Endemic SIR Model in Random Media

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Abstract: We consider an averaging principle for the endemic SIR model in a semi-Markov random media. Under stationary conditions of a semi-Markov media we show that the perturbed endemic SIR model converges to the classic endemic SIR model with averaged coefficients. Novelty of the paper lies in the study of an endemic SIR model in semi-Markov random media.

Keywords: endemic SIR model; semi-Markov random media; averaging principle; averaged endemic SIR model

1 Introduction

In the last years, deterministic and stochastic epidemic models, in both discrete and continuous time, have been studied (Nasel, 1985 and 2002; Ball and Lyne, 2001). Both model types are needed, and both have their advantages and weaknesses (Hethcote, 2000; Allen and Burguin, 2000). The deterministic models lead to powerful qualitative results with important threshold behavior. They can serve as a useful inside into the stochastic models as well.

Even with large population, chance fluctuation may not average out, especially when these fluctuations have some spatial nature. Therefore, it may be important to take these variability under consideration. Allowance should be made for complicating feature of real infections, such as population structure and duration of disease stages - the assumed homogeneous mixing and exponential distribution of simple models are seldom appropriate. A particular challenge for the future now is to extend the epidemic model types, to allow structured population where assumptions of homogeneous mixing do not apply or partially apply.

The model described in this paper is a variation on a SIR theme, with a simple and relatively tractable mathematical structure. In particular, we assume that the hosts are identical and homogeneously mixing, but not in the entire population. We divide the population of interest into subgroups/clusters, where that hosts mix homogeneously. It is straightforward to generalize this type of mixing structure to allow the distinct subgroups to have different rates of disease spreading. The groups are not isolated from one another. We allow contacts between groups that are modeled by use of transition
probabilities. A particular host while traveling in space and time randomly appears in different groups - changes environment. Therefore we introduce randomness not directly through $S$, $I$, and $R$, but indirectly, through the coefficients of the SIR model. These coefficients are directed by a semi-Markov process which serves as a switching process (Swishchuk and Wu, 2003). The choice of a semi-Markov process is made for the purpose of generalization. In some particular situation, when the state space is finite, a Markov process can play the role of a switching process. Semi-Markovian properties have one more advantage: sojourn time must not be exponentially distributed.

2 Classic Endemic SIR Model

Let $S(t)$, $I(t)$ and $R(t)$ be the number of individuals in each class of susceptible, infectives and removed, respectively. We follow the approach suggested by Hethcote (2001), taking under consideration demography and introducing $\beta$, $\mu$, $\gamma$ as infective, mortality/birth, and removal rates. The deterministic SIR endemic model is:

$$\begin{align*}
    \frac{dS}{dt} &= -\beta SI + \mu(N - S), \quad S(0) = S_0 \\
    \frac{dI}{dt} &= \beta SI - \gamma I - \mu I, \quad I(0) = I_0 \\
    \frac{dR}{dt} &= \gamma I - \mu R, \quad R(0) = R_0
\end{align*}$$

(1)

In the classical endemic SIR model the various classes are uniformly mixed, that is, every pair of individuals has equal probability of coming into contact with each other and the total population size is constant. For many diseases with transmission taking place within some particular groups, it is logical to divide the host population into groups, where it is assumed that hosts mix homogeneously within the group. Contacts among groups are modeled by use of a transition probability matrix whose $(i, j)$ element specifies the probability that host in group $i$ will have a potential contact with host in group $j$ by visiting this group. As a good example of the described above situation an epidemic on some finite amount of islands with birds populations on each can be used. Another example is diseases spreading among big cities joined with some transportation systems.

If we take under consideration that one particular host may visit different groups by moving in space and time, then an important concern is how to generalize the concept of the reproduction ratio for such a heterogeneous structured population.

One of the stochastic models capable to incorporate distinct subgroups with different contact rates is the epidemic SIR model in random environment (Swishchuk and Wu, 2002). In this model we presume that the coefficients of transmission, recovery, and mortality depend on semi-Markov process that
switches the coefficient values depending on the state of the process. It looks like the system is submerged into some random media.

3 Random Media

Let \((y_n)_{n \in \mathbb{Z}^+}\) be a homogeneous Markov chain in a measurable space \((Y, \mathcal{Y})\) with transition probabilities \(P(y, A), y \in Y, A \in \mathcal{Y}\), and ergodic distribution \(p(A), A \in \mathcal{Y}\); \(\beta(y), \gamma(y), \) and \(\mu(y)\) are non-negative, bounded measurable functions defined on \(Y\);

\((y_n; \theta_n)_{n \in \mathbb{Z}^+}\) is a Markov renewal process in the phase space \((Y \times \mathbb{R}^+, \mathcal{Y} \times \mathcal{R}^+)\) with stochastic kernel \(Q(y, dz, t) = P(y, dz)G_y(t), y \in Y, dz \in \mathcal{Y}, t \in \mathbb{R}^+;\)

\(\nu(t) := \max \{n : \tau_n \leq t\}\) is a counting process, \(\tau_n := \sum_{k=0}^{n} \theta_k, \theta_0 = 0;\)

\(G_y(t)\) is the distribution function of the sojourn times.

The Markov renewal process is a convenient constructive tool to define a semi-Markov process \((y(t))_{t \in \mathbb{R}^+}, y(t) = y_{\nu(t)}\). As \(\nu(t) = n, \tau_n \leq t < \tau_{n+1}, y(t)\) also assumes constant values on the same intervals and is continuous from the right. Namely, \(y(t) = y_n, \tau_n \leq t < \tau_{n+1}, y(\tau_n) = y_n, n \geq 0\). For the semi-Markov process \((y(t))_{t \in \mathbb{R}^+}\), the renewal time \(\theta_n := \tau_{n+1} - \tau_n\) may be naturally interpreted as the occupation time (life-time) in the state \(y_n\). That explains the choice of the process: semi-Markov process differs from a Markov process by the distribution of time, for a Markov process a distribution function is exponential while for a semi-Markov process it can be any distribution function. Therefore, by choosing a semi-Markov process for a role of a switching process, we have wider possibilities for the occupation time intervals. We consider only a regular semi-Markov process, this is a process that with probability 1 has a finite number of renewals on a finite period of time. Just as in the right-continuous Markov process, the moments of jumps are regeneration points erasing the influence of the past. The only difference is that sojourn time at a point \(y\) has an arbitrary distribution \(G_y(t), y \in Y, t \in \mathbb{R}^+\), which depends on the terminal state.

The ergodic theorem for a semi-Markov process \((y(t))_{t \in \mathbb{R}^+}\) states (Swishchuk and Wu, 2003) that for any measured and bounded function \(f(y)\)

\[
P\left(\frac{1}{t} \int_0^t f(y(s)) ds \to \hat{f}, t \to \infty\right) = 1
\]

where

\[
\hat{f} = \frac{1}{m} \int_Y m(y) f(y)p(dy), \quad m = \int_Y m(y)p(dy), \quad m(y) = \int_0^{+\infty} tG_y(dt)
\]
4 Endemic SIR model in Random Media (RM)

The model in semi-Markov renewal random environment is defined as

\[
\begin{align*}
\frac{dS}{dt} &= -\beta(y(t))SI + \mu(y(t))(N - S), \\
\frac{dI}{dt} &= \beta(y(t))SI - \gamma(y(t))I - \mu(y(t)) \\
\frac{dR}{dt} &= \gamma(y(t))I - \mu(y(t))
\end{align*}
\]  

(2)

It is important to note that now the coefficients \(\alpha, \beta, \) and \(\gamma\) are not constant. The state of the semi-Markov process defines their value. We may say that \(y(t)\) is serving as a switching process: depending on the time this process takes its values in different states, defining corresponding to this state coefficients of disease spreading. \(S, I,\) and \(R\) are random processes as well.

For the finite (n-elements) set of states we have: \(S = (S_i), I = (I_i),\) and \(R = (R_i)\) with \(i = 1, 2, ..., n.\) In this case, we may consider \(n\) subgroups/clusters of the population under investigation. In each group we assume homogeneous mixing, but the coefficients of disease spreading may be different for different groups, taking their values as \(\beta_i, \mu_i,\) and \(\gamma_i, \) \(i = 1, 2, ..., n.\)

5 Averaging of the SIR model in RM

In order to investigate the system’s (2) equilibrium we perturb this system in the following way:

\[
\begin{align*}
\frac{dS^\varepsilon}{dt} &= \varepsilon(-\beta(y(t))S^\varepsilon I^\varepsilon + \mu(y(t))(N - S^\varepsilon)) \\
\frac{dI^\varepsilon}{dt} &= \varepsilon(\beta(y(t))S^\varepsilon I^\varepsilon - \gamma(y(t))I^\varepsilon - \mu(y(t))I^\varepsilon) \\
\frac{dR^\varepsilon}{dt} &= \varepsilon(\gamma(y(t))I^\varepsilon - \mu(y(t))R^\varepsilon)
\end{align*}
\]  

(3)

where \(\varepsilon\) is a small positive parameter.

Changing the time scale \(t \rightarrow \frac{t}{\varepsilon}\) we transform the perturbed system (3) into the system

\[
\begin{align*}
\frac{dS^\varepsilon}{dt} &= -\beta(y(t/\varepsilon))S^\varepsilon I^\varepsilon + \mu(y(t/\varepsilon))(N - S^\varepsilon) \\
\frac{dI^\varepsilon}{dt} &= \beta(y(t/\varepsilon))S^\varepsilon I^\varepsilon - \gamma(y(t/\varepsilon))I^\varepsilon - \mu(y(t/\varepsilon))I^\varepsilon \\
\frac{dR^\varepsilon}{dt} &= \gamma(y(t/\varepsilon))I^\varepsilon - \mu(y(t/\varepsilon))R^\varepsilon
\end{align*}
\]  

(4)

which can be averaged in the following way:

when \(\varepsilon \rightarrow 0:\) \((S^\varepsilon, I^\varepsilon, R^\varepsilon) \rightarrow (\hat{S}, \hat{I}, \hat{R}),\) in the sense:
for any $\delta \geq 0$ \( \lim_{\varepsilon \to 0} P\{(|S^\varepsilon - \hat{S}| + |I^\varepsilon - \hat{I}| + |R^\varepsilon - \hat{R}|) > \delta \} = 0 \).

The averaged system is

\[
\begin{cases}
\frac{d\hat{S}}{dt} = -\beta\hat{S}\hat{I} + \mu(N - \hat{S}) \\
\frac{d\hat{I}}{dt} = \beta\hat{S}\hat{I} - \gamma\hat{I} - \mu\hat{I} \\
\frac{d\hat{R}}{dt} = \gamma\hat{I} - \mu\hat{R}
\end{cases}
\]

(5)

Coefficients of the averaged system can be found by using the **ergodic theorem** for a semi-Markov process

\[
\hat{\mu} = \frac{1}{m} \int_Y m(y)\mu(y)p(dy), \quad \hat{\beta} = \frac{1}{m} \int_Y m(y)\beta(y)p(dy),
\]

\[
\hat{\gamma} = \frac{1}{m} \int_Y m(y)\gamma(y)p(dy),
\]

\[
m = \int_Y m(y)p(dy), \quad m(y) = \int_0^{+\infty} tG_y(dt)
\]

where \(p(y)\) is a unique invariant distribution.

In the case when the state space of a semi-Markov process is finite, \(n\)-element, the above integrals become the following sums:

\[
\hat{\mu} = \frac{1}{m} \sum_{i=1}^{n} m_i\mu(i)\pi_i, \quad \hat{\beta} = \frac{1}{m} \sum_{i=1}^{n} m_i\beta(i)\pi_i, \quad \hat{\gamma} = \frac{1}{m} \sum_{i=1}^{n} m_i\gamma(i)\pi_i,
\]

where \(m_i = \int_0^{+\infty} tG_i(dt)\) with a distribution function

\[
G_i(t) = P(\tau_n < t : y_n = i)
\]

and the stationary probability \(\pi = \begin{pmatrix} \pi_1 \\ \pi_2 \\ \vdots \\ \pi_n \end{pmatrix}\).

Here, \(m = \sum_{i=1}^{n} p_im_i\), where \(p_i\) are ergodic distribution of \(n\)-state semi-Markov process.

**Example: Two-state Markov Chain.** If \(y(t)\) is a Markov Chain with two states and transition matrix

\[
P = \begin{pmatrix}
1 - \alpha & \alpha \\
\beta & 1 - \beta 
\end{pmatrix},
\]

the stationary probability now is \(\pi = \begin{pmatrix} \pi_1 \\ \pi_2 \end{pmatrix} = \begin{pmatrix} \frac{\beta}{\alpha + \beta} \\ \frac{\alpha}{\alpha + \beta} \end{pmatrix}\).

For the distribution function \(G_y(t) = 1 - e^{-\lambda t}\) we have \(m(y) = \frac{1}{\lambda}\pi_1 + \frac{1}{\lambda}\pi_2 = \frac{1}{\lambda} = m\), therefore, \(\hat{\mu} = \mu_1\pi_1 + \mu_2\pi_2\), \(\hat{\beta} = \beta_1\pi_1 + \beta_2\pi_2\), \(\hat{\gamma} = \gamma_1\pi_1 + \gamma_2\pi_2\).

The averaged system (5), being a deterministic, can be used for a regular analysis. For example, an endemic equilibrium solution and a basic reproductive number for the averaged system may be found by regular method. They are: \(\hat{I} = \frac{\hat{\mu}N}{\hat{\gamma} + \hat{\mu}} - \frac{\hat{\mu}}{\hat{\beta}}\) and \(R_0 = \frac{\hat{\beta}N}{\hat{\gamma} + \hat{\mu}}\).
6 Discussion

In this paper, we considered a random media as a semi-Markov process because in some cases the distribution functions of being in states (for models, for example, for birds migrating between some islands, or people migrating between several cities, etc.) are not exponentially distributed (Swishchuk and Wu, 2003). From the other side, it is more general mathematical model than Markov model.

The result of the paper says, that if we have many states (e.g., islands, cities, etc.) for the endemic SIR model in random media and transition between states are fast than the whole system with many states can be regarded with fast migration as a system with one state or deterministic system, we called it averaged system, and this system can be studied by standard methods for classical endemic SIR models.

7 Conclusion and Future Work

We considered the averaging principle for endemic SIR model in semi-Markov random media. Under stationary conditions of semi-Markov media we shown that the perturbed endemic SIR model converges to the classic SIR model with averaged coefficients.

This research paper is just a first step in the investigation of endemic SIR model in random media. The future work will be devoted to the merging, diffusion approximation, normal deviations and stability of endemic SIR models in semi-Markov random media.

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