ABSTRACT

未感染媒介体の不均一分布下における伝染病流行様式に関する
確率過程モデル解析

A Simple Stochastic Model for Epidemic Transmission
among
Heterogeneously Distributed Susceptible Units

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In our modeling analysis, we focus on how the extent of epidemic damage depends on the spatial distribution of susceptible units.

We assume that the unit of infection is immobile, as town, plant, etc. We call the unit by *the site*. We classify the sites into three classes, depending on the state of site in terms of the epidemics: *susceptible*, *infective* and *recovered*. We ignore any time delay about the epidemic dynamics, including the latent period. Infection rate depends only on the total number of *infective* sites. Only susceptible site could be infected. Recovered site is never infected again. Besides, infection and recovery of a site is independent of that of any other ones. With these assumptions, we consider $P(k, h, t)$ that means the probability for the state such that k *infected* and h *infective* sites exist at time t. Considering the possible transitions of state in sufficiently small time interval $(t, t + \Delta t]$, we can get the differential equation to describe the temporal variation of $P(k, h, t)$, which can be analyzed by means of the moment generating function. As for the initial condition, we assume that the epidemic begins with a site at time 0.

Next, we consider the mathematical modeling for the range expanded by infected sites, say, the *infected range*. We characterize the infected range at time t by the minimal diameter R which includes all infected sites at t. Then, we assume the generalized relation between the infected range and the total number of infected sites as follows: $k \propto R^d$ $(1 \leq d \leq 2)$, where the power d characterizes the spatial pattern of infected region occupied by infected sites. Power d is called *cluster dimension* or *mass dimension*, that is a sort of *fractal dimension*. When $d \approx 2$, the spatial distribution of infected sites can be approximated by a disc. When $d \approx 1$, the distribution can be approximately regarded as one dimensional, that is, the infected sites can be regarded to be arrayed along a curve. With the relation, $k \propto R^d$, and $P(k, h, t)$, we can obtain the temporal variations of expected infected range and expected expansion velocity of infected range.

From the results of our modeling analysis, we try to discuss the effects of spatial distribution of susceptible sites and characteristics of the epidemic on the nature of its expansion. Further, we try to mention the contribution of treatment and prevention for it, too.

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