

Spread of infectious diseases with and without a latent period

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1 Metapopulation epidemic models

Spread of infectious disease is often modeled on a complex network. In a metapopulation network, each node corresponds to a subpopulation or patch, which contains a population of individuals, and each edge expresses connection between patches. Individuals can move between connected patches. However, infection dynamics occurs only within each patch. We here consider a Susceptible-Infected-Recovered (SIR) model and a modified SIR model with a latent period, which we call a SHIR model [1], on a metapopulation network.

In the SIR model, the number of susceptible, infected and recovered individuals in the j th patch are denoted by S_j , I_j and R_j , respectively. Each susceptible individual becomes infected at a rate $\beta I_j/N_j$, where β is the transmission rate and N_j is the population in the j th patch. The epidemic threshold in a patch is given by $R_0 = \beta/\gamma$, where γ is the recovery rate, in the SIR model. In the metapopulation SIR model, all individuals can move between patches.

In the SHIR model, the infection period is divided into two stages: an infected stage, which corresponds to a latent period, and a seriously ill stage, in which each individual is infected and cannot move to another patch. Each susceptible individual becomes infected at a rate $\beta(H_j + I_j)/N_j$, where H_j and I_j are the numbers of the infected and seriously ill individuals, respectively. Each infected individual becomes seriously ill at a rate μ , and seriously ill individual recovers at the recovery rate γ . The epidemic threshold in a patch is given by $R_0 = \beta(\mu + \gamma)/(\mu\gamma)$ in the SHIR model [1].

2 Epidemic and global invasion thresholds

The epidemic threshold in each patch is given by the basic reproduction number, which is independent of the mobility (or traveling) rate between connected patches. The metapopulation system is characterized by not only the epidemic threshold but also the global invasion threshold, which depends on the mobility rate and the network structure as well as the basic reproduction number [2]. However, the results we reported in Ref. [1] showed that the attack ratio and thus the global invasion threshold were almost independent of the mobility rate. We will show that this contradiction came of a mean-field approach that corresponds to the limit of $N \rightarrow \infty$.

Another unexpected result reported in Ref. [1] is the discontinuous final size distribution in the SHIR model. The discontinuous jump of attack ratio occurred at $\beta = \gamma$, which is different from the expected epidemic threshold. The attack ratio was almost zero for $\beta < \gamma$, and it was the same as expected for $\beta > \gamma$. We will demonstrate that the result is affected by the termination condition of computation. In fact, the termination condition in Ref. [1] was $\sum_j (H_j + I_j) < 1$. If the termination threshold is changed from 1 to ϵ ($\epsilon \simeq 10^{-14}$ in double precision), the discontinuous jump disappears and the global invasion occurs above the epidemic threshold.

References

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