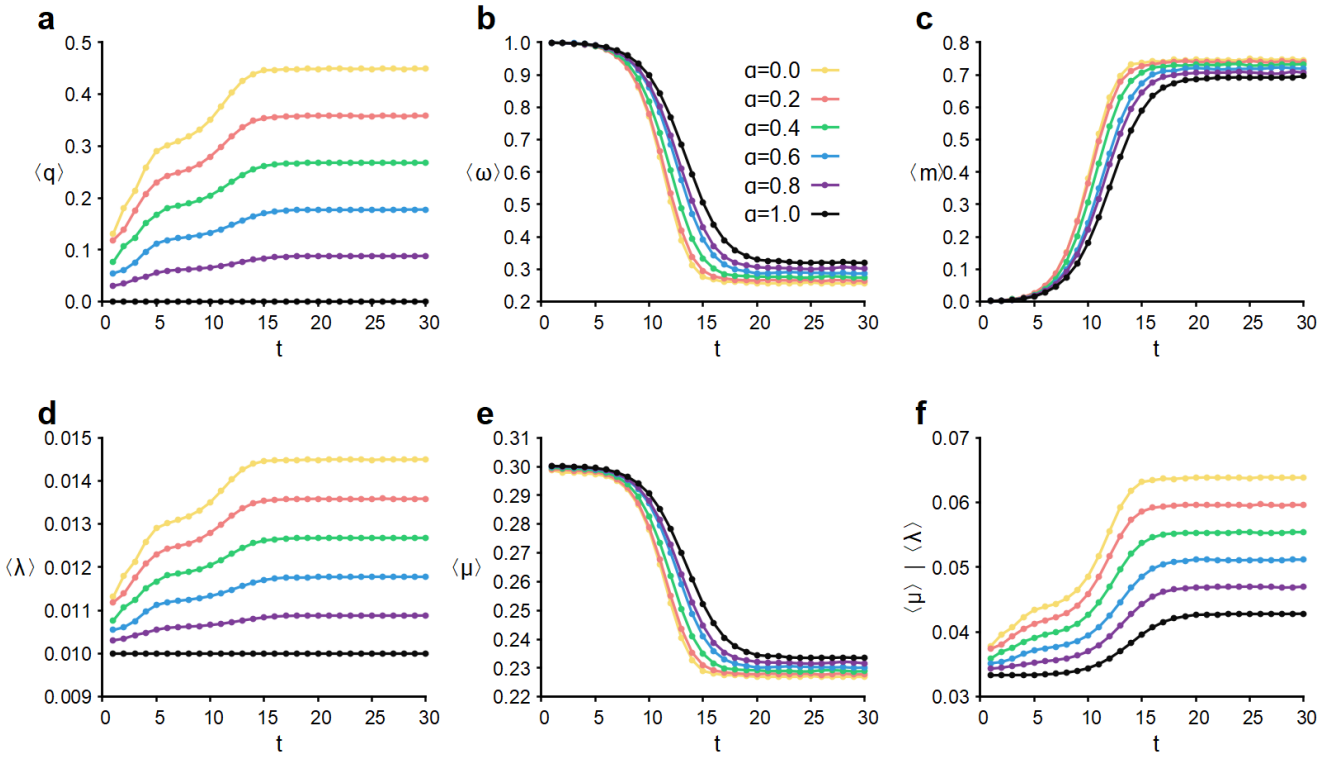


Fig. S2 The time evolution of six average values of all subpopulations for various values of α by MC simulation under HOD when λ=0.01 (the legend in (b)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

The average infection ratio of individuals in neighboring subpopulations increases promptly as shown in (c), and the lower α is, the faster it increases. When infected individuals emerge in subpopulations, they will release/receive resources to/from neighbors. As we can see from (a), the average donation will increases with time when α is not equal to 1, and a lower α induces a higher donation will. However, a higher donation will of one subpopulation induces a higher infection rate as shown in (d). At the same time, because the increasing of infected individuals induces a lower ability of resource production, the average resources of each subpopulation become fewer and fewer as shown in (b). Meanwhile, the recovery rate of one subpopulation is positive correlated to its current resources, so we can see a same trend shown in (e). In order to clearly present the relationship between average infection rate and average recovery rate, the time evolution of average effective infection rate is shown in (f), and we can see the growth whatever the value of α is.

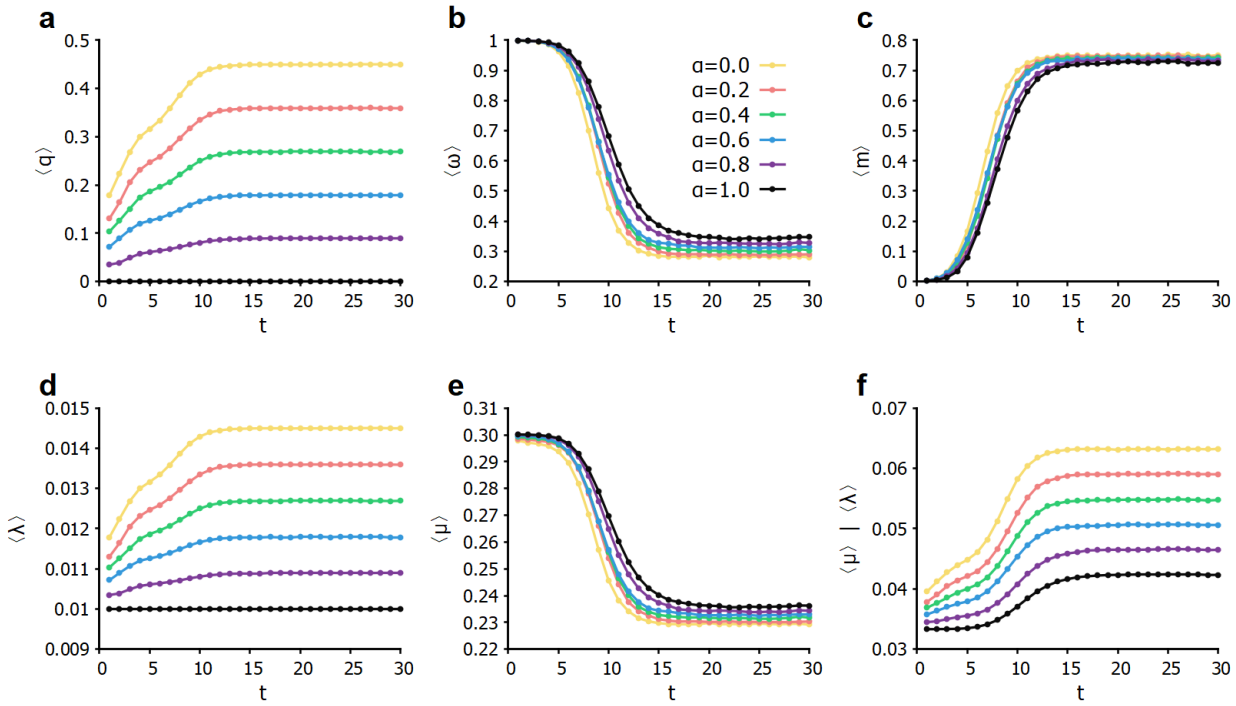


Fig. S3 The time evolution of six average values of all subpopulations for various values of α by MC simulation under HED when λ=0.01 (the legend in (b)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

The figures appear a similar trend with previous HOD, but the epidemic reaches a steady state in a shorter time.

Prevalence ρ for five subpopulation groups under HED

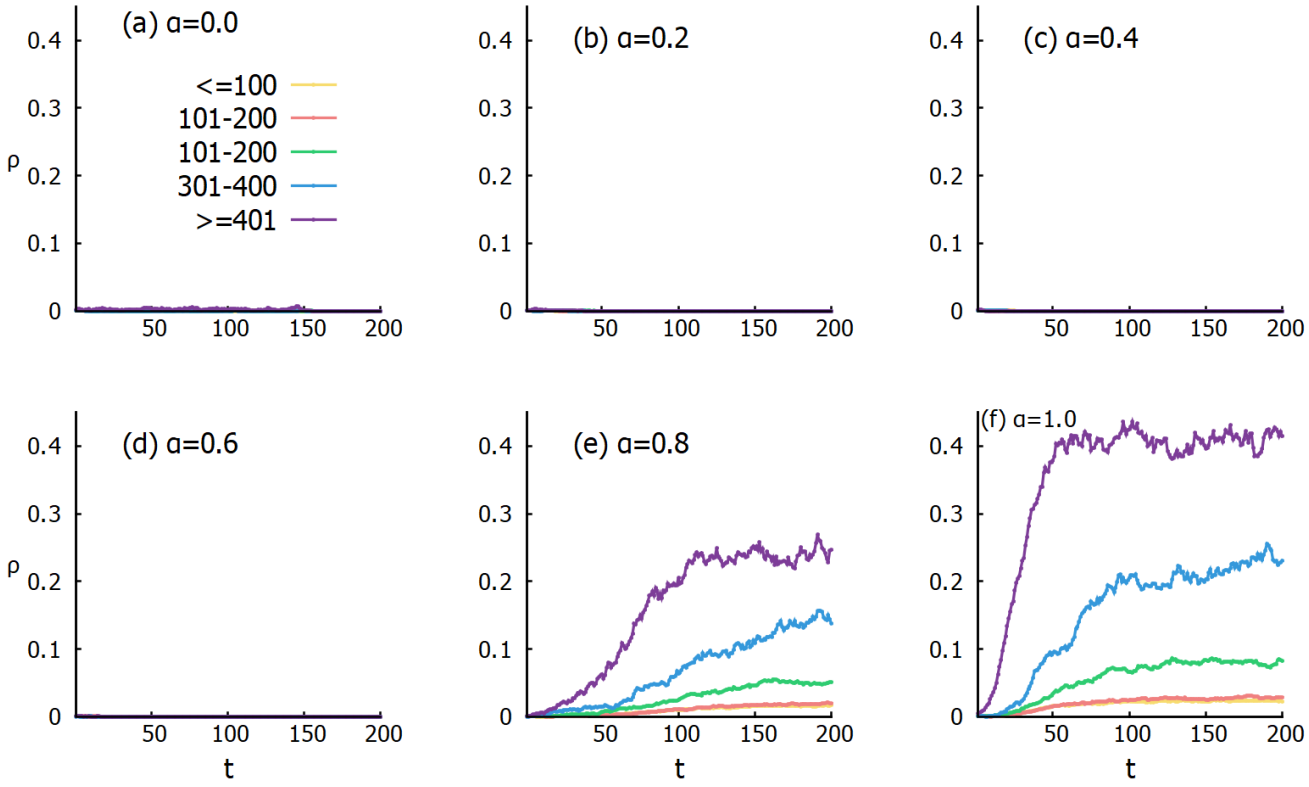


Fig. S4 The time evolution of the prevalence ρ for five subpopulation groups under various values of α when λ=0.0015. (a)-(f) correspond to parameter α=0.0, 0.2, 0.4, 0.6, 0.8, and 1.0, respectively (The legend represents subpopulation groups shown in (a)).

As the population distribution is heterogeneous under HED, for further interpreting the role of awareness α when close to threshold, we group subpopulations according to its population, and set λ at 0.0015. Apparently, α=1.0 denotes there is no resource donation. From (a)-(d), the epidemic can't spread in all the subpopulation groups under α=0.0, 0.2, 0.4, and 0.6, respectively; whereas the epidemic breaks out, particular subpopulations with more population, when awareness α=0.8 and 1.0 as shown in (e) and (f), respectively.

Effects of the parameter β

The time evolution of epidemic under HOD and HED

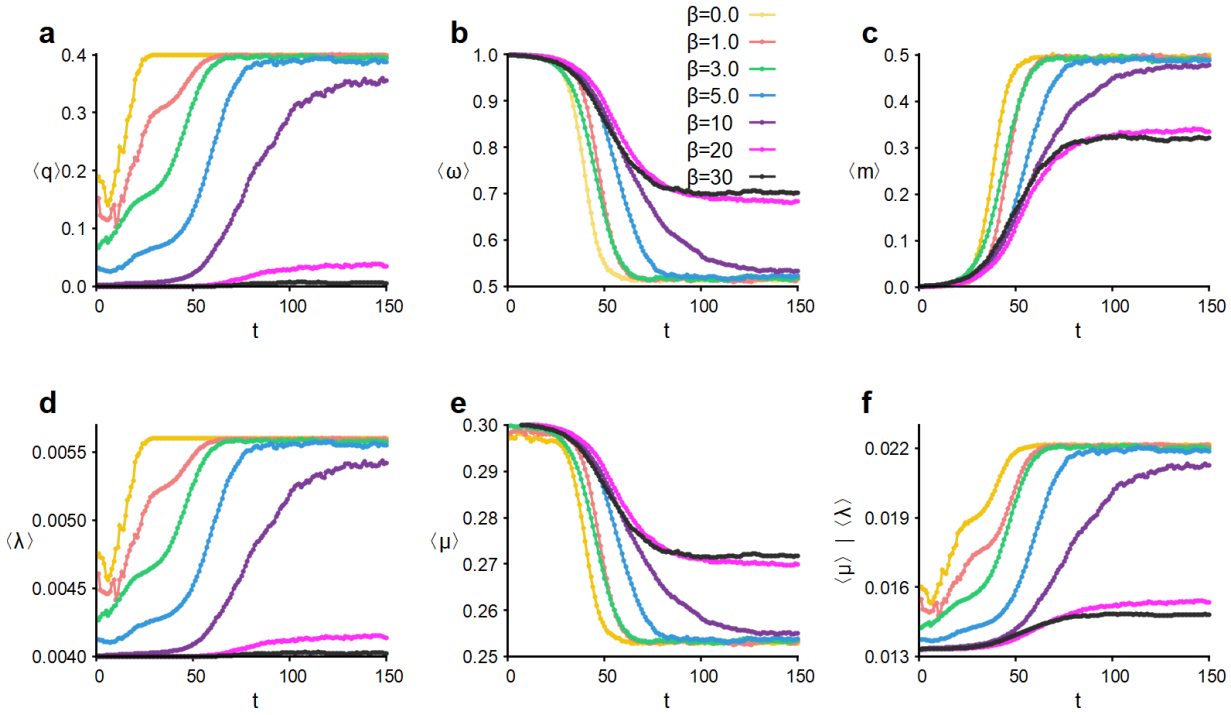


Fig. S5 The time evolution of six average values of all subpopulations for various values of β by MC simulation under **HOD** when λ=0.004 (the legend in (b)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

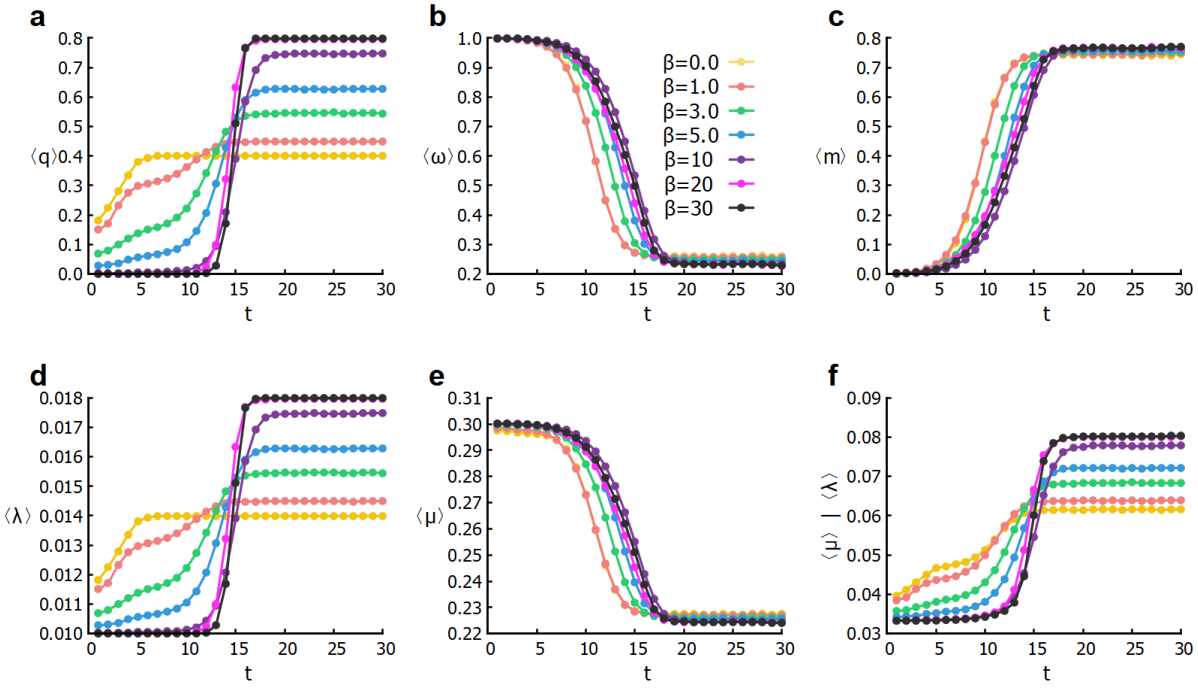


Fig. S6 The time evolution of six average values of all subpopulations for various values of β by MC simulation under HOD when λ=0.01 (the legend in (b)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

With time evolution, more infected individuals emerge as shown in Fig. S6 (c). Once infected individuals emerge, subpopulations would increase their donation will to donate resources to others as shown in (a), and a lower β indicates a higher initial donate will. Besides, average infection rate has a similar trend as shown in (d). At the same time, average resources of each subpopulation become less and less as shown in (b) because of the increasing of infected individuals. Hence, average recover rate of the system become lower and lower as shown in (e). We can see the growth of average effective infection rate in (f), and the higher the β is, the higher final average effective infection rate is.

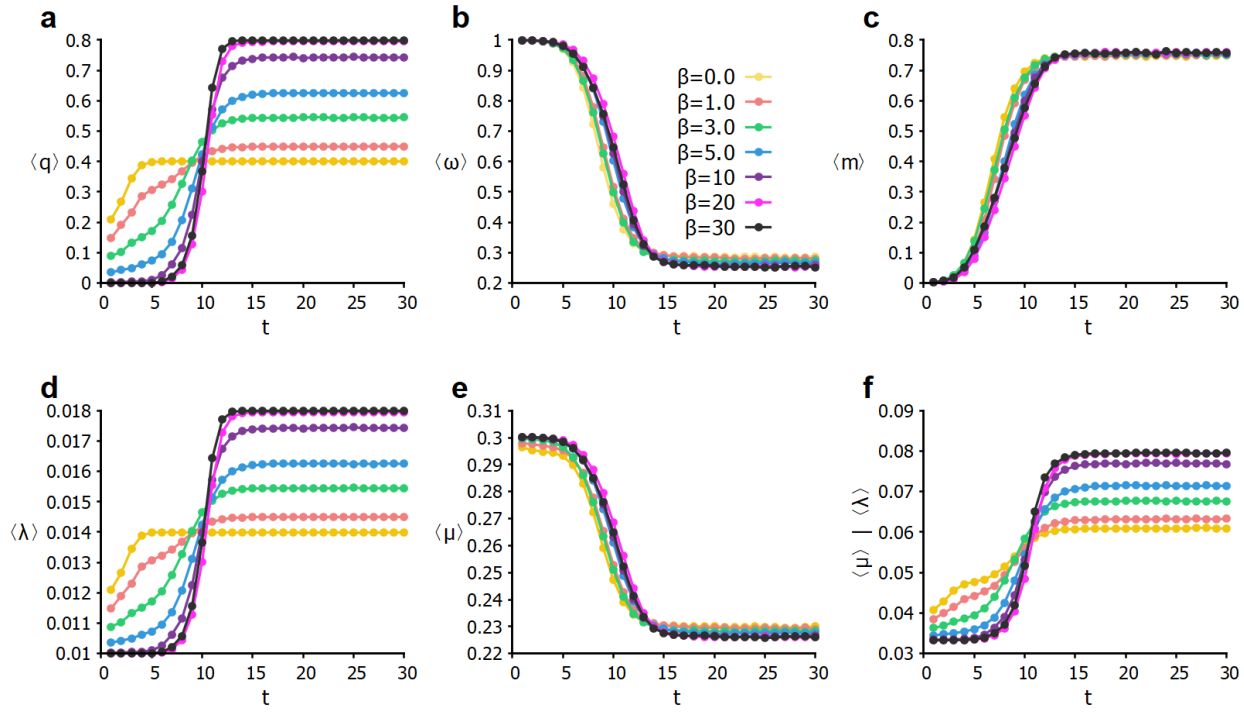


Fig. S7 The time evolution of six average values of all subpopulations for various values of β by MC simulation under HED when λ=0.01 (the legend in (b)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

The figures appear a similar trend as previous situation.

Prevalence ρ for five subpopulation groups under HED

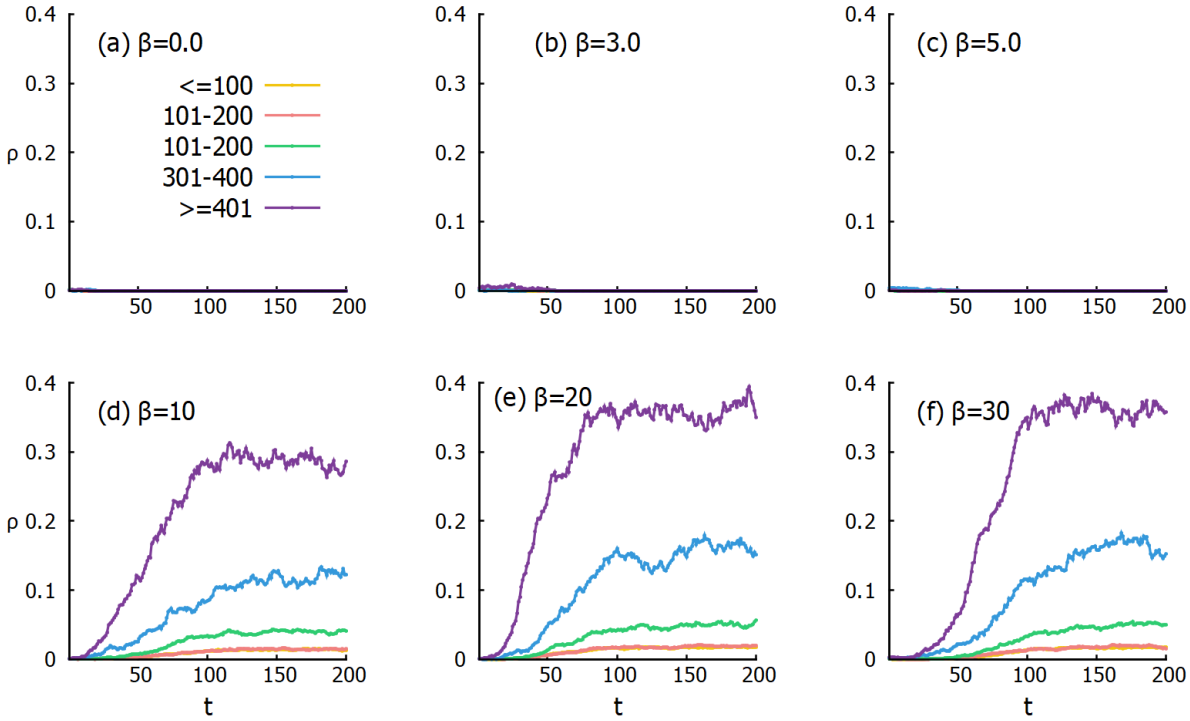


Fig. S8 The time evolution of the prevalence ρ f for five subpopulation groups under various values of β when λ=0.0015. (a)-(f) correspond to parameter β=0.0, 3.0, 5.0, 10, 20, and 30, respectively (The legend represents subpopulation groups shown in (a)).

Because the population distribution is heterogeneous under HED, for further interpreting the role of the donation sensitivity β when closed to threshold, we group subpopulations according to its population, and set λ at 0.0015. The donation will keeps a constant when β=0.0. From (a)-(c), the curves just presents a slight fluctuation initially and finally approach to 0 with time evolution, which suggests that epidemic cannot spread. From (d)-(f), the epidemic easily diffuses especially in subpopulations with more population, and the curves firstly go up then present steady with the time evolution.

Effects of the parameter θ

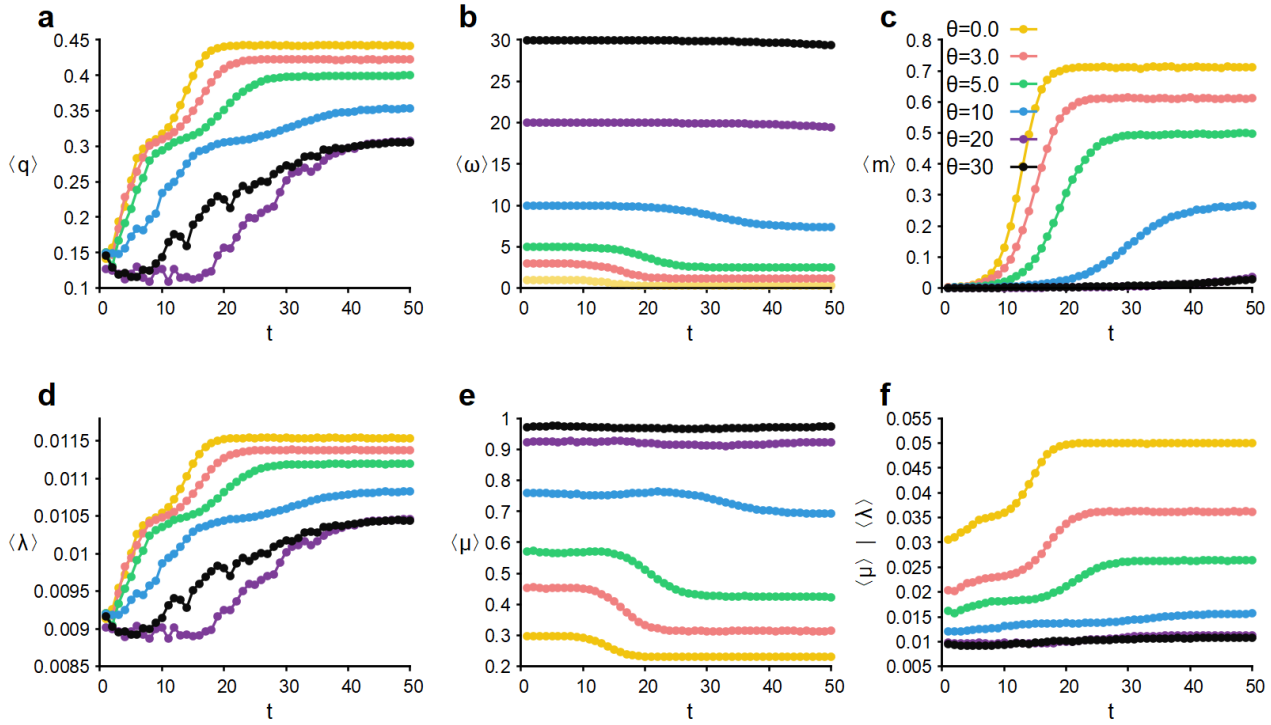


Fig. S9 The time evolution of six average values of all subpopulations for various values of θ by MC simulation under HOD when λ=0.01 (the legend in (c)). (a)-(f) are average values corresponding to donation will <q>, holding resources <ω>, infection ratio of individuals in neighboring subpopulations <m>, infection rate <λ>, recover rate <μ>, and effective infection rate <λ>/<μ>, respectively.

In order to explore the time evolution of the epidemic under various values of parameter θ when basic infection rate λ is close to thresholds, we set λ=0.004. As we can see from (b) and (e), higher θ can effectively increase the average holding resources and average recover rate. From (c) and (f), there is a lower average effective infection rate with a higher θ, suppressing the spread of the epidemic validly.

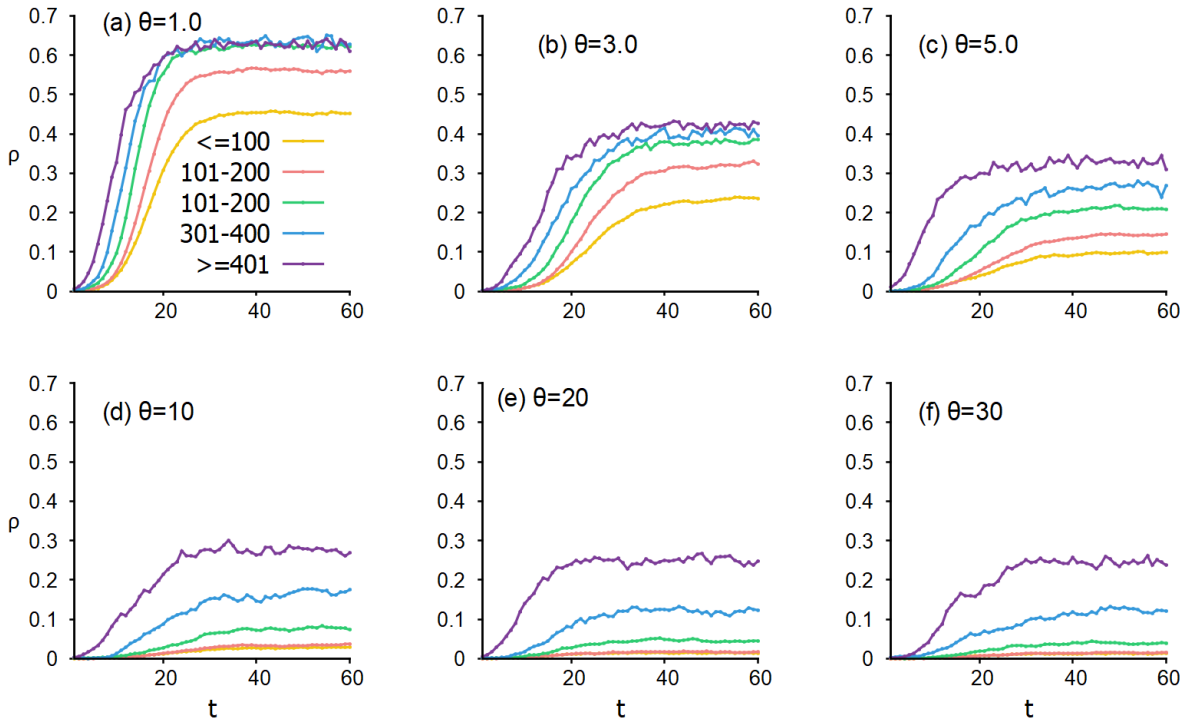


Fig. S10 The time evolution of the prevalence ρ for five subpopulation groups under various values of θ when λ=0.01. (a)-(f) correspond to parameter θ=1.0, 3.0, 5.0, 10, 20, and 30, respectively (The legend represents subpopulation groups shown in (a)).

As the population distribution is heterogeneous under HED, for further interpreting the role of the productive strength θ, we group subpopulations according to its population, and set λ at 0.01. From (a)-(d), we can obviously find that high θ can effectively reduce final prevalence. However, when θ=20 or larger as shown in (e) and (f), there is few changes on reducing final prevalence because of not obviously increase of the recovery rate. These results suggest it is conducive to control epidemic when we strengthen the speed of resource production such as extending working hours properly.

Supplementary References

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